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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:32:59 ; Search time 27 Seconds  
(without alignments)  
34.387 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71  
Sequence: 1 TSLDASIIWAMQN 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 145874

Minimum DB seq length: 0  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2.6/prodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2.6/prodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2.6/prodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2.6/prodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2.6/prodata/1/iaa/PCUS\_COMB.pep.\*  
6: /cgn2.6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	39.4	12	1	US-08-241-054-34
2	28	39.4	12	1	US-08-241-054-50
3	28	39.4	12	1	US-08-390-156A-14
4	28	39.4	12	1	US-08-390-156A-22
5	28	39.4	12	1	US-08-439-817-14
6	28	39.4	12	1	US-08-439-817-30
7	28	39.4	12	1	US-08-485-508-34
8	28	39.4	12	1	US-08-485-508-50
9	26	36.6	12	1	US-08-241-054-5
10	26	36.6	12	1	US-08-390-156A-76
11	26	36.6	12	1	US-08-439-817-4
12	26	36.6	12	1	US-08-485-508-5
13	26	36.6	12	4	US-09-428-082B-149
14	25	35.2	12	4	US-09-842-164A-10
15	25	35.2	14	4	US-09-053-611-29
16	24	33.8	6	1	US-08-133-020-3
17	24	33.8	8	3	US-08-444-818-563
18	24	33.8	8	3	US-08-444-818-564
19	24	33.8	8	3	US-08-160-604-112
20	24	33.8	9	3	US-09-171-705-76
21	24	33.8	10	2	US-08-617-929-24
22	24	33.8	10	4	US-08-388-852B-6
23	24	33.8	10	4	US-08-234-784B-77
24	24	33.8	12	1	US-08-241-054-7
25	24	33.8	12	1	US-08-241-054-68
26	24	33.8	12	1	US-08-241-054-100
27	24	33.8	12	1	US-08-241-054-117

28	24	33.8	12	1	US-08-390-156A-10	Sequence 10, Appl
29	24	33.8	12	1	US-08-390-156A-64	Sequence 64, Appl
30	24	33.8	12	1	US-08-390-156A-88	Sequence 88, Appl
31	24	33.8	12	1	US-08-390-156A-103	Sequence 103, Appl
32	24	33.8	12	1	US-08-439-817-6	Sequence 6, Appl
33	24	33.8	12	1	US-08-439-817-48	Sequence 48, Appl
34	24	33.8	12	1	US-08-439-817-80	Sequence 80, Appl
35	24	33.8	12	1	US-08-439-817-99	Sequence 99, Appl
36	24	33.8	12	1	US-08-439-817-209	Sequence 209, Appl
37	24	33.8	12	1	US-08-485-508-7	Sequence 7, Appl
38	24	33.8	12	1	US-08-485-508-68	Sequence 68, Appl
39	24	33.8	12	1	US-08-485-508-100	Sequence 100, Appl
40	24	33.8	12	1	US-08-485-508-117	Sequence 117, Appl
41	24	33.8	12	2	US-08-461-990B-27	Sequence 27, Appl
42	24	33.8	12	3	US-08-817-869-5	Sequence 5, Appl
43	24	33.8	12	3	US-08-160-604-109	Sequence 109, Appl
44	24	33.8	12	4	US-09-205-258-304	Sequence 304, Appl
45	24	33.8	12	4	US-09-428-082B-150	Sequence 150, Appl

ALIGNMENTS

RESULT 1  
US-08-241-054-34  
; Sequence 34, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Gerald F. Swiss  
REGISTRATION NUMBER: 30,113  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-241-054-34

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWMWQ 13  
Db :|||  
7 LWVWQ 12

## RESULT 2

US-08-241-054-50  
; Sequence 50, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirila, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selections Including Endothelium Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule 1  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 520  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Gerald F. Swiss  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-002  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-241-054-50

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWMWQ 13  
:::|

Db 5 NWLWMMQ 12

## RESULT 3

US-08-390-156A-14  
; Sequence 14, Application US/08390156A  
; Patent No. 5648458  
; GENERAL INFORMATION:  
; APPLICANT: Cwirila, Steven E.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Dower, William J.  
; APPLICANT: Martens, Christine L.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to  
; TITLE OF INVENTION: ELAM-1  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, N.V.  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-156A-14

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWMWQ 13  
:|  
Db 7 LWVWQ 12

## RESULT 4

US-08-390-156A-22  
; Sequence 22, Application US/08390156A  
; Patent No. 5648458  
; GENERAL INFORMATION:  
; APPLICANT: Cwirila, Steven E.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Dower, William J.  
; APPLICANT: Martens, Christine L.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to  
; TITLE OF INVENTION: ELAM-1  
; NUMBER OF SEQUENCES: 113

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Affymax Technologies, N.V.  
;; STREET: 4001 Miranda Ave.  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/390,156A  
;; FILING DATE: 16-FEB-1996  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/057,295  
;; FILING DATE: 05-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/881,395  
;; FILING DATE: 06-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Swiss, Gerald F.  
;; REGISTRATION NUMBER: 30,113  
;; REFERENCE/DOCKET NUMBER: 1023.1A  
;; TELEPHONE: 415-496-2300  
;; TELEFAX: 415-424-0832  
;; INFORMATION FOR SEQ ID NO: 22:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-390-156A-22

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWMMQ 13  
DB 5 NMLWMMQ 12

RESULT 5  
US-08-439-817-14  
; Sequence 14, Application US/08439817  
; Patent No. 5728802  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I (ELAM-1)  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/439,817  
;; FILING DATE: 12-MAY-1995  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/241,054  
;; FILING DATE: 11-MAY-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/057,295  
;; FILING DATE: 05-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/881,395  
;; FILING DATE: 06-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Stevens, Lauren L.  
;; REGISTRATION NUMBER: 36,691  
;; REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
;; TELEPHONE: 415-496-2300  
;; TELEFAX: 415-424-0832  
;; INFORMATION FOR SEQ ID NO: 14:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-439-817-14

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWMMQ 13  
DB 7 LWMMQ 12

RESULT 6  
US-08-439-817-30  
; Sequence 30, Application US/08439817  
; Patent No. 5728802  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I (ELAM-1)  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,817  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054

;; FILING DATE: 11-MAY-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/057,295  
;; FILING DATE: 05-MAY-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/881,395  
;; FILING DATE: 06-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Stevens, Lauren L.  
;; REGISTRATION NUMBER: 36,691  
;; REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
;; TELEPHONE: 415-496-2300  
;; TELEFAX: 415-424-0832  
;; INFORMATION FOR SEQ ID NO: 30:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-439-817-30

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWMMQ 13  
DB 5 NMLWMMQ 12

RESULT 7  
US-08-485-508-34  
; Sequence 34, Application US/08485508  
; Patent No. 5786322  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule 1  
; NUMBER OF SEQUENCES: 162  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,508  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395

;; FILING DATE: 06-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Stevens, Lauren L.  
;; REGISTRATION NUMBER: 36,691  
;; REFERENCE/DOCKET NUMBER: 000324-002/1056  
;; TELEPHONE: 415-496-2300  
;; TELEFAX: 415-424-0832  
;; INFORMATION FOR SEQ ID NO: 34:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-485-508-34

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWMMQ 13  
DB 7 LWVMMQ 12

RESULT 8  
US-08-485-508-50  
; Sequence 50, Application US/08485508  
; Patent No. 5786322  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule 1  
; NUMBER OF SEQUENCES: 162  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,508  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 000324-002/1056  
; TELECOMMUNICATION INFORMATION:



DT 17-MAY-2001 (first entry)  
DE CD66 peptide CD66f (11)-10.  
KW CD66; CEACAM; adhesion molecule; antiviral; antibacterial;  
KW antiinflammatory; cytostatic; neutrophil activation; proliferation;  
KW differentiation; cancer; angiogenesis.  
XX Unidentified.  
OS WO200113937-A1.  
PN 01-MAR-2001.  
PD 25-AUG-2000; 2000WO-US023482.  
PF 26-AUG-1999; 99US-0150791P.  
PR 02-SEP-1999; 99US-0152501P.  
XX (SKUB/). SKUBITZ K M.  
PA (SKUB/). SKUBITZ A P N.  
PI Skubitz KM, Skubitz APN;  
XX WPI; 2001-234981/24.  
DR Novel peptides useful for activating neutrophils or blocking activation  
XX of neutrophils, modulating homotypic or heterotypic adhesion of CD66  
PT polypeptides, and modulating immune cell activation.  
XX Claim 1; Page 54; 102pp; English.  
PS The present sequence is an isolated peptide that was tested for its  
CC ability to modulate the function of CD66 family polypeptides and CD66  
CC ligands. 106 sequences of 13 or 14 amino acids in length, and their  
CC analogues, were identified that modulate the function of at least one  
CC CD66 family polypeptide and/or at least one ligand of the polypeptide.  
CC The peptides are capable of modulating activation of neutrophils,  
CC activation or inhibition, proliferation and/or differentiation of T-  
CC cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune  
CC system cells, proliferation and/or differentiation of epithelial cells,  
CC homotypic and/or heterotypic adhesion among CD66 family polypeptides and  
CC adhesion of CD66 family polypeptides to other ligands. The peptides are  
CC useful for delivering a therapeutically active agent to a patient, for  
CC modifying the metastasis of malignant cells, for altering bacterial or  
CC viral binding to cells or a biomaterial, for altering cell adhesion to a  
CC biomaterial, for detecting tumours, for detecting inflammation, for  
CC detecting a CD66 protein or its ligand, for altering angiogenesis by  
CC contacting endothelial cells, tumour cells or immune cells, for altering  
CC an immune response, and for altering keratinocyte proliferation  
XX Sequence 14 AA;  
SQ  
Query Match 46.5%; Score 33; DB 4; Length 14;  
Best Local Similarity 60.0%; Pred. No. 55;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 2 SLDASIIWAM 11  
Db : : : : :  
3 TLDASYLWMM 12  
RESULT 10  
ADM73036  
ID ADM73036 standard; peptide; 9 AA.  
XX ADM73036;  
AC  
XX 03-JUN-2004 (first entry)  
DT Human GAGE-1 epitope SEQ ID NO:295.  
DE epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;  
XX

KW cancer; tumour; human; GAGE-1.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO2004022709-A2.  
XX 18-MAR-2004.  
XX 05-SEP-2003; 2003WO-US027706.  
XX 06-SEP-2002; 2002US-0409123P.  
XX (MANN-) MANNKIND CORP.  
XX Simard JTL, Diamond DC, Liu L, Liu Z;  
XX WPI; 2004-315564/29.  
XX New polypeptides and encoding nucleic acids that are useful epitopes of  
PT target-associated antigens, useful for diagnosing and/or treating viral  
PT infections, cancers and tumors.  
XX Claim 1; SEQ ID NO 295; 357pp; English.  
PS The present invention describes a polypeptide (I) comprising a component  
CC selected from: (a) a polypeptide epitope having any of the 503 fully  
CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope  
CC cluster comprising the polypeptide of (a); (c) a polypeptide having  
CC substantial similarity to (a) or (b); (d) a polypeptide having functional  
CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the  
CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and  
CC can be used in vaccines. The methods and compositions of the present  
CC invention are useful for the diagnosis and/or treatment of viral  
CC infections, cancers and tumors. The present sequence is used in the  
CC exemplification of the present invention.  
XX Sequence 9 AA;  
SQ  
Query Match 40.8%; Score 29; DB 8; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 7 IIVAMQON 14  
Db 1 ILWLLMNN 8  
RESULT 11  
ADM73041  
ID ADM73041 standard; peptide; 9 AA.  
XX ADM73041;  
AC  
XX 03-JUN-2004 (first entry)  
DT Human GAGE-1 epitope SEQ ID NO:300.  
XX  
XX epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;  
KW cancer; tumour; human; GAGE-1.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO2004022709-A2.  
XX 18-MAR-2004.  
XX 05-SEP-2003; 2003WO-US027706.  
XX 06-SEP-2002; 2002US-0409123P.  
XX (MANN-) MANNKIND CORP.  
PA

XX PI Simard JLL, Diamond DC, Liu L, Liu Z;  
 XX DR WPI; 2004-315564/29.  
 XX CC New polypeptides and encoding nucleic acids that are useful epitopes of  
 PT target-associated antigens, useful for diagnosing and/or treating viral  
 PT infections, cancers and tumors.  
 XX PS Claim 1; SEQ ID NO 300; 357pp; English.  
 XX CC The present invention describes a polypeptide (I) comprising a component  
 CC selected from: (a) a polypeptide epitope having any of the 503 fully  
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope  
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having  
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional  
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the  
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and  
 CC can be used in vaccines. The methods and compositions of the present  
 CC invention are useful for the diagnosis and/or treatment of viral  
 CC infections, cancers and tumors. The present sequence is used in the  
 CC exemplification of the present invention.  
 XX CC Sequence 9 AA;  
 CC Query Match 40.8%; Score 29; DB 8; Length 9;  
 CC Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 CC Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 7 IIAWMQN 14  
 Db 1 ILWLLMNN 8  
 RESULT 12  
 ADM73042  
 ID ADM73042 standard; peptide; 10 AA.  
 XX AC ADM73042;  
 XX DT 03-JUN-2004 (first entry)  
 XX DE Human GAGE-1 epitope SEQ ID NO:301.  
 XX KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;  
 KW cancer; tumour; human; GAGE-1.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO2004022709-A2.  
 XX PD 18-MAR-2004.  
 XX PF 05-SEP-2003; 2003WO-US027706.  
 XX PR 06-SEP-2002; 2002US-0409123P.  
 XX PA (MANN-) MANNKIND CORP.  
 XX PI Simard JLL, Diamond DC, Liu L, Liu Z;  
 XX DR WPI; 2004-315564/29.  
 XX CC New polypeptides and encoding nucleic acids that are useful epitopes of  
 PT target-associated antigens, useful for diagnosing and/or treating viral  
 PT infections, cancers and tumors.  
 XX PS Claim 1; SEQ ID NO 301; 357pp; English.  
 XX CC The present invention describes a polypeptide (I) comprising a component  
 CC selected from: (a) a polypeptide epitope having any of the 503 fully  
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope

CC cluster comprising the polypeptide of (a); (c) a polypeptide having  
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional  
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the  
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and  
 CC can be used in vaccines. The methods and compositions of the present  
 CC invention are useful for the diagnosis and/or treatment of viral  
 CC infections, cancers and tumors. The present sequence is used in the  
 CC exemplification of the present invention.  
 XX CC Sequence 10 AA;  
 CC Query Match 40.8%; Score 29; DB 8; Length 10;  
 CC Best Local Similarity 50.0%; Pred. No. 2e+02;  
 CC Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 7 IIAWMQN 14  
 Db 2 ILWLLMNN 9  
 RESULT 13  
 ADM73040  
 ID ADM73040 standard; peptide; 10 AA.  
 XX AC ADM73040;  
 XX DT 03-JUN-2004 (first entry)  
 XX DE Human GAGE-1 epitope SEQ ID NO:299.  
 XX KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;  
 KW cancer; tumour; human; GAGE-1.  
 XX OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO2004022709-A2.  
 XX PD 18-MAR-2004.  
 XX PF 05-SEP-2003; 2003WO-US027706.  
 XX PR 06-SEP-2002; 2002US-0409123P.  
 XX PA (MANN-) MANNKIND CORP.  
 XX PI Simard JLL, Diamond DC, Liu L, Liu Z;  
 XX DR WPI; 2004-315564/29.  
 XX CC New polypeptides and encoding nucleic acids that are useful epitopes of  
 PT target-associated antigens, useful for diagnosing and/or treating viral  
 PT infections, cancers and tumors.  
 XX PS Claim 1; SEQ ID NO 299; 357pp; English.  
 XX CC The present invention describes a polypeptide (I) comprising a component  
 CC selected from: (a) a polypeptide epitope having any of the 503 fully  
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope  
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having  
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional  
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the  
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and  
 CC can be used in vaccines. The methods and compositions of the present  
 CC invention are useful for the diagnosis and/or treatment of viral  
 CC infections, cancers and tumors. The present sequence is used in the  
 CC exemplification of the present invention.  
 XX CC Sequence 10 AA;  
 CC Query Match 40.8%; Score 29; DB 8; Length 10;  
 CC Best Local Similarity 50.0%; Pred. No. 2e+02;  
 CC Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14  
 Db 1 ILWLLMNN 8

RESULT 14  
 ADM73035  
 ID ADM73035 standard; peptide; 10 AA.  
 XX  
 AC ADM73035;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Human GAGE-1 epitope SEQ ID NO:294.  
 XX  
 KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;  
 KW cancer; tumour; human; GAGE-1.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO2004022709-A2.  
 XX  
 PD 18-MAR-2004.  
 XX  
 PF 05-SEP-2003; 2003WO-US027706.  
 XX  
 PR 06-SEP-2002; 2002US-0409123P.  
 XX  
 PA (MANN-) MANNKIND CORP.  
 XX  
 PI Simard JUL, Diamond DC, Liu L, Liu Z;  
 XX  
 DR WPI; 2004-315564/29.  
 XX  
 PT New polypeptides and encoding nucleic acids that are useful epitopes of  
 PT target-associated antigens, useful for diagnosing and/or treating viral  
 PT infections, cancers and tumors.  
 XX  
 PS Claim 1; SEQ ID NO 294; 357pp; English.  
 XX  
 CC The present invention describes a polypeptide (I) comprising a component  
 CC selected from: (a) a polypeptide epitope having any of the 503 fully  
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope  
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having  
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional  
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the  
 CC polypeptide of (a)-(d). (i) has virucide and cytostatic activities, and  
 CC can be used in vaccines. The methods and compositions of the present  
 CC invention are useful for the diagnosis and/or treatment of viral  
 CC infections, cancers and tumors. The present sequence is used in the  
 CC exemplification of the present invention.  
 XX  
 SQ Sequence 10 AA;

Query Match 40.8%; Score 29; DB 8; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 2e+02;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14  
 Db 2 ILWLLMNN 9

RESULT 15  
 AAY93007  
 ID AAY93007 standard; peptide; 12 AA.  
 XX  
 AC AAY93007;  
 XX  
 DT 08-NOV-2000 (first entry)  
 XX  
 XX

DE Transforming growth factor inhibitory peptide P53.  
 XX  
 KW Hepatotropic; antagonist; transforming growth factor betai; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200031135-A1.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 23-NOV-1999; 99WO-ES000375.  
 XX  
 PR 24-NOV-1998; 98ES-00002465.  
 XX  
 PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 XX  
 PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borras Cuesta F;  
 XX  
 DR WPI; 2000-411935/35.  
 XX  
 PT Peptides that antagonize binding of transforming growth factor betai,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 XX  
 PS Disclosure; Page 27; 86pp; Spanish.  
 XX  
 CC The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betai (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 12 AA;

Query Match 40.8%; Score 29; DB 3; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASII 8  
 Db 5 TSLDATMI 12

Search completed: November 14, 2004, 13:44:57  
 Job time : 112.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 13:18:48 ; Search time 110.5 Seconds  
(without alignments)  
45.450 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71  
Sequence: 1 TSLDASIIWMMQN 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 543373

Minimum DB seq length: 0  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003ae:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	14	3 AAY93098	Aay93098 Transform
2	71	100.0	14	3 AAY92950	Aay92950 Transform
3	50	70.4	12	3 AAY93009	Aay93009 Transform
4	50	70.4	12	3 AAY92947	Aay92947 Transform
5	50	70.4	12	3 AAY93008	Aay93008 Transform
6	40	56.3	12	3 AAY93093	Aay93093 Transform
7	37	52.1	11	3 AAY93094	Aay93094 Transform
8	37	52.1	12	3 AAY93010	Aay93010 Transform
9	33	46.5	14	4 AAB88161	Aab88161 CD66 pept
10	29	40.8	9	4 ADM73036	Adm73036 Human GAG
11	29	40.8	9	8 ADM73041	Adm73041 Human GAG
12	29	40.8	10	8 ADM73042	Adm73042 Human GAG
13	29	40.8	10	8 ADM73040	Adm73040 Human GAG
14	29	40.8	10	8 ADM73035	Adm73035 Human GAG
15	29	40.8	12	3 AAY93007	Aay93007 Transform
16	28	39.4	12	2 AAR86049	Aar86049 Anti-ELAM
17	28	39.4	12	2 AAR86065	Aar86065 Anti-ELAM
18	28	39.4	12	2 AAW26857	Aaw26857 ELAM-1 bi
19	28	39.4	12	2 AAW26865	Aaw26865 ELAM-1 bi
20	28	39.4	12	2 AAW63875	Aaw63875 ELAM-1 pe
21	28	39.4	12	2 AAW63859	Aaw63859 ELAM-1 pe
22	27.5	38.7	9	3 AAY93096	Aay93096 Transform
23	27.5	38.7	9	3 AAY92949	Aay92949 Transform
24	27	38.0	7	3 AAW46010	Aaw46010 Peptide #
25	27	38.0	7	3 AAY93095	Aay93095 Transform

26	27	38.0	11	5 ABB05301	Abb05301 Polyureth
27	27	38.0	12	2 AAR83343	Aar83343 K0-bindin
28	27	38.0	14	4 ABB56643	Abb56643 Human SNP
29	26	36.6	9	5 AAO14709	Aao14709 Human cri
30	26	36.6	9	5 AAG80179	Aag80179 HER-2 mim
31	26	36.6	10	5 AAO14645	Aao14645 Human cri
32	26	36.6	11	5 ABR52334	Abr52334 Peptide r
33	26	36.6	11	5 ABJ07364	Abj07364 Hepatitis
34	26	36.6	12	2 AAR72136	Aar72136 Endotheli
35	26	36.6	12	2 AAR86025	Aar86025 Anti-ELAM
36	26	36.6	12	2 AAR86041	Aar86041 Anti-ELAM
37	26	36.6	12	2 AAW26845	Aaw26845 ELAM-1 bi
38	26	36.6	12	2 AAW63849	Aaw63849 ELAM-1 pe
39	26	36.6	12	3 AAB17093	Aab17093 Selectin
40	26	36.6	12	5 AAU81139	Aau81139 Selectin-
41	26	36.6	12	5 ABB72976	Abb72976 Selectin
42	26	36.6	12	7 ADJ73130	Adj73130 Integrin
43	26	36.6	12	8 ADJ52765	Adj52765 CHI delet
44	26	36.6	12	8 ADJ51726	Adj51726 CHI delet
45	26	36.6	13	2 AAR86115	Aar86115 Anti-ELAM

ALIGNMENTS

RESULT 1  
AAY93098  
ID AAY93098 standard; peptide; 14 AA.  
XX  
AC AAY93098;  
XX  
DT 08-NOV-2000 (first entry)  
XX  
DE Transforming growth factor inhibitory peptide P144.  
XX  
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;  
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200031135-A1.  
XX  
PD 02-JUN-2000.  
XX  
PF 23-NOV-1999; 99WO-ES000375.  
XX  
PR 24-NOV-1998; 98ES-0002465.  
(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
Borras Cuesta F;  
WPI; 2000-411935/35.  
Peptides that antagonize binding of transforming growth factor beta1,  
useful for treatment of liver disease, especially cirrhosis, are partial  
sequences of the factor or its receptors.  
Disclosure; Page 31; 86pp; Spanish.  
The invention relates to synthetic peptides that antagonise the binding  
of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in  
vivo which have partial amino acid sequences identical, or similar, with  
those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent  
examples of the peptides of the invention. The peptides act by  
competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.  
they are inhibitors of stimulation of collagen synthesis in liver cells  
and inhibitors of synthesis of proteolytic enzymes able to degrade the  
extracellular matrix. The peptides, their mimetopes and/or DNA (or  
expression systems) encoding the peptides are used for treatment of liver  
disease, specifically cirrhosis

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XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 71; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASIIWAMQON 14
DB 1 TSLDASIIWAMQON 14

RESULT 2
AA92950
ID AAY92950 standard; peptide; 14 AA.
XX
AC AAY92950;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #6.
XX
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
PS (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
DR WPI; 2000-411935/35.
XX
PT Peptides that antagonize binding of transforming growth factor beta1,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
PS Claim 7; Page 81; 86pp; Spanish.
XX
CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 14 AA;
Query Match 100.0%; Score 71; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASIIWAMQON 14
DB 1 TSLDASIIWAMQON 14

RESULT 3
AA92947
ID AAY92947 standard; peptide; 12 AA.
XX
AC AAY92947;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #3.
XX
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX

AA93009
ID AAY93009 standard; peptide; 12 AA.
XX
AC AAY93009;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P55.
XX
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Rattus sp.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
PS (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
DR WPI; 2000-411935/35.
XX
PT Peptides that antagonize binding of transforming growth factor beta1,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
PS Disclosure; Page 27; 86pp; Spanish.
XX
CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 12 AA;
Query Match 70.4%; Score 50; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 0.046;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLDASIIWAMQ 13
DB 1 SLDATMIWTMMQ 12

RESULT 4
AA92947
ID AAY92947 standard; peptide; 12 AA.
XX
AC AAY92947;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #3.
XX
KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
```



CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 12 AA;

Query Match 56.3%; Score 40; DB 3; Length 12;  
 Best Local Similarity 77.8%; Pred. No. 2.7;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLDASIIW 9  
 DB 1 TSLDATMIW 9  
 |||||:|

RESULT 7  
 AAY93094  
 ID AAY93094 standard; peptide; 11 AA.  
 XX  
 AC AAY93094;

XX  
 DT 08-NOV-2000 (first entry)  
 XX

DE Transforming growth factor inhibitory peptide P140.

XX Hepatotrophic; antagonist; transforming growth factor betai; TGF- $\beta$ 1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betai,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betai (TGF- $\beta$ 1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX

SQ Sequence 11 AA;

Query Match 52.1%; Score 37; DB 3; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 8.4;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 OY 4 DASIIWMM 12  
 ||:| |  
 DB 3 DATMIWTMM 11

RESULT 8  
 AAY93010  
 ID AAY93010 standard; peptide; 12 AA.  
 XX  
 AC AAY93010;

XX  
 DT 08-NOV-2000 (first entry)  
 XX

DE Transforming growth factor inhibitory peptide P56.

XX Hepatotrophic; antagonist; transforming growth factor betai; TGF- $\beta$ 1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Rattus sp.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betai,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX Disclosure; Page 27; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betai (TGF- $\beta$ 1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX

SQ Sequence 12 AA;

Query Match 52.1%; Score 37; DB 3; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 9.2;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 IIVWMMQN 14  
 ||:| |  
 DB 1 MIWTMMQN 8

RESULT 9  
 AAB88161  
 ID AAB88161 standard; peptide; 14 AA.  
 XX  
 AC AAB88161;

XX



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RN SEQUENCE FROM N.A.
RP MEDLINE=22404279; PubMed=12516573;
RA Kurth J., Pernik A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RT Thompson K.M., Winkler T., Rajewsky K., Kueppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; D31968; BAA28850.1; -
DR EMBL; AJ279011; CAC35539.1; -
DR EMBL; AJ279012; CAC35540.1; -
DR EMBL; AJ279013; CAC35541.1; -
DR EMBL; AJ509179; CAD48929.1; -
DR EMBL; AJ509180; CAD48930.1; -
FT NON_TER
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 26.8%; Score 19; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 8 IWMM 12
Db 4 IWTL 8

RESULT 15
Q9TWX6 PRELIMINARY; PRT; 11 AA.
AC Q9TWX6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide
DE (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=92134256; PubMed=1734862;
RA Touhara K.; Prestwich G.D.;
RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
RT Binding protein.";
RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
FT NON_TER 1
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

Query Match 26.8%; Score 19; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.4e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SLDASII 8
Db 1 NIQASII 7

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Search completed: November 14, 2004, 13:41:10  
 Job time : 124.5 secs

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FT  NON TER      1      1
FT  NON TER     14     14
SQ  SEQUENCE    14 AA; 1544 MW; 0BC0478DBE55A33B CRC64;

Query Match      29.6%; Score 21; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.5e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY  1 TSLDASII 8
Db  1 TSLESSYL 8

RESULT 11
Q841R8 PRELIMINARY; PRT; 13 AA.
AC Q841R8; 2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ccch (Fragment).
GN Name-cpch;
OS Synecococcus sp. (strain PCC 6301) (Anacystis nidulans).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=1139;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9321540; PubMed=7682531;
RA Kalla R., Bhalarao R.P., Gustafsson P.;
RT "Regulation of phycobilisome rod proteins and mRNA at different light
RT intensities in the cyanobacterium Synecococcus 6301.";
RL Gene 126:77-83(1993).
DR EMBL; S58974; RAP13908.1; -.
FT NON TER      13
SQ SEQUENCE     13 AA; 1439 MW; D586F2E86F2D0DDD CRC64;

Query Match      28.2%; Score 20; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY  1 TSLDAS 6
Db  2 TSLEAA 7

RESULT 12
P823B3 PRELIMINARY; PRT; 10 AA.
AC P823B3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Larval cuticle LCP2A protein (Minor band protein) (Fragment).
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE.
RC STRAIN=OREGON-R; TISSUE=LARVA;
RA Chihara C.J.;
RT "Third instar cuticle proteins.";
RL Submitted (XXX-2000) to Swiss-Prot.
CC -1- FUNCTION: COMPONENT OF THE CUTICLE OF THE LARVA OF FRUIT FLY.
DR FlyBase; FBgn0061208; Lcp2a.
DR GO; GO:0042302; F:structural constituent of cuticle; IEA.
DR InterPro; IPR000618; Insect cuticle.
DR PROSITE; PS00233; CUTICLE; PARTIAL.
KW Cuticle; Structural protein.
FT NON TER      10
SQ SEQUENCE     10 AA; 1100 MW; 9DCF320732C44DDA CRC64;

Query Match      26.8%; Score 19; DB 2; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.3e+04;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY  2 SLDASIIWA 10
Db  1 NVDANVLRA 9

RESULT 13
Q25356 PRELIMINARY; PRT; 10 AA.
ID Q25356;
AC Q25356;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Vitellogenin B (Fragment).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88003971; PubMed=2820677;
RA Locke J., White B.N., Wyatt G.R.;
RT "Cloning and 5' end nucleotide sequences of two juvenile hormone-
RT inducible vitellogenin genes of the African migratory locust.";
RL DNA 6:331-342(1987).
DR EMBL; M17334; AAA29285.1; -.
FT NON TER      10
SQ SEQUENCE     10 AA; 1116 MW; D1B31165B720572D CRC64;

Query Match      26.8%; Score 19; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY  8 IWAMM 12
Db  1 MWALI 5

RESULT 14
Q9UEL0 PRELIMINARY; PRT; 11 AA.
ID Q9UEL0;
AC Q9UEL0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Fas antigen (CD95 antigen) (Fragment).
GN Name=CD95;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95355401; PubMed=7543095;
RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
RA Nakanishi Y.;
RT "Transcription Stimulation of the Fas-encoding gene by nuclear factor
RT for interleukin-6 expression upon influenza virus infection.";
RL J. Biol. Chem. 270:18007-18012(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
RA Kuppers R., Rajewsky K.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; AY128666; AAM96953.1; -.  
 FT NON TER 8 8  
 SQ SEQUENCE 8 AA; 965 MW; F99DC37B1046D876 CRC64;

Query Match 29.6%; Score 21; DB 2; Length 8;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 IIVAM 11  
 | : : :  
 Db 4 IEWAM 8

## RESULT 7

APE\_CAPGI STANDARD; PRT; 10 AA.

AC P80474;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Aminopeptidase (EC 3.4.11.-) (Fragment).  
 OS Capnocytophaga gingivalis.  
 OC Bacteria; Bacteroidetes; Flavobacteriales; Flavobacteriaceae;  
 OC Flavobacteriaceae; Capnocytophaga.  
 OX NCBI\_TaxID=1017;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=ATCC 33624;  
 RX MEDLINE=96118234; PubMed=8574402;  
 RA Spratt D.A., Greenman J., Schaffer A.G.;  
 RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence factor."  
 RL Microbiology 141:3087-3093(1995).  
 CC -1- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N-terminal amino acid residues but not N-terminal blocked ones.  
 CC Optimum activity is measured at pH 7.5. May be important in the nutrition and pathogenesis of the organism in the human oral cavity.  
 CC -1- COFACTOR: Requires magnesium or calcium.  
 KW Aminopeptidase; Calcium; Direct protein sequencing; Hydrolase;  
 KM Magnesium.  
 FT NON TER 1 1  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 29.6%; Score 21; DB 1; Length 10;  
 Best Local Similarity 33.3%; Pred. No. 5.2e+03;  
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 DASIIW 9  
 | : : :  
 Db 1 DVNMLW 6

## RESULT 8

Q7M1J3 PRELIMINARY; PRT; 10 AA.

AC Q7M1J3;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Cystathionine gamma-synthase (Fragment).  
 OS Spinacia oleracea (spinach).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Amaranthaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=95142682; PubMed=7840669;  
 RA Ravanel S., Droux M., Douce R.;

RT "Methionine biosynthesis in higher plants. I. Purification and characterization of cystathionine gamma-synthase from spinach

RT chloroplasts.";  
 RL Arch. Biochem. Biophys. 316:572-584(1995).  
 DR PIR; S69159; S69159. 1  
 FT NON TER 1 1  
 FT NON TER 10 10  
 SQ SEQUENCE 10 AA; 873 MW; D88458DDDDAB2CD CRC64;

Query Match 29.6%; Score 21; DB 2; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 5.2e+03;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASII 8  
 | : : : :  
 Db 2 TAVDAAA 9

## RESULT 9

O77895 PRELIMINARY; PRT; 11 AA.

AC O77895;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 12 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.;  
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC class II B loci."  
 RT Genetics 149:1527-1537(1998).  
 RL EMBL; AF050005; AAC41344.1; -.  
 FT NON TER 1 1  
 FT NON TER 11 11  
 SQ SEQUENCE 11 AA; 1367 MW; 3F47C9EA772045A3 CRC64;

Query Match 29.6%; Score 21; DB 2; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 5.8e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SIIW 9  
 | : : :  
 Db 5 SIIW 8

## RESULT 10

O9R5Q6 PRELIMINARY; PRT; 14 AA.

AC O9R5Q6;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 2-HALOGENOATE 1,2-dioxygenase component A beta subunit (Fragment).  
 OS Burkholderia cepacia (Pseudomonas cepacia).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
 OC Burkholderiaceae; Burkholderia.  
 OX NCBI\_TaxID=292;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=92104974; PubMed=1370284;  
 RA Fetzner S., Muller R., Lingens F.;

RT "Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a two-component enzyme system from Pseudomonas cepacia 2CBS.";  
 RL J. Bacteriol. 174:279-290(1992).  
 DR PIR; A44920; A44920.

RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.,  
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC  
 class II B loci.",  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050004; AAC41343.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 31.0%; Score 22; DB 2; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SIIV 9  
 ||:|  
 Db 5 SIVW 8

## RESULT 3

O77898 PRELIMINARY; PRT; 11 AA.  
 AC O77898;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE MHC class II B locus 12 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;  
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
 RA Figueroa F., Sultmann H., Klein J.,  
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC  
 class II B loci",  
 RL Genetics 149:1527-1537(1998).  
 DR EMBL; AF050008; AAC41347.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 31.0%; Score 22; DB 2; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 3.7e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SIIV 9  
 ||:|  
 Db 5 SIVW 8

## RESULT 4

O7M1U2 PRELIMINARY; PRT; 11 AA.  
 AC O7M1U2;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Unidentified 5-7/35K protein (Fragment).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE.

RA Komatsu S., Kajiwarra H., Hirano H.;  
 RT "A rice protein library; a data-file of rice proteins separated by  
 RT two-dimensional electrophoresis.";

RL Theor. Appl. Genet. 86:935-942(1993).  
 DR PIR; P00731; P00731.1  
 FT NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1319 MW; CBE97F0E53277362 CRC64;

Query Match 31.0%; Score 22; DB 2; Length 11;  
 Best Local Similarity 40.0%; Pred. No. 3.7e+03;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 ASIIV 9  
 ||:|  
 Db 1 ATVVW 5

## RESULT 5

Q99902 PRELIMINARY; PRT; 14 AA.  
 AC Q99902;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)  
 DE ERG/EWS protein (Fragment).  
 GN Name=ERG/EWS;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Liver;  
 RX MEDLINE=96321017; PubMed=8707406;  
 RA Peter M., Mugneret F., Aurias A., Thomas G., Magdelenat H.,  
 RA Delattre O.,  
 RT "An EWS/ERG fusion with a truncated N-terminal domain of EWS in a  
 Ewing's tumor";  
 RL Int. J. Cancer 67:339-342(1996).  
 DR EMBL; S82338; AAD15010.2; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1624 MW; D8808FFB7C07C61D CRC64;

Query Match 31.0%; Score 22; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 4.8e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LDASIWA 10  
 ||:|  
 Db 5 LSAEHLWA 12

## RESULT 6

Q86SL0 PRELIMINARY; PRT; 8 AA.  
 AC Q86SL0;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Flavocytochrome b-558 alpha polypeptide (fragment).  
 GN Name=CYBA;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22615572; PubMed=12729892;  
 RA Moreno M.U., San Jose G., Orbe J., Paramo J.A., Belouqui O., Diez J.,  
 RA Zalba G.;  
 RT "Preliminary characterisation of the promoter of the human p22phox  
 RT gene: identification of a new polymorphism associated with  
 RT hypertension.";

FEBS Lett. 542:27-31(2003).

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:17:28 ; Search time 122.5 Seconds  
(without alignments)  
65.757 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71

Sequence: 1 TSLDASIWAMQMN 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 6764

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	31.0	10	2 Q9ESU5	Q9esU5 mus musculus
2	22	31.0	11	2 Q77894	Q77894 oreochromis
3	22	31.0	11	2 Q77898	Q77898 oreochromis
4	22	31.0	11	2 Q7MIU2	Q7mlU2 oryza sativ
5	22	31.0	14	2 Q99902	Q99902 homo sapien
6	21	29.6	8	2 Q86SL0	Q86SL0 homo sapien
7	21	29.6	10	1 APE_CAPGI	P80474 capnocytoph
8	21	29.6	10	2 Q7MLJ3	Q7mlJ3 spinacia ol
9	21	29.6	11	2 Q77895	Q77895 oreochromis
10	21	29.6	14	2 Q9RS06	Q9rsQ6 burkholderi
11	20	28.2	13	2 Q841R8	Q841R8 synechococc
12	19	26.8	10	2 P82383	P82383 drosophila
13	19	26.8	10	2 Q25356	Q25356 locusta mig
14	19	26.8	11	2 Q9UELO	Q9ueL0 homo sapien
15	19	26.8	11	2 Q9TWX6	Q9twX6 manduca sex
16	19	26.8	11	2 Q77896	Q77896 oreochromis
17	19	26.8	12	2 Q9UCR3	Q9ucr3 homo sapien
18	19	26.8	12	2 Q6X7V1	Q6x7V1 canis fam
19	19	26.8	12	2 AAP79619	AP79619 canis fam
20	19	26.8	13	2 Q7RFA9	Q7rfA9 plasmodium
21	19	26.8	14	2 Q9SAP8	Q9sap8 plasmu sativ
22	18	25.4	8	2 Q70V57	Q70V57 fuerstia af
23	18	25.4	8	2 CAD45547	Cad45547 fuerstia
24	18	25.4	9	2 Q85DB0	Q85db0 lepilemur s
25	18	25.4	9	2 Q85DB8	Q85db8 lepilemur e
26	18	25.4	9	2 Q94NR9	Q94nr9 daubentonia
27	18	25.4	9	2 Q94NB0	Q94nb0 microcebus
28	18	25.4	9	2 Q94NB1	Q94nb1 microcebus
29	18	25.4	9	2 Q94NB2	Q94nb2 microcebus
30	18	25.4	10	2 Q7M501	Q7m501 aspergillus
31	18	25.4	10	2 Q6EEZ7	Q6eeZ7 homo sapien

32	18	25.4	10	2 Q25355	Q25355 locusta mig
33	18	25.4	10	2 Q7ZZJ2	Q7zzJ2 motacilla f
34	18	25.4	11	2 Q78118	Q78118 oreochromis
35	18	25.4	11	2 Q78120	Q78120 oreochromis
36	18	25.4	11	2 Q56972	Q56972 yersinia pe
37	18	25.4	11	2 Q7LZ10	Q7Lz10 gadus sp. a
38	18	25.4	11	2 Q7ZZI6	Q7zzI6 motacilla f
39	18	25.4	11	2 Q7ZZI9	Q7zzI9 motacilla f
40	18	25.4	11	2 Q8ADI8	Q8adi8 human immun
41	18	25.4	12	2 Q7M348	Q7m348 pan troglod
42	18	25.4	12	2 Q7M350	Q7m350 callithrix
43	18	25.4	12	2 Q7M351	Q7m351 macaca fusc
44	18	25.4	12	2 Q7M352	Q7m352 hylobates l
45	18	25.4	12	2 Q7M353	Q7m353 pongo pygma

#### ALIGNMENTS

##### RESULT 1

Q9ESU5 PRELIMINARY; PRT; 10 AA.  
 ID Q9ESU5  
 AC Q9ESU5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Fas death receptor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SFRAIN=C3H/He;  
 RX MEDLINE=20127858; PubMed=10660538;  
 RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,  
 RA Yonish-Rouach E., Reisdorf P.;  
 RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a  
 RT p53-responsive element that is activated by p53 mutants unable to  
 RT induce apoptosis.";  
 RL J. Biol. Chem. 275:3867-3872 (2000).  
 DR EMBL; AF282865; AAG02410.1; -;  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 31.0%; Score 22; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWAMM 12  
 DB 4 IWAVL 8

##### RESULT 2

O77894 PRELIMINARY; PRT; 11 AA.  
 ID O77894;  
 AC O77894;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DE MHC class II B locus 12 (Fragment).  
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;  
 OC Cichlidae; Oreochromis.  
 OX NCBI\_TaxID=8128;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98315113; PubMed=9649539;

A;Reference number: PH1754; MUID:93301585; PMID:8391057  
A;Accession: PH1768  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-14 <POR>

Query Match 26.8%; Score 19; DB 2; Length 14;  
Best Local Similarity 33.3%; Pred. No. 2.3e+03;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TSLDASIIW 9  
| : : :  
Db 5 TDSNYQLIW 13

RESULT 15

S66195  
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragment)  
C;Species: Gadus sp. (cod)  
C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 12-Jun-1998  
C;Accession: S66195  
R;Hjelmqvist, L.; Hackett, M.; Shafqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;  
FEBS Lett. 367, 237-240, 1995  
A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M  
nzyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314  
A;Accession: S66195  
A;Molecule type: protein  
A;Residues: 1-6 <HJE>  
C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 25.4%; Score 18; DB 2; Length 6;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ASIIW 9  
| : :  
Db 1 AAVAW 5

Search completed: November 14, 2004, 13:45:47  
Job time : 22.5 secs

A;Note: sequence extracted from NCBI backbone (NCBIP:75379)

Query Match 29.6%; Score 21; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 9.6e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASII 8  
|||::||  
DB 1 TSLESSYL 8

## RESULT 9

PH1769

T cell receptor alpha chain V region (clone 2V alpha 7.2-4) - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999  
C;Accession: PH1769  
R;Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.  
J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A;Reference number: PH1754; MUID:93301585; PMID:8391057

A;Accession: PH1769

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-14 <PDR>

Query Match 28.2%; Score 20; DB 2; Length 14;  
Best Local Similarity 40.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 4; Mismatches 0; Indels 2; Gaps 1;

QY 2 SLDAS--IIW 9  
|:::|  
DB 4 SMDSNYQLIW 13

## RESULT 10

PT0519

T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0519

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0519

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-6 <FEE>

A;Experimental source: adult thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 26.8%; Score 19; DB 2; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIW 9  
||:|  
DB 1 ASSLW 5

## RESULT 11

S09652

hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)

C;Species: Enterobacter cloacae

C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 08-Oct-1999

C;Accession: S09652

R;Vliegenthart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.

Antimicrob. Agents Chemother. 33, 1153-1159, 1989

A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant inv

A;Reference number: S09651; MUID:90024972; PMID:2552900

A;Accession: S09652

A;Molecule type: DNA

A;Residues: 1-7 <VLI>

A;Cross-references: EMBL:X51534; NID:g40878; PIDN:CAA35914.1; PID:g581034

Query Match 26.8%; Score 19; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIW 9  
|||  
DB 2 IIW 4

## RESULT 12

PH1602

Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1602

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1602

A;Molecule type: DNA

A;Residues: 1-7 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 26.8%; Score 19; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIW 9  
||:|  
DB 2 ASSLW 6

## RESULT 13

S66248

processing enzyme, 33K - black gram (fragment)

C;Species: Vigna mungo (black gram)

C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S66248

R;Okamoto, T.; Minamikawa, T.

Eur. J. Biochem. 231, 300-305, 1995

A;Title: Purification of a processing enzyme (VmPE-1) that is involved in post-translat

A;Reference number: S66248; MUID:95361851; PMID:7635141

A;Accession: S66248

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <OKA>

A;Cross-references: UNIPROT:Q9XFZ4

Query Match 26.8%; Score 19; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 1.8e+03;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 DASIIWAMM 12  
|||::|  
DB 1 DEGTWAVL 9

## RESULT 14

PH1768

T cell receptor alpha chain V region (clone 2V alpha 7.2-3) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Jul-1999

C;Accession: PH1768

R;Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood



Db 2 TAVDAAAI 9

RESULT 3  
S69123  
proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)  
C:Species: Rhodospirillum rubrum  
C>Date: 10-Mar-1998 #sequence\_revision 24-Apr-1998 #text\_change 24-Apr-1998  
C:Accession: S69123  
R:Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.  
Eur. J. Biochem. 228, 719-726, 1995  
A:Title: Properties of the soluble polypeptide of the proton-translocating transhydrogenase  
A:Reference number: S69123; MUID:95255277; PMID:7737169  
A:Accession: S69123  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <DIG>

Query Match 31.0%; Score 22; DB 2; Length 12;  
Best Local Similarity 22.2%; Pred. No. 5.2e+02;  
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 ASIIWAMQ 13  
| : : : :  
Db 2 ADVVWKVQR 10

RESULT 4  
PT0586  
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0586; PT0592  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0586  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-7 <FEE>  
A:Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)  
C:Keywords: T-cell receptor

Query Match 29.6%; Score 21; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIW 9  
| : : : :  
Db 1 ASSIW 5

RESULT 5  
S69159  
cystathionine gamma-synthase - spinach (fragment)  
C:Species: Spinacia oleracea (spinach)  
C>Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
C:Accession: S69159  
R:Ravanel, S.; Droux, M.; Douce, R.  
Arch. Biochem. Biophys. 316, 572-584, 1995  
A:Title: Methionine biosynthesis in higher plants. I. Purification and characterization  
A:Reference number: S69159; MUID:95142682; PMID:7840669  
A:Accession: S69159  
A:Molecule type: protein  
A:Residues: 1-10 <RAV>  
A:Cross-references: UNIPROT:Q7M1J3  
C:Keywords: chloroplast

Query Match 29.6%; Score 21; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 6.6e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASII 8  
| : : : :|

Db 2 TAVDAAAI 9

RESULT 6  
I64829  
gene HEXA protein - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
C:Accession: I64829  
R:Boles, D.J.; Proia, R.L.  
Am. J. Hum. Genet. 56, 716-724, 1995  
A:Title: The molecular basis of HEXA mRNA deficiency caused by the most common Tay-Sachs  
A:Reference number: I51882; MUID:95193801; PMID:7887427  
A:Accession: I64829  
A:Status: preliminary; translated from GB/EMBL/DBBJ  
A:Molecule type: mRNA  
A:Residues: 1-12 <RES>  
A:Cross-references: GB:S76984; NID:g912781; PIDN:AAD14243.1; PID:g4261943  
C:Genetics:  
A:Gene: GDB:HEXA  
A:Cross-references: GDB:120040; OMIM:272800  
A:Map position: 15q23-15q24  
C:Superfamily: beta-hexosaminidase

Query Match 29.6%; Score 21; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 8.1e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 SIIW 9  
| : : : :  
Db 8 SILW 11

RESULT 7  
PHI327  
Ig heavy chain DJ region (clone C113-105) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PHI327  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma  
A:Reference number: PHI302; MUID:93094761; PMID:1460419  
A:Accession: PHI327  
A:Molecule type: DNA  
A:Residues: 1-14 <WAS>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.6%; Score 21; DB 2; Length 14;  
Best Local Similarity 75.0%; Pred. No. 9.6e+02;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 WAMM 12  
| : : : :  
Db 2 WYMM 5

RESULT 8  
A44920  
2-halobenzoate 1,2-dioxygenase component A beta chain - Pseudomonas cepacia (fragment)  
C:Species: Pseudomonas cepacia  
C>Date: 01-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: A44920  
R:Fetner, S.; Muller, R.; Lingens, F.  
J. Bacteriol. 174, 279-290, 1992  
A:Title: Purification and some properties of 2-halobenzoate 1,2-dioxygenase, a two-component  
A:Reference number: A44920; MUID:92104974; PMID:1370284  
A:Contents: 2CBS  
A:Accession: A44920  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <FET>  
A:Cross-references: UNIPROT:Q9RSQ6

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:32:33 ; Search time 22.5 Seconds  
(without alignments)  
59.868 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71

Sequence: 1 TSLDASIIWMMQN 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2096

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	36.6	14	2 A35105	hypothetical prote
2	22	31.0	11	2 PQ0731	unidentified 5.7/3
3	22	31.0	12	2 S69123	proton-translocati
4	21	29.6	7	2 PT0586	T-cell receptor be
5	21	29.6	10	2 S69159	cystathionine gamm
6	21	29.6	12	2 I64829	gene HEXA protein
7	21	29.6	14	2 PH1327	Ig heavy chain DJ
8	21	29.6	14	2 A44920	2-halobenzoate 1,2
9	20	28.2	14	2 PH1769	T cell receptor al
10	19	26.8	6	2 PT0519	T-cell receptor be
11	19	26.8	7	2 S09652	hypothetical prote
12	19	26.8	7	2 PH1502	Ig H chain V-D-J r
13	19	26.8	10	2 S66248	processing enzyme,
14	19	26.8	14	2 PH1768	T cell receptor al
15	18	25.4	6	2 S66195	alcohol dehydrogen
16	18	25.4	9	2 S13889	phosphoenolpyruvat
17	18	25.4	10	2 D61440	polygalacturonase
18	18	25.4	11	2 S66196	alcohol dehydrogen
19	18	25.4	12	2 PN0581	tyrosine 3-monooxy
20	18	25.4	12	2 PN0580	tyrosine 3-monooxy
21	18	25.4	12	2 PN0579	tyrosine 3-monooxy
22	18	25.4	12	2 PN0577	tyrosine 3-monooxy
23	18	25.4	12	2 PN0576	tyrosine 3-monooxy
24	18	25.4	12	2 PN0578	tyrosine 3-monooxy
25	18	25.4	13	2 I54984	aeg-46.5 protein -
26	18	25.4	14	2 PH1758	T cell receptor al
27	18	25.4	14	2 PH1766	T cell receptor al
28	18	25.4	14	2 S14336	mastoparan B - hor
29	17	23.9	9	2 S07241	litorin - Rohde's

30 17 23.9 9 2 I58350  
31 17 23.9 10 2 S48182  
32 17 23.9 10 2 A35556  
33 17 23.9 10 2 B33143  
34 17 23.9 10 2 A33143  
35 17 23.9 12 2 A29169  
36 17 23.9 13 2 S57567  
37 17 23.9 14 2 PH1757  
38 17 23.9 14 2 PH1759  
39 17 23.9 14 2 PH1767  
40 16 22.5 7 2 PX0008  
41 16 22.5 8 2 A39308  
42 16 22.5 9 2 S07205  
43 16 22.5 9 2 S07204  
44 16 22.5 10 2 A60647  
45 16 22.5 10 2 PQ0177

#### ALIGNMENTS

##### RESULT 1

A35105

hypothetical protein - Neurospora crassa mitochondrion (fragment)

C;Species: mitochondrion Neurospora crassa

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 07-Dec-1999

C;Accession: A35105

R;Saville, B.J.; Collins, R.A.

Cell 61, 685-696, 1990

A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora

A;Reference number: A35105; MUID:90263093; PMID:2160856

A;Accession: A35105

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-14 <SAV>

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC3

C;Keywords: mitochondrion

Query Match 36.6%; Score 26; DB 2; Length 14;  
Best Local Similarity 37.5%; Pred. No. 11e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 SIWMMQ 13  
DB 2 SFLWTLQ 9

##### RESULT 2

PQ0731

unidentified 5.7/35K protein [imported] - rice (fragment)

C;Species: Oryza sativa (rice)

C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C;Accession: PQ0731

R;Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensio

A;Reference number: PQ0696

A;Accession: PQ0731

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <KOM>

A;Cross-references: UNIPROT:Q7M1U2

Query Match 31.0%; Score 22; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 4.7e+02;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 ASIIW 9  
DB 1 ATVW 5

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ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,141A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: CARTY, CHRISTINE E.  
REGISTRATION NUMBER: 36,099  
REFERENCE/DOCKET NUMBER: 174611B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)-594-6734  
TELEFAX: (908)-594-4720  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
US-08-469-141A-32

Query Match 38.0%; Score 27; DB 3; Length 15;  
Best Local Similarity 71.4%; Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DASIWA 10  
|  
|  
|  
|  
|  
Db 7 DNGIWA 13

Search completed: November 14, 2004, 12:08:49  
Job time : 12.0213 secs

REFERENCE/DOCKET NUMBER: 0233 US  
TELEPHONE: (515) 245-3594  
TELEFAX: (515) 245-3634  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-179-632-15

Query Match 39.4%; Score 28; DB 1; Length 23;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIWMM 12  
Db 12 LIWALM 17

RESULT 13  
US-08-440-174A-15  
Sequence 15, Application US/08440174A  
Patent No. 5717061  
GENERAL INFORMATION:  
APPLICANT: Rao, Gururaj A.  
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.  
STREET: 7100 N.W. 62nd Avenue  
CITY: Johnston  
STATE: Iowa  
COUNTRY: USA  
ZIP: 50131  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,174A  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/079,512  
FILING DATE: 18-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bobrowicz, Donna  
REGISTRATION NUMBER: 32,196  
REFERENCE/DOCKET NUMBER: 0234R2D-US  
TELEPHONE: (515) 334-6883  
TELEFAX: (515) 334-6883  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-440-174A-15

Query Match 39.4%; Score 28; DB 1; Length 23;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIWMM 12  
Db 12 LIWALM 17

RESULT 14  
PCT-US95-00062-15  
Sequence 15, Application PC/TUS9500062  
GENERAL INFORMATION:  
APPLICANT: Pioneer Hi-Bred International, Inc.  
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pioneer Hi-Bred International, Inc.  
STREET: 700 Capital Square, 400 Locust Street  
CITY: Des Moines  
STATE: Iowa  
COUNTRY: United States  
ZIP: 50309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS/Microsoft Windows  
SOFTWARE: Microsoft Windows Notepad  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/00062  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Yates, Michael E.; Sweeney, Patricia A.;  
NAME: Roth, Michael J.; & Simon, Soma G.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 234R2-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (515) 248-4800  
TELEFAX: (515) 248-4844  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-00062-15

Query Match 39.4%; Score 28; DB 5; Length 23;  
Best Local Similarity 66.7%; Pred. No. 2.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIWMM 12  
Db 12 LIWALM 17

RESULT 15  
US-08-469-141A-32  
Sequence 32, Application US/08469141A  
Patent No. 6124107  
GENERAL INFORMATION:  
APPLICANT: MUMFORD, RICHARD A.  
APPLICANT: DAVIES, D.T. PHILIP  
APPLICANT: DAHLGREN, MARY E.  
APPLICANT: BOGER, JOSHUA S.  
APPLICANT: HUMES, JOHN L.  
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN  
TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY  
NUMBER OF SEQUENCES: 71  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DR. CHRISTINE E. CARTY  
STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000  
CITY: RAHWAY  
STATE: NEW JERSEY  
COUNTRY: USA

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-485-508-34

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13  
Db 7 LWVMMQ 12

## RESULT 10

US-08-485-508-50  
; Sequence 50, Application US/08485508  
; Patent No. 5786322

## ; GENERAL INFORMATION:

; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I  
; NUMBER OF SEQUENCES: 162

## ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/485,508  
; FILING DATE: Herewith  
; CLASSIFICATION: 514

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994

## ; CLASSIFICATION: 514

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992

## ; ATTORNEY/AGENT INFORMATION:

; NAME: Stevens, Lauren L.

## ; REGISTRATION NUMBER: 36,691

; REFERENCE/DOCKET NUMBER: 000324-002/1056

## ; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-496-2300

; TELEFAX: 415-424-0832

## ; INFORMATION FOR SEQ ID NO: 50:

## ; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-485-508-50

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWAMMQ 13  
Db 5 NMLWNMMQ 12

## RESULT 11

US-09-255-501-108  
; Sequence 108, Application US/09255501  
; Patent No. 6596525

## ; GENERAL INFORMATION:

; APPLICANT: Estell, David  
; APPLICANT: Harding, Fiona  
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN  
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND  
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS  
; FILE REFERENCE: GC527  
; CURRENT APPLICATION NUMBER: US/09/255,501  
; CURRENT FILING DATE: 1999-02-23  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 108  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; US-09-255-501-108

Query Match 39.4%; Score 28; DB 4; Length 15;  
Best Local Similarity 44.4%; Pred. No. 1.6e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 LDASIIWAM 11  
Db 1 LQADVLWQM 9

## RESULT 12

US-08-179-632-15  
; Sequence 15, Application US/08179632  
; Patent No. 5607914

## ; GENERAL INFORMATION:

; APPLICANT: Rao, A. Gururaj; Zhong, Lingxiu  
; TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pioneer Hi-Bred International, Inc.  
; STREET: 700 Capital Square, 400 Locust Street  
; CITY: Des Moines

; STATE: Iowa

; COUNTRY: United States

; ZIP: 50309

## ; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: MS-DOS/Microsoft Windows

; SOFTWARE: Microsoft Windows No. 5607914epad

## ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/179,632

; FILING DATE: 07-JAN-1994

## ; CLASSIFICATION: 530

## ; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/079,512

; FILING DATE: 06/18/93

## ; ATTORNEY/AGENT INFORMATION:

; NAME: Roth, Michael J.

; REGISTRATION NUMBER: 29,342

APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-439-817-14

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13  
Db 7 LWVMMQ 12

RESULT 8  
US-08-439-817-30  
Sequence 30, Application US/08439817  
Patent No. 5728802  
GENERAL INFORMATION:  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice  
TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule I (ELAM-1)  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, NV  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,817  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,054  
FILING DATE: 11-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.

REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-439-817-30

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWAMMQ 13  
Db 5 NMLWNMQ 12

RESULT 9  
US-08-485-508-34  
Sequence 34, Application US/08485508  
Patent No. 5786322  
GENERAL INFORMATION:  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice  
TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule I  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, NV  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,508  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,054  
FILING DATE: 11-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 000324-002/1056  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 34:

APPLICANT: Barrett, Ronald W.  
APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
TITLE OF INVENTION: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-156A-14

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13  
:| |||  
Db 7 LWVMMQ 12

RESULT 6  
US-08-390-156A-22  
Sequence 22, Application US/08390156A  
Patent No. 5648458  
GENERAL INFORMATION:  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
TITLE OF INVENTION: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-156A-22

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWAMMQ 13  
:| |||  
Db 5 NMLWNMMQ 12

RESULT 7  
US-08-439-817-14  
Sequence 14, Application US/08439817  
Patent No. 5728802  
GENERAL INFORMATION:  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhlman-Fritsch, Beatrice  
TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule I (ELAM-1)  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, NV  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/439,817  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,054  
FILING DATE: 11-MAY-1994  
PRIOR APPLICATION DATA:



Qy 8 IWAMMQ 13

8 IWAMMQ 13

; APPLICANT: Cwirla, Steven E.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 11.0213 Seconds  
(without alignments)  
84.242 Million cell updates/sec

Title: US-09-831-253F-6  
Sequence: 1 TSLDASIIWAMQW 14

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	40.8	15	4	US-09-255-501-106
2	29	40.8	15	4	US-09-255-501-107
3	28	39.4	12	1	US-08-241-054-34
4	28	39.4	12	1	US-08-241-054-50
5	28	39.4	12	1	US-08-390-156A-14
6	28	39.4	12	1	US-08-390-156A-22
7	28	39.4	12	1	US-08-439-817-14
8	28	39.4	12	1	US-08-439-817-30
9	28	39.4	12	1	US-08-485-508-34
10	28	39.4	12	1	US-08-485-508-50
11	28	39.4	15	4	US-09-255-501-108
12	28	39.4	23	1	US-08-179-632-15
13	28	39.4	23	1	US-08-440-174A-15
14	28	39.4	23	5	PCT-US95-00062-15
15	27	38.0	15	4	US-08-469-141A-32
16	27	38.0	15	4	US-09-073-009-38
17	27	38.0	15	4	US-09-073-010-38
18	27	38.0	15	4	US-09-069-827A-162
19	27	38.0	15	5	PCT-US95-13794-32
20	27	38.0	20	1	US-07-654-839-4
21	27	38.0	20	4	US-09-664-945-39
22	26	36.6	12	1	US-08-241-054-5
23	26	36.6	12	1	US-08-390-156A-76
24	26	36.6	12	1	US-08-439-817-4
25	26	36.6	12	1	US-08-485-508-5
26	26	36.6	12	4	US-09-428-082B-149
27	26	36.6	15	1	US-08-241-054-110

28	26	36.6	15	1	US-08-390-156A-92	Sequence 92, Appl
29	26	36.6	15	1	US-08-439-817-90	Sequence 90, Appl
30	26	36.6	15	1	US-08-485-508-110	Sequence 110, App
31	26	36.6	18	4	US-09-082-358B-16	Sequence 16, Appl
32	26	36.6	20	3	US-08-504-538A-13	Sequence 13, Appl
33	26	36.6	20	3	US-08-464-496-2	Sequence 2, Appli
34	26	36.6	20	3	PCT-US92-07218-2	Sequence 13, Appl
35	26	36.6	20	5	PCT-US95-09307-13	Sequence 13, Appl
36	26	36.6	23	1	US-08-383-753-27	Sequence 27, Appl
37	26	36.6	23	2	US-08-586-772-27	Sequence 27, Appl
38	26	36.6	23	2	US-08-959-512-27	Sequence 27, Appl
39	26	36.6	23	3	US-09-512-983-27	Sequence 10, Appl
40	26	36.6	23	3	US-09-842-164A-10	Sequence 10, Appl
41	25	35.2	12	4	US-09-053-611-29	Sequence 29, Appl
42	25	35.2	12	4	US-09-053-611-19	Sequence 19, Appl
43	25	35.2	15	4	US-09-009-953-244	Sequence 244, App
44	25	35.2	15	4	US-09-073-009-39	Sequence 39, Appl
45	25	35.2	15	4		

ALIGNMENTS

RESULT 1

US-09-255-501-106  
; Sequence 106, Application US/092555501  
; Patent No. 6596525  
; GENERAL INFORMATION:  
; APPLICANT: Batell, David  
; APPLICANT: Harding, Fiona  
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND  
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS  
; FILE REFERENCE: GC527  
; CURRENT APPLICATION NUMBER: US/09/255,501  
; CURRENT FILING DATE: 1999-02-23  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 106  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-255-501-106

Query Match 40.8%; Score 29; DB 4; Length 15;  
Best Local Similarity 40.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 SLDASIIWAM 11  
:|:|:|:  
DB 6 TLQADVLMQM 15

RESULT 2

US-09-255-501-107  
; Sequence 107, Application US/092555501  
; Patent No. 6596525  
; GENERAL INFORMATION:  
; APPLICANT: Batell, David  
; APPLICANT: Harding, Fiona  
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND  
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS  
; FILE REFERENCE: GC527  
; CURRENT APPLICATION NUMBER: US/09/255,501  
; CURRENT FILING DATE: 1999-02-23  
; NUMBER OF SEQ ID NOS: 211  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 107  
; LENGTH: 15  
; TYPE: PRT

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; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 296  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo-sapiens  
US-09-759-130B-296

Query Match 39.4%; Score 28; DB 10; Length 20;  
Best Local Similarity 50.0%; Pred. No. 6.6e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SLDASIIWAM 11  
||:||||:  
Db 5 SLRTVVIWAL 14

## RESULT 15

US-10-189-123-26  
; Sequence 26, Application 'US/10189123  
; Publication No. US20030082586A1  
; GENERAL INFORMATION:  
; APPLICANT: KIRST, Susan J.  
; APPLICANT: HOLTZMAN, Douglas A.  
; APPLICANT: FRASER, Christopher C.  
; APPLICANT: SHARP, John D.  
; APPLICANT: BARNES, Thomas S.  
; TITLE OF INVENTION: ANTIBODIES HAVING DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; FILE REFERENCE: 10147-1103  
; CURRENT APPLICATION NUMBER: US/10/189,123  
; CURRENT FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: US 09/596,194  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 09/342,364  
; PRIOR FILING DATE: 1999-06-29  
; NUMBER OF SEQ ID NOS: 100  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-189-123-26

Query Match 39.4%; Score 28; DB 14; Length 20;  
Best Local Similarity 50.0%; Pred. No. 6.6e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SLDASIIWAM 11  
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Db 5 SLRTVVIWAL 14

Search completed: November 14, 2004, 12:26:59  
Job time : 33.0638 secs

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RESULT 11
US-10-225-567A-1338
; Sequence 1338, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR FILING DATE: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1338
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1338

Query Match      40.8%; Score 29; DB 14; Length 20;
Best Local Similarity 55.6%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 ASIIWAMQ 13
Db      1 ARIIWSLRQ 9

RESULT 12
US-10-280-066-90
; Sequence 90, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR FILING DATE: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 90
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Escherichia coli
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DGI-2-20R-4-E6
US-10-280-066-90

Query Match      40.8%; Score 29; DB 14; Length 20;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 DASIIWAM 11
Db      5 DAGMIWFM 12

RESULT 13
US-10-296-734-1234
; Sequence 1234, Application US/10296734
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; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1234
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: GAGE-1 segment 9
US-10-296-734-1234

Query Match      40.8%; Score 29; DB 15; Length 22;
Best Local Similarity 50.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      7 IIWAMQON 14
Db      3 ILWLLMNN 10

RESULT 14
US-09-759-130B-296
; Sequence 296, Application US/09759130B
; Publication No. US20030022279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; FILE REFERENCE: MPI00-535OMNIM
; CURRENT APPLICATION NUMBER: US/09/759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
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; SEQ ID NO 294  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homosapiens  
US-10-657-022-294

Query Match 40.8%; Score 29; DB 16; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14  
| : | : |  
Db 2 ILWLLMNN 9

RESULT 7  
US-10-657-022-299  
; Sequence 299, Application US/10657022  
; Publication No. US20040180354A1  
; GENERAL INFORMATION:  
; APPLICANT: Simard, John J. L.  
; APPLICANT: Diamond, David C.  
; APPLICANT: Liu, Liping  
; APPLICANT: Liu, Zheng  
; TITLE OF INVENTION: EPIPTOPE SEQUENCES  
; FILE REFERENCE: MANNK.032A  
; CURRENT APPLICATION NUMBER: US/10/657,022  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: 60/409123  
; PRIOR FILING DATE: 2002-09-06  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; NUMBER OF SEQ ID NOS: 610  
; SEQ ID NO 299  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homosapiens  
US-10-657-022-299

Query Match 40.8%; Score 29; DB 16; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14  
| : | : |  
Db 1 ILWLLMNN 8

RESULT 8  
US-10-657-022-301  
; Sequence 301, Application US/10657022  
; Publication No. US20040180354A1  
; GENERAL INFORMATION:  
; APPLICANT: Simard, John J. L.  
; APPLICANT: Diamond, David C.  
; APPLICANT: Liu, Liping  
; APPLICANT: Liu, Zheng  
; TITLE OF INVENTION: EPIPTOPE SEQUENCES  
; FILE REFERENCE: MANNK.032A  
; CURRENT APPLICATION NUMBER: US/10/657,022  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: 60/409123  
; PRIOR FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 610  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 301  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homosapiens  
US-10-657-022-301

Query Match 40.8%; Score 29; DB 16; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14  
| : | : |  
Db 2 ILWLLMNN 9

RESULT 9  
US-10-176-791A-76  
; Sequence 76, Application US/10176791A  
; Publication No. US20030237101A1  
; GENERAL INFORMATION:  
; APPLICANT: IMHOF, BEAT A.  
; APPLICANT: WEHRLE-HALLER, BERNHARD M.  
; TITLE OF INVENTION: Basolateral Sorting Signal and  
; TITLE OF INVENTION: Inhibitors Thereof  
; FILE REFERENCE: 50275/002001  
; CURRENT APPLICATION NUMBER: US/10/176,791A  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: PCT/EP00/13141  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: PCT/CH99/00624  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 76  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Junction of Tac-Tyr Chimera  
US-10-176-791A-76

Query Match 40.8%; Score 29; DB 14; Length 17;  
Best Local Similarity 66.7%; Pred. No. 3.7e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSLDASIIW 9  
| : | : | : | : | : |  
Db 5 TDLQASRIW 13

RESULT 10  
US-10-657-022-606  
; Sequence 606, Application US/10657022  
; Publication No. US20040180354A1  
; GENERAL INFORMATION:  
; APPLICANT: Simard, John J. L.  
; APPLICANT: Diamond, David C.  
; APPLICANT: Liu, Liping  
; APPLICANT: Liu, Zheng  
; TITLE OF INVENTION: EPIPTOPE SEQUENCES  
; FILE REFERENCE: MANNK.032A  
; CURRENT APPLICATION NUMBER: US/10/657,022  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: 60/409123  
; PRIOR FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 610  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 606  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homosapiens  
US-10-657-022-606

Query Match 40.8%; Score 29; DB 16; Length 18;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIWAMMON 14  
| : | : | : | : | : |  
Db 6 ILWLLMNN 13

Publication No. US2003014492A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et. al  
; TITLE OF INVENTION: 101 Human Secreted Proteins  
; FILE REFERENCE: PZ017P1  
; CURRENT APPLICATION NUMBER: US/10/195,730  
; CURRENT FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: US/09/281,976  
; PRIOR FILING DATE: 1999-03-31  
; PRIOR APPLICATION NUMBER: 60/060,837  
; PRIOR FILING DATE: 1997-10-02  
; PRIOR APPLICATION NUMBER: 60/060,862  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 390  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 319  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-195-730-319

Query Match 47.9%; Score 34; DB 14; Length 22;  
Best Local Similarity 50.0%; Pred. No. 65;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASIWA 10  
:|:|:|:  
Db 4 STLDRSVIS 13

## RESULT 3

US-10-799-747-319  
; Sequence 319, Application US/10799747  
; Publication No. US20040157258A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et. al  
; TITLE OF INVENTION: 101 Human Secreted Proteins  
; FILE REFERENCE: PZ017P1  
; CURRENT APPLICATION NUMBER: US/10/799,747  
; CURRENT FILING DATE: 2004-03-15  
; PRIOR APPLICATION NUMBER: US/10/195,730  
; PRIOR FILING DATE: 2002-07-16  
; PRIOR APPLICATION NUMBER: US/09/281,976  
; PRIOR FILING DATE: 1999-03-31  
; PRIOR APPLICATION NUMBER: 60/060,837  
; PRIOR FILING DATE: 1997-10-02  
; PRIOR APPLICATION NUMBER: 60/060,862  
; PRIOR FILING DATE: 1997-10-02  
; NUMBER OF SEQ ID NOS: 390  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 319  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-799-747-319

Query Match 47.9%; Score 34; DB 16; Length 22;  
Best Local Similarity 50.0%; Pred. No. 65;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASIWA 10  
:|:|:|:  
Db 4 STLDRSVIS 13

## RESULT 4

US-10-657-022-295  
; Sequence 295, Application US/10657022  
; Publication No. US20040180354A1  
; GENERAL INFORMATION:  
; APPLICANT: Simard, John J. L.  
; APPLICANT: Diamond, David C.  
; APPLICANT: Liu, Liping

; APPLICANT: Liu, Zheng  
; TITLE OF INVENTION: EPITOPE SEQUENCES  
; FILE REFERENCE: MANNK.032A  
; CURRENT APPLICATION NUMBER: US/10/657,022  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: 60/409123  
; PRIOR FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 610  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 295  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homosapiens  
US-10-657-022-295

Query Match 40.8%; Score 29; DB 16; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIVAMQON 14  
|:|:|:  
Db 1 ILWLLMNN 8

## RESULT 5

US-10-657-022-300  
; Sequence 300, Application US/10657022  
; Publication No. US20040180354A1  
; GENERAL INFORMATION:  
; APPLICANT: Simard, John J. L.  
; APPLICANT: Diamond, David C.  
; APPLICANT: Liu, Liping  
; APPLICANT: Liu, Zheng  
; TITLE OF INVENTION: EPITOPE SEQUENCES  
; FILE REFERENCE: MANNK.032A  
; CURRENT APPLICATION NUMBER: US/10/657,022  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: 60/409123  
; PRIOR FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 610  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 300  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homosapiens  
US-10-657-022-300

Query Match 40.8%; Score 29; DB 16; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIVAMQON 14  
|:|:|:  
Db 1 ILWLLMNN 8

## RESULT 6

US-10-657-022-294  
; Sequence 294, Application US/10657022  
; Publication No. US20040180354A1  
; GENERAL INFORMATION:  
; APPLICANT: Simard, John J. L.  
; APPLICANT: Diamond, David C.  
; APPLICANT: Liu, Liping  
; APPLICANT: Liu, Zheng  
; TITLE OF INVENTION: EPITOPE SEQUENCES  
; FILE REFERENCE: MANNK.032A  
; CURRENT APPLICATION NUMBER: US/10/657,022  
; CURRENT FILING DATE: 2003-09-04  
; PRIOR APPLICATION NUMBER: 60/409123  
; PRIOR FILING DATE: 2002-09-06  
; NUMBER OF SEQ ID NOS: 610  
; SOFTWARE: FastSeq for Windows Version 4.0

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Query Match          50.7%; Score 36; DB 16; Length 22;
Best Local Similarity 38.5%; Pred. No. 29;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1  TSLDASIIWAMMQ 13
      ||| | | | | | | | | | | | | | | |
Db      1  TSRDMSLLWELLE 13

RESULT 2
US-10-195-730-319
Sequence 319, Application US/10195730

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Pending Appl.  
Interference  
Searches

Query Match 32.4%; Score 23; DB 2; Length 23;  
 Best Local Similarity 25.0%; Pred. No. 5.3e+03;  
 Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TSLDASIIWMM 12  
 | : : : : :  
 Db 12 TIINRLFWAI 23

RESULT 15

Q9UEK9 PRELIMINARY; PRT; 23 AA.  
 AC Q9UEK9;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Keratin (Fragment).  
 GN Name-KRT5;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Blood;  
 RX MEDLINE=96121606; PubMed=8595431;  
 RA Matsuki M., Hashimoto K., Yoshikawa K., Yasuno H., Yamanishi K.;  
 RT "Epidermolysis bullosa simplex (Weber-Cockayne) associated with a  
 RT novel missense mutation of Asp328 to Val in Linker 12 domain of  
 RT keratin 5.";  
 RL Hum. Mol. Genet. 4:1999-2000(1995).  
 DR EMBL; D50666; BAA09320.1; -;  
 DR GO; GO:0005882; C:intermediate filament; IEA.  
 KW Keratin.  
 FT NON TER 1  
 FT NON TER 23  
 SQ SEQUENCE 23 AA; 2546 MW; 6BA5FFB4FC7E511E CRC64;

Query Match 32.4%; Score 23; DB 2; Length 23;  
 Best Local Similarity 36.4%; Pred. No. 5.3e+03;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 DASIIWMMON 14  
 | : : : : :  
 Db 5 DTSVLSDMNN 15

Search completed: November 14, 2004, 12:07:34  
 Job time : 38.383 secs

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AC Q9S8L0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE CUSATIVIN (Fragment).
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE.
RX MEDLINE=95003967; PubMed=7765423;
RA Rojo M.A., Arias F.J., Iglesias R., Ferreras J.M., Munoz R.,
RA Escarmis C., Soriano F., Lopez-Pando J., Mendez E., Girbes T.,
RL Planta 194:328-338(1994).
SQ SEQUENCE 21 AA; 2347 MW; FCD26FB44DB60ACC CRC64;

Query Match 32.4%; Score 23; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 4.8e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 DASIIW 9
Db |::|
7 DLNVVW 12

RESULT 12
Q38287 PRELIMINARY; PRT; 22 AA.
ID Q38287
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E10 protein.
GN Name=e10;
OS Lactococcus bacteriophage c2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
OC c2-like viruses.
OX NCBI_TaxID=31537;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94036453; PubMed=8221377;
RA Ward L.J., Beresford T.P., Lubbers M.W., Jarvis B.D., Jarvis A.W.;
RT "Sequence analysis of the lysin gene region of the prolate lactococcal
RT bacteriophage c2.";
RL Can. J. Microbiol. 39:767-774(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95115663; PubMed=7816023;
RA Lubbers M.W., Ward L.J., Beresford T.P., Jarvis B.D., Jarvis A.W.;
RT "Sequencing and analysis of the cos region of the lactococcal
RT bacteriophage c2.";
RL Mol. Gen. Genet. 245:160-166(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96086019; PubMed=8534101;
RA Lubbers M.W., Waterfield N.R., Beresford T.P., Le Page R.W.,
RA Jarvis A.W.;
RT "Sequencing and analysis of the prolate-headed lactococcal
RT bacteriophage c2 genome and identification of the structural genes.";
RL Appl. Environ. Microbiol. 61:4348-4356(1995).
DR EMBL; L48605; AAA92170.1; -.
SQ SEQUENCE 22 AA; 2631 MW; 1DFF1FA427364C93 CRC64;

Query Match 32.4%; Score 23; DB 2; Length 22;
Best Local Similarity 18.2%; Pred. No. 5e+03;
Matches 2; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 LDASIIWMMQ 13
Db ::|::|
10 IETLILWLVLE 20

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```

RESULT 13
Q80GP4 PRELIMINARY; PRT; 22 AA.
ID Q80GP4
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Gene 7.
GN Name=gene 7;
OS Human rotavirus A.
OC Viruses; dsRNA viruses; Reoviridae; Rotavirus.
OX NCBI_TaxID=10941;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=wa;
RX MEDLINE=92352338; PubMed=1339264;
RA Mendez E., Arias C.F., Lopez S.;
RT "Genomic rearrangements in human rotavirus strain wa; analysis of
RT rearranged RNA segment 7.";
RL Arch. Virol. 125:331-338(1992).
DR EMBL; S41238; AAP13880.1; -.
DR GO; GO:0003723; rRNA binding; IEA.
DR InterPro; IPR002873; Rota_NSP3.
SQ SEQUENCE 22 AA; 2242 MW; 22CC217A1F6BD3AA CRC64;

Query Match 32.4%; Score 23; DB 2; Length 22;
Best Local Similarity 40.0%; Pred. No. 5e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLDASIIWA 10
Db ||::|
8 TSFEAAVVAA 17

RESULT 14
Q7S8F9 PRELIMINARY; PRT; 23 AA.
ID Q7S8F9
AC Q7S8F9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU05174.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kotha G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamyssekis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glass I., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000232; EAA32642.1; -.
SQ SEQUENCE 23 AA; 2598 MW; 7EA10217A542BCC5 CRC64;

```

Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DASIIW 9  
| | | | |  
Db 10 DESVLW 15

RESULT 7  
Q9S818 PRELIMINARY; PRT; 18 AA.  
AC Q9S818  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE 40 kDa PI 8.5 ABCSSISIC acid-induced protein (Fragment).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoidae; Oryzeae; Oryza.  
OX NCBI\_TaxID=4530;  
[1]  
RN SEQUENCE.  
RP MEDLINE=95175599; PubMed=7870812;  
RX Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;  
RA "Molecular and physiological responses to abscisic acid and salts in  
RT roots of salt-sensitive and salt-tolerant indica rice varieties.";  
RL Plant Physiol. 107:177-186(1995).  
DR Gramine; Q9S818; -  
SQ SEQUENCE 18 AA; 2097 MW; 146450D9A97E6D83 CRC64;

Query Match 35.2%; Score 25; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DASIIW 9  
| | | | |  
Db 10 DESVLW 15

RESULT 8  
Q9ZV83 PRELIMINARY; PRT; 18 AA.  
AC Q9ZV83  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome oxidase II (Fragment).  
OS Xylocopa virginica (Carpenter bee).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
OC Apidae; Xylocopa.  
OX NCBI\_TaxID=28638;  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=95152621; PubMed=10028295;  
RX Downton M., Austin A.D.;  
RA "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in  
RT the hymenoptera.";  
RL Mol. Biol. Evol. 16:298-309(1999).  
DR ENBL; AF082318; AAD1778.1; -  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 18 AA; 2202 MW; F695A5FD1C36CA16 CRC64;

Query Match 33.8%; Score 24; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.6e+03;  
Matches 7; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 1 TSLDASIIWAMQON 14  
| | | | |

Db 6 TSYDLFINW--MKN 17

RESULT 9  
Q69074 PRELIMINARY; PRT; 17 AA.  
AC Q69074  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HSV-1 glycoprotein C (Fragment).  
OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).  
OC Viruses; GADNA viruses; no RNA stage; Herpesviridae;  
OC Alphaherpesvirinae; Simplexvirus.  
OX NCBI\_TaxID=10298;  
[1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=87089706; PubMed=3025606;  
RX Homa F.L., Otal T.M., Glorioso J.C., Levine M.;  
RA "Transcriptional control signals of a herpes simplex virus type 1 late  
RT (gamma-2) gene lie within bases -34 to +124 relative to the 5'  
RT terminus of the mRNA.";  
RL Mol. Cell. Biol. 6:3652-3666(1986).  
DR ENBL; M14128; AAA45784.1; -  
FT NON TER 17  
SQ SEQUENCE 17 AA; 1868 MW; B4ED3CEC6ABAEC92 CRC64;

Query Match 32.4%; Score 23; DB 2; Length 17;  
Best Local Similarity 25.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIWMM 12  
| | | | |  
Db 9 AVVLMSLL 16

RESULT 10  
Q7MOC6 PRELIMINARY; PRT; 19 AA.  
AC Q7MOC6  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Cytochrome P450-C-M/F, hepatic (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
[1]  
RN SEQUENCE.  
RP MEDLINE=88163652; PubMed=3349056;  
RX Sugita O., Sassa S., Miyairi S., Fishman J., Kubota I., Noguchi T.,  
RA Kappas A.;  
RT "Cytochrome P-450-C-M/F, a new constitutive form of microsomal  
RT cytochrome P-450 in male and female rat liver with estrogen 2- and 16-  
RT alpha-hydroxylase activity.";  
RL Biochemistry 27:678-686(1988).  
DR FIR; A28702; A28702.  
FT NON TER 19  
SQ SEQUENCE 19 AA; 2242 MW; FF1DD2C9CDF9C8FA CRC64;

Query Match 32.4%; Score 23; DB 2; Length 19;  
Best Local Similarity 60.0%; Pred. No. 4.3e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWAVM 12  
| | | | |  
Db 8 LWAVM 12

RESULT 11  
Q9S8L0 PRELIMINARY; PRT; 21 AA.  
ID Q9S8L0

DR GO: GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 19 AA; 2291 MW; B964CCC7FDAC36C3 CRC64;

Query Match 38.0%; Score 27; DB 2; Length 19;  
Best Local Similarity 42.9%; Pred. No. 7.4e+02;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 TSLDASIIWAMQON 14  
|||:|:|:|:  
DB 6 TSLNSFFNWKMFN 19

RESULT 3  
Q9TWP7 PRELIMINARY; PRT; 20 AA.  
AC Q9TWP7  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE Cathepsin B-like cysteine protease (Fragment).  
OS Leishmania mexicana.  
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
OX NCBI\_TaxID=5665;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94187801; PubMed=8139620;  
RA Robertson C.D.; Coombs G.H.;  
RT "Cathepsin B-like cysteine proteases of Leishmania mexicana."  
RL Mol. Biochem. Parasitol. 62:271-279(1993).  
SQ SEQUENCE 20 AA; 2203 MW; FE1A260FA1DBE41F CRC64;

Query Match 38.0%; Score 27; DB 2; Length 20;  
Best Local Similarity 60.0%; Pred. No. 7.8e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 SLDASIIWAM 11  
|||:|:|:|:  
DB 5 SFDASEKQPM 14

RESULT 4  
Q8ZS29 PRELIMINARY; PRT; 18 AA.  
AC Q8ZS29  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein PAE3501a.  
GN Name=PAE3501a;  
OS Pyrobaculum aerophilum.  
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
OC Thermoproteaceae; Pyrobaculum.  
OX NCBI\_TaxID=13773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IM2 / DSM 7523;  
RX MEDLINE=21664397; PubMed=11792869;  
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
RA Miller J.H.;  
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
aerophilum";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).  
RL EMBL; AE009934; AL64964.1; -;  
RW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 18 AA; 2262 MW; BCF4D6D923A98943 CRC64;

Query Match 36.6%; Score 26; DB 2; Length 18;  
Best Local Similarity 40.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 LDASIIWAM 12

DB 1 MDESIVPIV 10  
|||:|:|:|:

RESULT 5  
Q25012 PRELIMINARY; PRT; 22 AA.  
AC Q25012  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein HP0225.  
GN OrderedLocNames=HP0225;  
OS Helicobacter pylori (Campylobacter pylori).  
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
OC Helicobacteraceae; Helicobacter.  
OX NCBI\_TaxID=210;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=26695 / ATCC 700392;  
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;  
RA Tomb J.-P., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,  
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,  
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,  
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,  
RA Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,  
RA Hickey E.K., Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D.,  
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,  
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,  
RA Smith H.O., Fraser C.M., Venter J.C.;  
RT "The complete genome sequence of the gastric pathogen Helicobacter  
pylori";  
RL Nature 388:539-547(1997).  
DR EMBL; AE000542; RAD07297.1; -;  
DR FIR; A64548; A64548.  
DR TIGR; HP0225; -;  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 22 AA; 2624 MW; 9B98024022F049BE CRC64;

Query Match 36.6%; Score 26; DB 2; Length 22;  
Best Local Similarity 25.0%; Pred. No. 1.3e+03;  
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 7 IIVAMQON 14  
|||:|:|:|:  
DB 9 VLVWILKN 16

RESULT 6  
Q9S817 PRELIMINARY; PRT; 18 AA.  
AC Q9S817  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE 40 kDa PI 8.5 ABSCISSIC acid-induced histidine rich protein  
DE (Fragment).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartioideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95175599; PubMed=7870812;  
RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;  
RT "Molecular and physiological responses to abscisic acid and salts in  
RT roots of salt-sensitive and salt-tolerant Indica rice varieties.";  
RL Plant Physiol. 107:177-186(1995).  
DR Gramene; Q9S817; -;  
SQ SEQUENCE 18 AA; 2094 MW; OCD245DB237E7520 CRC64;

Query Match 35.2%; Score 25; DB 2; Length 18;

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 37.383 Seconds  
(without alignments)  
215.479 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71

Sequence: 1 TSLDASIIWAMQN 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot 02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	39.4	23	2	Q9UR71
2	27	38.0	19	2	Q9ZYW5
3	27	38.0	20	2	Q9TWP7
4	26	36.6	18	2	Q8ZS29
5	26	36.6	22	2	O25012
6	25	35.2	18	2	Q9S817
7	25	35.2	18	2	Q9S818
8	24	33.8	18	2	Q9ZY83
9	23	32.4	17	2	Q69074
10	23	32.4	19	2	Q7M0C6
11	23	32.4	21	2	Q9S8L0
12	23	32.4	22	2	Q38287
13	23	32.4	22	2	Q80GP4
14	23	32.4	23	2	Q7S8F9
15	23	32.4	23	2	Q9UEK9
16	23	32.4	23	2	Q8HA22
17	23	32.4	23	2	Q07939
18	22	31.0	10	2	Q9ESU5
19	22	31.0	11	2	Q77894
20	22	31.0	11	2	Q77898
21	22	31.0	11	2	Q7MIU2
22	22	31.0	14	2	Q99902
23	22	31.0	15	2	Q8HIF6
24	22	31.0	15	2	Q8HIF8
25	22	31.0	17	1	LPW_AZOBR
26	22	31.0	17	2	Q6LAP9
27	22	31.0	17	2	CAA65527
28	22	31.0	19	2	Q7S645
29	22	31.0	19	2	Q8W128
30	22	31.0	19	2	Q9QV70
31	22	31.0	20	2	Q49132

32 22 31.0 21 2 Q6LERS  
33 22 31.0 21 2 Q9PRQ1  
34 22 31.0 21 2 BAA00902  
35 22 31.0 22 2 Q6YID4  
36 22 31.0 22 2 AAN52159  
37 22 31.0 23 2 Q8NPF7  
38 21 29.6 8 2 Q86SL0  
39 21 29.6 10 1 APE\_CAPGI  
40 21 29.6 10 2 Q7MIJ3  
41 21 29.6 11 2 Q77895  
42 21 29.6 14 2 Q9RSQ6  
43 21 29.6 15 2 Q8SL36  
44 21 29.6 16 2 Q9TWC0  
45 21 29.6 16 2 Q9AXW2

Q6LERS homo sapien  
Q9PRQ1 oncorhynchu  
BAA00902 homo sapi  
Q6YID4 theromyzo  
AAN52159 theromyzo  
Q8NPF7 homo sapien  
Q86SL0 homo sapien  
P80474 capnocytoph  
Q7MIJ3 spinacia ol  
Q77895 oreochromis  
Q9RSQ6 burkholderi  
Q8SL36 monanthes i  
Q9TWC0 acanthamoeb  
Q9AXW2 brassica na

## ALIGNMENTS

## RESULT 1

Q9UR71 PRELIMINARY; PRT; 23 AA.  
ID Q9UR71 AC Q9UR71;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE 5'-nucleotide-forming nuclease (Fragment).  
OS Lentinula edodes (Shiitake mushroom) (Lentinus edodes).  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Agaricales; Tricholomataceae; Lentinula.  
OX NCBI\_TaxID=5353;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=95337563; PubMed=7613009;  
RX Kobayashi H., Inokuchi N., Koyama T., Tomita M., Irie M.;  
RT "Purification and characterization of the 2nd 5'-nucleotide-forming  
RT nuclease from Lentinus edodes";  
RL Biosci. Biotechnol. Biochem. 59:1169-1171(1995).  
DR PIR; PC4030; PC4030.  
DR InterPro; IPR008947; PLC\_Nuclease.  
SQ SEQUENCE 23 AA; 2535 MW; 978082B3B161FCC6 CRC64;

Query Match 39.4%; Score 28; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 5.9e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SLDASIIW 9  
DB 16 ALDPSFVW 23

## RESULT 2

Q9ZYW5 PRELIMINARY; PRT; 19 AA.  
ID Q9ZYW5 AC Q9ZYW5;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome oxidase II (Fragment).  
OS Jarra phorocantha.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;  
OC Braconidae; Doryctinae; Jarra.  
OX NCBI\_TaxID=64830;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=99152621; PubMed=10028295;  
RA Downton M., Austin A.D.;  
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in  
RT the hymenoptera";  
RL Mol. Biol. Evol. 16:298-309(1999).  
DR EMBL; AF034596; AAC79744.1; -.

TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-485-508-50

Query Match 39.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIWAMMQ 13  
: : : : :  
Db 5 NMLWMMQ 12

RESULT 9  
US-08-241-054-5  
; Sequence 5, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule 1  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gerald P. Swiss  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-241-054-5

Query Match 36.6%; Score 26; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13  
: : : : :  
Db 7 LWDMMQ 12

RESULT 10  
US-08-390-156A-76  
; Sequence 76, Application US/08390156A  
; Patent No. 5648458  
; GENERAL INFORMATION:  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Dower, William J.  
; APPLICANT: Martens, Christine L.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to  
; TITLE OF INVENTION: ELAM-1  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, N.V.  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/390,156A  
; FILING DATE: 16-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald P.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 1023.1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 76:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-156A-76

Query Match 36.6%; Score 26; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13  
: : : : :  
Db 7 LWDMMQ 12

RESULT 11  
US-08-439-817-4  
; Sequence 4, Application US/08439817  
; Patent No. 5728802  
; GENERAL INFORMATION:

APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven B.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice  
TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule I (ELAM-1)  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, NV  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/439,817  
FILING DATE: 12-MAY-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,054  
FILING DATE: 11-MAY-1994  
PRIOR APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-439-817-4

Query Match 36.6%; Score 26; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMQ 13  
DB 7 LWDMMQ 12

RESULT 12  
US-08-485-508-5  
Sequence 5, Application US/08485508  
Patent No. 5786322  
GENERAL INFORMATION:  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven B.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice

TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule I  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, NV  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION NUMBER: US/08/485,508  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 000324-002/1056  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-485-508-5

Query Match 36.6%; Score 26; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMQ 13  
DB 7 LWDMMQ 12

RESULT 13  
US-09-428-082B-149  
Sequence 149, Application US/09428082B  
Patent No. 6660843  
GENERAL INFORMATION:  
APPLICANT: FEIGE, ULRICH  
APPLICANT: LIU, CHUAN-FA  
APPLICANT: CHEETHAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/09/428,082B  
CURRENT FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 149



; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: SELECTIN ANTAGONIST PEPTIDE  
US-09-428-082B-149

Query Match 36.6%; Score 26; DB 4; Length 12;  
Best Local Similarity 66.7%; Pred. No. 2.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IWAMMQ 13  
Db 7 LWDMMQ 12

## RESULT 14

US-09-842-164A-10  
; Sequence 10, Application US/09842164A  
; Patent No. 6544754  
; GENERAL INFORMATION:  
; APPLICANT: INOUE, SATOSHI  
; TITLE OF INVENTION: LUCIFERASE AND PHOTOPROTEIN  
; FILE REFERENCE: 206497US0  
; CURRENT APPLICATION NUMBER: US/09/842,164A  
; PRIOR FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: JP 2000-125053  
; PRIOR FILING DATE: 2000-04-26  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Oplophorus gracilorostris  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (11)..(11)  
; OTHER INFORMATION: Xaa = any amino acid  
US-09-842-164A-10

Query Match 35.2%; Score 25; DB 4; Length 12;  
Best Local Similarity 41.7%; Pred. No. 4e+02;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SLDASIIWAMQ 13  
Db 1 NLDPAVFHAMXQ 12

## RESULT 15

US-09-053-611-29  
; Sequence 29, Application US/09053611  
; Patent No. 6410245  
; GENERAL INFORMATION:  
; APPLICANT: No. 6410245throp, Jeffrey P.  
; APPLICANT: Hart, Charles P.  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Glaxo Group Limited  
; TITLE OF INVENTION: Compositions and Methods for Detecting Ligand Dependent  
; FILE REFERENCE: 2064  
; CURRENT APPLICATION NUMBER: US/09/053,611  
; CURRENT FILING DATE: 1998-04-01  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 29  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Selected clone  
US-09-053-611-29

Query Match 35.2%; Score 25; DB 4; Length 14;  
Best Local Similarity 42.9%; Pred. No. 4.7e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 SIIWAMM 12  
Db 5 SLLWKML 11

Search completed: November 14, 2004, 13:46:47  
Job time : 27.5 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 14, 2004, 11:57:25 ; Search time 8.6383 Seconds  
(without alignments)  
155.938 Million cell updates/sec

Title: US-09-831-253F-6  
Perfect score: 71  
Sequence: 1 TSLDASIIWMMQN 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	39.4	23	2 PC4030	rRNA endonuclease
2	26	36.6	14	2 A35105	hypothetical prote
3	26	36.6	22	2 A64548	hypothetical prote
4	24	33.8	22	2 S07966	T-cell receptor be
5	23	32.4	19	2 A28702	cytochrome P450-C
6	23	32.4	20	2 PH1326	Ig heavy chain DJ
7	23	32.4	23	2 T03261	glutamate-ammonia
8	22	31.0	11	2 PQ0731	unidentified 5.7/3
9	22	31.0	12	2 S69123	proton-translocati
10	22	31.0	19	2 B46592	lactase-phlorizin
11	22	31.0	20	2 A44921	hydroxypyruvate re
12	22	31.0	21	2 S62893	cold-inducible pro
13	22	31.0	22	2 PQ0007	killer toxin - yea
14	21	29.6	7	2 PT0586	T-cell receptor be
15	21	29.6	10	2 S69159	cystathionine gamm
16	21	29.6	12	2 I64829	gene HEXA protein
17	21	29.6	14	2 PH1327	Ig heavy chain DJ
18	21	29.6	14	2 A44920	2-halobenzoate 1,2
19	21	29.6	19	2 I49422	L-lactate dehydrog
20	21	29.6	20	2 DIRT	dental fluid tra
21	20	28.2	14	2 PH1769	T cell receptor al
22	20	28.2	15	2 A45103	7 alpha-hydroxy-4-
23	20	28.2	19	2 S61279	nikkomycin synthe
24	20	28.2	19	2 S29212	protein C - oat (f
25	20	28.2	20	2 S50175	kallikrein (PK-120
26	20	28.2	21	2 B53035	probable bacteriop
27	20	28.2	22	2 I58038	MHC class I transp
28	20	28.2	23	2 S34739	trans-cinnamate 4-
29	19.5	27.5	21	2 S01816	hemoglobin BIV - t

30 19 26.8 6 2 PT0519 T-cell receptor be  
31 19 26.8 7 2 S09652 hypothetical prote  
32 19 26.8 7 2 PH1602 Ig H chain V-D-J r  
33 19 26.8 10 2 S66248 processing enzyme,  
34 19 26.8 14 2 PH1768 T cell receptor al  
35 19 26.8 15 2 PH0782 T-cell receptor al  
36 19 26.8 15 2 PL0109 complement factor  
37 19 26.8 16 2 A46236 transforming prote  
38 19 26.8 20 2 AC0269 probable trp opero  
39 19 26.8 21 2 S23361 protein-tyrosine k  
40 19 26.8 21 2 A44139 RNA-polymerase-  
41 18 25.4 6 2 S66195 alcohol dehydrogen  
42 18 25.4 9 2 S13889 phosphoenolpyruvat  
43 18 25.4 10 2 D61440 polygalacturonase  
44 18 25.4 11 2 S66196 alcohol dehydrogen  
45 18 25.4 12 2 PN0581 tyrosine 3-monoxy

ALIGNMENTS

RESULT 1

PC4030  
rRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)  
N;Alternate names: nuclease Le3  
C;Species: Lentinula edodes (shiitake mushroom)  
C;Date: 21-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: PC4030

R;Kobayashi, H.; Inokuchi, N.; Koyama, T.; Tomita, M.; Irie, M.  
Bioeci. Biotechnol. Biochem. 59, 1169-1171, 1995  
A;Title: Purification and characterization of the 2nd 5'-nucleotide-forming nuclease fr.  
A;Reference number: PC4030; MUID:95337563; PMID:7613009  
A;Accession: PC4030

A;Molecule type: DNA

A;Residues: 1-23 <KOB>

A;Cross-references: UNIPROT:Q9UR71

C;Comment: This enzyme has 3'-nucleotidase activity.

C;Keywords: endonuclease; hydrolase

Query Match 39.4%; Score 28; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 81;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SLDASIIW 9  
:|:|:|:  
Db 16 ALDPSFW 23

RESULT 2

A35105  
hypothetical protein - Neurospora crassa mitochondrion (fragment)

C;Species: mitochondrion Neurospora crassa

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 07-Dec-1999

C;Accession: A35105

R;Saville, B.J.; Collins, R.A.

Cell 61, 685-696, 1990

A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora

A;Reference number: A35105; MUID:90263093; PMID:2160856

A;Accession: A35105

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-14 <SAV>

C;Genetics:

A;Genome: mitochondrion

A;Genetic code: SGC3

C;Keywords: mitochondrion

Query Match 36.6%; Score 26; DB 2; Length 14;  
Best Local Similarity 37.5%; Pred. No. 11e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 SIIWMMQ 13  
|:|:|:  
|:|:|:

Db 2 SFLWTLQ 9

RESULT 3  
A:Species: Helicobacter pylori (strain 26695)  
C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: A64548  
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne-son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.  
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.  
A:Reference number: A64520; MUID:97394467; PMID:9252185  
A:Accession: A64548  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-22 <TOM>  
A:Cross-references: UNIPROT:O25012; GB:AE000542; GB:AE000511; NID:G2313310; PIDN:AAD0729

Query Match 36.6%; Score 26; DB 2; Length 22;  
Best Local Similarity 25.0%; Pred. No. 1.8e+02;  
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 7 IIVMMQN 14  
: : : : :  
Db 9 VLVVILKN 16

RESULT 4  
S07966  
T-cell receptor beta chain V-D-J region (clone 15 BEM 21) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
A:Variety: strain C57BL/10  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 23-Jul-1999  
C:Accession: S07966; S08057  
R:Bill, J.; Yaguee, J.; Appel, V.B.; White, J.; Horn, G.; Erlich, H.A.; Palmer, E. J. Exp. Med. 169, 115-133, 1989  
A:Title: Molecular genetic analysis of 178 I-A(bm12)-reactive T cells.  
A:Reference number: S05590; MUID:89080476; PMID:2783331  
A:Accession: S07966  
A:Molecule type: mRNA  
A:Residues: 1-22 <BIL>  
A:Cross-references: EMBL:X14936  
A:Note: this sequence was determined from the differentiated gene  
R:Bill, J.  
submitted to the EMBL Data Library, April 1989  
A:Reference number: S08057  
A:Accession: S08057  
A:Molecule type: mRNA  
A:Residues: 1-19, 21-22 <BIW>  
A:Cross-references: EMBL:X14936; PIDN:CAA33062.1; PID:G773251  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor  
F;1-4/Domain: V region (V-beta 14) (fragment) #status predicted <VRE>  
F;6-7/Domain: D region #status predicted <DRE>  
F;8-21/Domain: J region (J-beta 1.1) #status predicted <JRE>

Query Match 33.8%; Score 24; DB 2; Length 22;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 WAMQON 14  
: : : : :  
Db 3 WSLRQN 8

RESULT 5  
A28702  
cytochrome P450-C-M/F, hepatic - rat (fragment)  
N:Contains: oxidoreductase (EC 1.-.-.-)

C:Species: Rattus norvegicus (Norway rat)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: A28702  
R:Sugita, O.; Sassa, S.; Miyairi, S.; Fishman, J.; Kubota, I.; Noguchi, T.; Kappas, A. Biochemistry 27, 678-686, 1988  
A:Title: Cytochrome P-450-C-M/F, a new constitutive form of microsomal cytochrome P-450  
A:Reference number: A28702; MUID:88163652; PMID:3349056  
A:Accession: A28702  
A:Molecule type: protein  
A:Residues: 1-19 <SUG>  
A:Cross-references: UNIPROT:Q7MOC6  
C:Genetics:  
A:Gene: CYP2D  
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
C:Keywords: electron transfer; heme; liver; monoxygenase; oxidoreductase; transmembrane

Query Match 32.4%; Score 23; DB 2; Length 19;  
Best Local Similarity 60.0%; Pred. No. 5.7e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWAMM 12  
: : : : :  
Db 8 LWAVM 12

RESULT 6  
PH1326  
Ig heavy chain DJ region (clone C515-116) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C:Accession: PH1326  
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G. J. Exp. Med. 176, 1577-1581, 1992  
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma  
A:Reference number: PH1302; MUID:93094761; PMID:1460419  
A:Accession: PH1326  
A:Molecule type: DNA  
A:Residues: 1-20 <WAS>  
C:Keywords: heterotetramer; immunoglobulin

Query Match 32.4%; Score 23; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 6e+02;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 SLDASIIWMMQ 13  
: : : : :  
Db 9 SNDAFDIWGQGQ 20

RESULT 7  
T03261  
glutamate-ammonia ligase (EC 6.3.1.2), cytosolic - common tobacco (fragment)  
N:Alternate names: glutamine synthetase  
C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T03261  
R:Hirel, B.; Marsollier, M.C.; Hoarau, A.; Hoarau, J.; Brangeon, J.; Schafer, R.; Verma, Plant Mol. Biol. 20, 207-218, 1992  
A:Title: Forcing expression of a soybean root glutamine synthetase gene in tobacco leaves  
A:Reference number: Z14867; MUID:93004474; PMID:1356501  
A:Accession: T03261  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-23 <HIR>  
A:Cross-references: UNIPROT:O07939; EMBL:X68604; NID:G312275; PIDN:CAA48594.1; PID:G3122  
C:Superfamily: glutamate-ammonia ligase  
C:Keywords: Cytosol; ligase

Query Match 32.4%; Score 23; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 7.1e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DASIIW 9

Db 16 DPTILW 21

## RESULT 8

PQ0731

unidentified 5.7/35K protein [imported] - rice (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: PQ0731  
R;Komatsu, S.; Kajiura, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993  
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensional

A;Reference number: PQ0696

A;Accession: PQ0731

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 &lt;KOW&gt;

A;Cross-references: UNIPROT:Q7M1U2

Query Match 31.0%; Score 22; DB 2; Length 11;

Best Local Similarity 40.0%; Pred. No. 4.7e+02;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ASIIW 9

| : | : |

Db 1 ATVW 5

## RESULT 9

S69123

proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)  
C;Species: Rhodospirillum rubrum  
C;Date: 10-Mar-1998 #sequence\_revision 24-Apr-1998 #text\_change 24-Apr-1998  
C;Accession: S69123  
R;Diggie, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.  
Eur. J. Biochem. 228, 719-726, 1995

A;Title: Properties of the soluble polypeptide of the proton-translocating transhydrogen

A;Reference number: S69123; MUID:95255277; PMID:7737169

A;Accession: S69123

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 &lt;DIG&gt;

Query Match

31.0%; Score 22; DB 2; Length 12;

Best Local Similarity 22.2%; Pred. No. 5.2e+02;

Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ASIIWMMQ 13

| : | : |

Db 2 ADVVVKVQR 10

## RESULT 10

B46592

lactase-phlorizin hydrolase 140K isoform - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)

C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 01-Nov-1996

C;Accession: B46592

R;Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutchens, T.W.; Nichols, B.L.; Rosenberger, J.

J. Biol. Chem. 268, 13609-13616, 1993

A;Title: In vivo sucrose-isomaltase and lactase-phlorizin hydrolase turnover in the fed

A;Reference number: A46592; MUID:93293888; PMID:8514793

A;Accession: B46592

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 &lt;DUP&gt;

A;Note: sequence extracted from NCBI backbone (NCBIP:134560)

C;Keywords: carbohydrate digestion; intestine

Query Match

31.0%; Score 22; DB 2; Length 19;

Best Local Similarity 60.0%; Pred. No. 8.8e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

A;Experimental source: strain KK1  
A;Note: the full activity of this toxin depends on NaCl or KCl

Query Match 31.0%; Score 22; DB 2; Length 22;  
Best Local Similarity 37.5%; Pred. No. 1e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 DASIIWAM 11  
:|:|:|:  
Db 2 EATIWGV 9

## RESULT 14

PT0586  
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0586; PT0592  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0586  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <FE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)  
C;Keywords: T-cell receptor

Query Match 29.6%; Score 21; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 ASIIW 9  
|||  
Db 1 ASSIW 5

## RESULT 15

S69159  
cystathionine gamma-synthase - spinach (fragment)  
C;Species: Spinacia oleracea (spinach)  
C;Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
C;Accession: S69159  
R;Ravanel, S.; Droux, M.; Douce, R.  
Arch. Biochem. Biophys. 316, 572-584, 1995  
A;Title: Methionine biosynthesis in higher plants. I. Purification and characterization  
A;Reference number: S69159; MUID:95142682; PMID:7840669  
A;Accession: S69159  
A;Molecule type: protein  
A;Residues: 1-10 <RAV>  
A;Cross-references: UNIPROT:Q7MLJ3  
C;Keywords: chloroplast

Query Match 29.6%; Score 21; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 6.6e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDASII 8  
|:|:|:  
Db 2 TAVDMAAI 9

Search completed: November 14, 2004, 12:03:13  
Job time : 9.6383 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 40.5106 Seconds  
(without alignments)  
123.973 Million cell updates/sec

Title: US-09-831-253F-6

Perfect score: 71

Sequence: 1 TSLDASIIWAMQON 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	14	3 AAY93098	Aay93098 Transform
2	71	100.0	14	3 AAY92950	Aay92950 Transform
3	50	70.4	12	3 AAY93009	Aay93009 Transform
4	50	70.4	12	3 AAY92947	Aay92947 Transform
5	50	70.4	12	3 AAY93008	Aay93008 Transform
6	40	56.3	12	3 AAY93093	Aay93093 Transform
7	37	52.1	11	3 AAY93094	Aay93094 Transform
8	37	52.1	12	3 AAY93010	Aay93010 Transform
9	33	46.5	14	4 AAB88161	Aab88161 CD66 pept
10	31	43.7	21	4 ABG25633	Abg25633 Novel hum
11	30	42.3	15	2 AAR13972	Aar13972 [Asp14]Me
12	30	42.3	15	2 AAR61463	Aar61463 [Asp-14]
13	29	40.8	9	8 ADM73036	Adm73036 Human GAG
14	29	40.8	9	8 ADM73041	Adm73041 Human GAG
15	29	40.8	10	8 ADM73042	Adm73042 Human GAG
16	29	40.8	10	8 ADM73040	Adm73040 Human GAG
17	29	40.8	10	8 ADM73035	Adm73035 Human GAG
18	29	40.8	12	3 AAY93007	Aay93007 Transform
19	29	40.8	15	3 AAY54720	Aay54720 Human sub
20	29	40.8	15	3 AAY54721	Aay54721 Human sub
21	29	40.8	15	3 AAY67084	Aay67084 Human pro
22	29	40.8	15	3 AAY67083	Aay67083 Human pro
23	29	40.8	15	4 AAU38622	Aau38622 Human sub
24	29	40.8	15	4 AAB38623	Aab38623 Human sub
25	29	40.8	15	5 AAB91198	Abg91198 Peptide a

ALIGNMENTS

RESULT 1

AAy93098

ID AAY93098 standard; peptide; 14 AA.

XX AC AAY93098;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide P144.

XX Hepatotropic; antagonist; transforming growth factor betaf; TGF-bi;  
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO2000031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz JJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

XX Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betaf.  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.

XX Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
XX of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in  
XX vivo which have partial amino acid sequences identical, or similar, with  
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
XX examples of the peptides of the invention. The peptides act by  
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
XX they are inhibitors of stimulation of collagen synthesis in liver cells  
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the  
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or  
XX expression systems) encoding the peptides are used for treatment of liver  
XX disease, specifically cirrhosis

Abg91199 Peptide a  
Aau06698 Peptide r  
Adm73347 Human GAG  
Aay54566 Peptide e  
Aap82665 G protein  
Adc92572 Cancer-re  
Aau85020 Human GAG  
Aar86049 Anti-ELAM  
Aar86065 Anti-ELAM  
Aaw26857 ELAM-1 bi  
Aaw26865 ELAM-1 bi  
Aaw63875 ELAM-1 pe  
Aaw63859 ELAM-1 pe  
Aay54722 Human sub  
Aay67085 Human pro  
Aau38624 Human sub  
Abg91200 Peptide a  
Aay67677 Peptide #  
Aab61209 Human INT  
Abo32652 Secreted

```

XX
SQ   Sequence 14 AA;
Query Match      100.0%; Score 71; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 TSLDASIIWAMQON 14
Db   1 TSLDASIIWAMQON 14

RESULT 2
AAY92950
ID   AAY92950 standard; peptide; 14 AA.
XX
AC   AAY92950;
XX
DT   08-NOV-2000 (first entry)
XX
DE   Transforming growth factor inhibitory peptide #6.
XX
KW   Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW   competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW   extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS   Homo sapiens.
XX
PN   WO200031135-A1.
XX
PD   02-JUN-2000.
XX
PF   23-NOV-1999; 99WO-ES000375.
XX
PR   24-NOV-1998; 98ES-00002465.
XX
PA   (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI   Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI   Borrás Cuesta F;
XX
WPI; 2000-411935/35.
XX
PT   Peptides that antagonize binding of transforming growth factor beta1,
PT   useful for treatment of liver disease, especially cirrhosis, are partial
PT   sequences of the factor or its receptors.
XX
PS   Claim 7; Page 81; 86pp; Spanish.
XX
CC   The invention relates to synthetic peptides that antagonise the binding
CC   of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
CC   vivo which have partial amino acid sequences identical, or similar, with
CC   those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC   examples of the peptides of the invention. The peptides act by
CC   competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
CC   they are inhibitors of stimulation of collagen synthesis in liver cells
CC   and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC   extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC   expression systems) encoding the peptides are used for treatment of liver
CC   disease, specifically cirrhosis
XX
SQ   Sequence 14 AA;
Query Match      100.0%; Score 71; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 TSLDASIIWAMQON 14
Db   1 TSLDASIIWAMQON 14

RESULT 3
AAY92947
ID   AAY92947 standard; peptide; 12 AA.
XX
AC   AAY92947;
XX
DT   08-NOV-2000 (first entry)
XX
DE   Transforming growth factor inhibitory peptide #3.
XX
KW   Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW   competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW   extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX

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AAY93009
ID   AAY93009 standard; peptide; 12 AA.
XX
AC   AAY93009;
XX
DT   08-NOV-2000 (first entry)
XX
DE   Transforming growth factor inhibitory peptide P55.
XX
KW   Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW   competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW   extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS   Rattus sp.
XX
PN   WO200031135-A1.
XX
PD   02-JUN-2000.
XX
PF   23-NOV-1999; 99WO-ES000375.
XX
PR   24-NOV-1998; 98ES-00002465.
XX
PA   (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI   Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI   Borrás Cuesta F;
XX
WPI; 2000-411935/35.
XX
PT   Peptides that antagonize binding of transforming growth factor beta1,
PT   useful for treatment of liver disease, especially cirrhosis, are partial
PT   sequences of the factor or its receptors.
XX
PS   Disclosure; Page 27; 86pp; Spanish.
XX
CC   The invention relates to synthetic peptides that antagonise the binding
CC   of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
CC   vivo which have partial amino acid sequences identical, or similar, with
CC   those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC   examples of the peptides of the invention. The peptides act by
CC   competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
CC   they are inhibitors of stimulation of collagen synthesis in liver cells
CC   and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC   extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC   expression systems) encoding the peptides are used for treatment of liver
CC   disease, specifically cirrhosis
XX
SQ   Sequence 12 AA;
Query Match      70.4%; Score 50; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 0.046;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY   2 SLDASIIWAMQO 13
Db   1 SLDATMIWTMMQ 12

RESULT 4
AAY92947
ID   AAY92947 standard; peptide; 12 AA.
XX
AC   AAY92947;
XX
DT   08-NOV-2000 (first entry)
XX
DE   Transforming growth factor inhibitory peptide #3.
XX
KW   Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW   competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW   extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX

```



OS Homo sapiens.  
 XX WO200031135-A1.  
 XX  
 PD 02-JUN-2000.  
 XX  
 XX 23-NOV-1999; 99WO-ES000375.  
 PF  
 XX 24-NOV-1998; 98ES-00002465.  
 PR  
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 PA  
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;  
 XX WPI; 2000-411935/35.  
 DR  
 XX Peptides that antagonize binding of transforming growth factor betal,  
 XX useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 PT  
 XX Claim 4; Page 80; 86pp; Spanish.  
 PS  
 XX The invention relates to synthetic peptides that antagonise the binding  
 XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 12 AA;  
 Query Match 70.4%; Score 50; DB 3; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 0.046;  
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TSLDASIIWMM 12  
 Db 1 TSLDATMIWTMM 12  
 |||||:|  
 |||||:|  
 RESULT 5  
 AAY93008  
 ID AAY93008 standard; peptide; 12 AA.  
 AC AAY93008;  
 XX  
 XX 08-NOV-2000 (first entry)  
 DT  
 XX Transforming growth factor inhibitory peptide P54.  
 DE  
 XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX  
 OS Rattus sp.  
 XX  
 XX WO200031135-A1.  
 PN  
 XX 02-JUN-2000.  
 PD  
 XX 23-NOV-1999; 99WO-ES000375.  
 PF  
 XX 24-NOV-1998; 98ES-00002465.  
 PR  
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 PA  
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;  
 XX WPI; 2000-411935/35.  
 DR  
 XX Peptides that antagonize binding of transforming growth factor betal,  
 XX useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 PT  
 XX Claim 4; Page 80; 86pp; Spanish.  
 PS  
 XX The invention relates to synthetic peptides that antagonise the binding  
 XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 12 AA;  
 Query Match 70.4%; Score 50; DB 3; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 0.046;  
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TSLDASIIWMM 12  
 Db 1 TSLDATMIWTMM 12  
 |||||:|  
 |||||:|  
 RESULT 6  
 AAY93093  
 ID AAY93093 standard; peptide; 12 AA.  
 AC AAY93093;  
 XX  
 XX 08-NOV-2000 (first entry)  
 DT  
 XX Transforming growth factor inhibitory peptide P139.  
 DE  
 XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200031135-A1.  
 PN  
 XX 02-JUN-2000.  
 PD  
 XX 23-NOV-1999; 99WO-ES000375.  
 PF  
 XX 24-NOV-1998; 98ES-00002465.  
 PR  
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 PA  
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;  
 XX WPI; 2000-411935/35.  
 DR  
 XX Peptides that antagonize binding of transforming growth factor betal,  
 XX useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 PT  
 XX Claim 4; Page 31; 86pp; Spanish.  
 PS  
 XX The invention relates to synthetic peptides that antagonise the binding  
 XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 12 AA;  
 Query Match 70.4%; Score 50; DB 3; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 0.046;  
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TSLDASIIWMM 12  
 Db 1 TSLDATMIWTMM 12  
 |||||:|  
 |||||:|

CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 12 AA;

Query Match 56.3%; Score 40; DB 3; Length 12;  
 Best Local Similarity 77.8%; Pred. No. 2.7;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDASIIW 9  
 Db 1 TSLDATMIW 9  
 |||:|:|

## RESULT 7

AA93094  
 ID AAY93094 standard; peptide; 11 AA.

XX  
 AC AAY93094;

XX  
 DT 08-NOV-2000 (first entry)

XX  
 DE Transforming growth factor inhibitory peptide PI40.

XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Homo sapiens.

XX PN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX PS Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis

XX SQ Sequence 11 AA;

Query Match 52.1%; Score 37; DB 3; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 8.4;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 DASIIWAMQ 12  
 Db 3 DATMIWTWM 11  
 ||:|:|

## RESULT 8

AA93010  
 ID AAY93010 standard; peptide; 12 AA.

XX  
 AC AAY93010;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide P56.

XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Rattus sp.

XX PN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX PS Disclosure; Page 27; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis

XX SQ Sequence 12 AA;

Query Match 52.1%; Score 37; DB 3; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 9.2;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 IIAWAMQN 14  
 Db 1 MIWTMWN 8  
 :|||:|

## RESULT 9

AAB88161  
 ID AAB88161 standard; peptide; 14 AA.

XX  
 AC AAB88161;

DT 17-MAY-2001 (first entry)  
 XX CD66 peptide CD66f(11)-10.  
 XX  
 XX CD66; CEACAM; adhesion molecule; antiviral; antibacterial;  
 KW antiinflammatory; cytostatic; neutrophil activation; proliferation;  
 KW differentiation; cancer; angiogenesis.  
 XX  
 XX Unidentified.  
 OS  
 XX WO200113937-A1.  
 PN  
 XX 01-MAR-2001.  
 PD  
 XX  
 XX 25-AUG-2000; 2000WO-US023482.  
 XX  
 XX 26-AUG-1999; 99US-0150791P.  
 PR  
 XX 02-SEP-1999; 99US-0152501P.  
 XX  
 XX (SKUB/) SKUBITZ K M.  
 PA (SKUB/) SKUBITZ A P N.  
 XX  
 XX Skubitz KM, Skubitz APN;  
 PI  
 XX WPI; 2001-234981/24.  
 DR  
 XX Novel peptides useful for activating neutrophils or blocking activation  
 PT of neutrophils, modulating homotypic or heterotypic adhesion of CD66  
 PT polypeptides, and modulating immune cell activation.  
 XX  
 PS Claim 1; Page 54; 102pp; English.  
 XX  
 CC The present sequence is an isolated peptide that was tested for its  
 CC ability to modulate the function of CD66 family polypeptides and CD66  
 CC ligands. 106 sequences of 13 or 14 amino acids in length, and their  
 CC analogues, were identified that modulate the function of at least one  
 CC CD66 family polypeptide and/or at least one ligand of the polypeptide.  
 CC The peptides are capable of modulating activation of neutrophils,  
 CC activation or inhibition, proliferation and/or differentiation of T-  
 CC cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune  
 CC system cells, proliferation and/or differentiation of epithelial cells,  
 CC homotypic and/or heterotypic adhesion among CD66 family polypeptides and  
 CC adhesion of CD66 family polypeptides to other ligands. The peptides are  
 CC useful for delivering a therapeutically active agent to a patient, for  
 CC modifying the metastasis of malignant cells, for altering bacterial or  
 CC viral binding to cells or a biomaterial, for altering cell adhesion to a  
 CC biomaterial, for detecting tumours, for detecting inflammation, for  
 CC detecting a CD66 protein or its ligand, for altering angiogenesis by  
 CC contacting endothelial cells, tumour cells or immune cells, for altering  
 CC an immune response, and for altering keratinocyte proliferation  
 XX  
 SQ Sequence 14 AA;  
 Query Match 46.5%; Score 33; DB 4; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 55;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 SLDASIIWAM 11  
 Db :|||:|  
 3 TLDASYLWWM 12  
 RESULT 10  
 ABG25633  
 ID ABG25633 standard; protein; 21 AA.  
 XX  
 AC ABG25633;  
 XX  
 XX 18-FEB-2002 (first entry)  
 DT  
 XX Novel human diagnostic protein #25624.  
 DE  
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW

KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.  
 XX WO200175067-A2.  
 PN  
 XX 11-OCT-2001.  
 PD  
 XX  
 XX 30-MAR-2001; 2001WO-US008631.  
 XX  
 XX 31-MAR-2000; 2000US-00540217.  
 PR  
 XX 23-AUG-2000; 2000US-00649167.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Drmanac RT, Liu C, Tang YT;  
 PI  
 XX WPI; 2001-639362/73.  
 DR N-PSDB; AAS89820.  
 XX  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX  
 PS Claim 20; SEQ ID NO 55992; 103pp; English.  
 XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 21 AA;  
 Query Match 43.7%; Score 31; DB 4; Length 21;  
 Best Local Similarity 42.1%; Pred. No. 1.9e+02;  
 Matches 8; Conservative 2; Mismatches 3; Indels 6; Gaps 1;  
 QY 1 TSLD-----ASIIWAMQ 13  
 Db :|||:|  
 1 TSLDEVOTGKPSLIWISQ 19  
 RESULT 11  
 AAR13972  
 ID AAR13972 standard; protein; 15 AA.  
 XX  
 AC AAR13972;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 27-NOV-1991 (first entry)  
 XX  
 XX [Asp14]Melittin-(7-21) (5).  
 DE  
 XX Bioassay; immunoassay; polystyrene; polyethylene; sheet; carrier;  
 KW support; solid-phase.  
 KW

11/27/99

XX OS Synthetic.  
 XX PN WO9113098-A.  
 XX PD 05-SEP-1991.  
 XX PF 02-MAR-1990; 90DK-00000559.  
 XX PR 02-MAR-1990; 90DK-00000559.  
 XX (RISO-) RISO FORSKNINGSCENTER.  
 XX PA (RISO-) RISO FORSKNINGSCENTER.  
 XX PI Berg RH, Almdal K, Pedersen W, Holm A;  
 XX WPI; 1991-281427/38.  
 XX PT Polymer substrate with grafted polystyrene chains - functionalised to  
 PT attach aminoacid(s), peptide(s) or proteins, for peptide synthesis, bio-  
 PT or immunoassays.  
 XX PS Disclosure; Fig 3; 92pp; English.  
 XX CC Protected melittin-(7-21) and twelve analogs (AAR13969-79) derived by  
 CC substitutions in position 12 and 14 were each assembled stepwise on a  
 CC labelled sheet. The sheet was an aminomethylated 285% polystyrene-  
 CC grafted polyethylene sheet labelled by graphite-based ink. The common  
 CC steps of deprotection, neutralisation, washing and coupling of identical  
 CC amino acids were performed simultaneously in a single reaction vessel,  
 CC while the coupling of different amino acids was carried out in separate  
 CC vessels. The polymer substrate serves as an efficient solid-phase carrier  
 CC on which the peptide may be synthesised or attached and remain covalently  
 CC bound in a stable, permanent manner. The resulting support can be used in  
 CC solid-phase bioassays, esp. immunoassays. See also AAR13968-79. (Updated  
 CC on 25-MAR-2003 to correct PA field.)  
 XX SQ Sequence 15 AA;  
 Query Match 42.3%; Score 30; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 2e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 TSLDASIIW 9  
 Db 5 TGLDALISW 13  
 RESULT 12  
 AAR61463  
 ID AAR61463 standard; peptide; 15 AA.  
 AC AAR61463;  
 XX 16-SEP-1995 (first entry)  
 XX [Asp-14] melittin-(7-21) analogue.  
 XX Peptide solid phase synthesis; polystyrene-grafted substrate; melittin.  
 XX Synthetic.  
 XX US5373053-A.  
 XX 13-DEC-1994.  
 XX 14-DEC-1992; 92US-009990584.  
 XX 01-SEP-1988; 88US-00239525.  
 XX 25-AUG-1989; 89US-00398846.  
 XX 12-WAY-1992; 92US-00882059.  
 XX (RISO-) RISO NAT LAB.

XX PI Berg RH, Holm A, Tam JP, Pedersen WB, Merrifield RB, Almdal K;  
 XX WPI; 1995-030351/04.  
 XX substrate grafted with polystyrene - used in peptide synthesis giving  
 XX high yields.  
 XX Example 9; Fig 3; 20pp; English.  
 XX The invention relates to a solid phase peptide synthesis method using a  
 CC support consisting of a functionalised polystyrene-grafted polymer  
 CC substrate. The peptides are prepared in high yield and purity. The  
 CC process may be used for compartmentalised synthesis of a number of  
 CC different peptides in parallel. The present sequence is one of 13  
 CC melittin-(7-21) analogues prepared in parallel by the process (AAR61460-  
 CC R61470)  
 XX SQ Sequence 15 AA;  
 Query Match 42.3%; Score 30; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 2e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 TSLDASIIW 9  
 Db 5 TGLDALISW 13  
 RESULT 13  
 ADM73036  
 ID ADM73036 standard; peptide; 9 AA.  
 AC ADM73036;  
 XX 03-JUN-2004 (first entry)  
 XX Human GAGE-1 epitope SEQ ID NO:295.  
 XX epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;  
 KW cancer; tumour; human; GAGE-1.  
 XX Homo sapiens.  
 OS Synthetic.  
 XX WO2004022709-A2.  
 XX 18-MAR-2004.  
 XX 05-SEP-2003; 2003WO-US027706.  
 XX 06-SEP-2002; 2002US-0409123P.  
 XX (MANN-) MANNKIND CORP.  
 XX Simard JLL, Diamond DC, Liu L, Liu Z;  
 XX WPI; 2004-315564/29.  
 XX New polypeptides and encoding nucleic acids that are useful epitopes of  
 PT target-associated antigens, useful for diagnosing and/or treating viral  
 PT infections, cancers and tumors.  
 XX Claim 1; SEQ ID NO 295; 357pp; English.  
 XX The present invention describes a polypeptide (I) comprising a component  
 CC selected from: (a) a polypeptide epitope having any of the 503 fully  
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope  
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having  
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional  
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the  
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and  
 CC can be used in vaccines. The methods and compositions of the present

CC invention are useful for the diagnosis and/or treatment of viral  
 CC infections, cancers and tumours. The present sequence is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 40.8%; Score 29; DB 8; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIVAMMON 14

Db 1 ILWLLMNN 8

RESULT 14

ADM73041  
 ID ADM73041 standard; peptide; 9 AA.

XX AC ADM73041;

XX DT 03-JUN-2004 (first entry)

XX DE Human GAGE-1 epitope SEQ ID NO:300.

XX KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;  
 XX cancer; tumour; human; GAGE-1.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004022709-A2.

XX PD 18-MAR-2004.

XX PF 05-SEP-2003; 2003WO-US027706.

XX PR 06-SEP-2002; 2002US-0409123P.

XX PA (MANN-) MANNKIND CORP.

XX PI Simard JYL, Diamond DC, Liu L, Liu Z;

XX DR WPI; 2004-315564/29.

XX PT New polypeptides and encoding nucleic acids that are useful epitopes of  
 PT target-associated antigens, useful for diagnosing and/or treating viral  
 PT infections, cancers and tumors.

XX PS Claim 1; SEQ ID NO 300; 357pp; English.

XX CC The present invention describes a polypeptide (I) comprising a component  
 CC selected from: (a) a polypeptide epitope having any of the 503 fully  
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope  
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having  
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional  
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the  
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and  
 CC can be used in vaccines. The methods and compositions of the present  
 CC invention are useful for the diagnosis and/or treatment of viral  
 CC infections, cancers and tumors. The present sequence is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 9 AA;

Query Match 40.8%; Score 29; DB 8; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIVAMMON 14

Db 1 ILWLLMNN 8

RESULT 15

ADM73042

ID ADM73042 standard; peptide; 10 AA.

XX AC ADM73042;

XX DT 03-JUN-2004 (first entry)

XX DE Human GAGE-1 epitope SEQ ID NO:301.

XX KW epitope; epitope cluster; virucide; cytostatic; vaccine; viral infection;  
 XX cancer; tumour; human; GAGE-1.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN WO2004022709-A2.

XX PD 18-MAR-2004.

XX PF 05-SEP-2003; 2003WO-US027706.

XX PR 06-SEP-2002; 2002US-0409123P.

XX PA (MANN-) MANNKIND CORP.

XX PI Simard JYL, Diamond DC, Liu L, Liu Z;

XX DR WPI; 2004-315564/29.

XX PT New polypeptides and encoding nucleic acids that are useful epitopes of  
 PT target-associated antigens, useful for diagnosing and/or treating viral  
 PT infections, cancers and tumors.

XX PS Claim 1; SEQ ID NO 301; 357pp; English.

XX CC The present invention describes a polypeptide (I) comprising a component  
 CC selected from: (a) a polypeptide epitope having any of the 503 fully  
 CC defined sequences of 8-33 amino acids (SEQ ID NO:108-610); (b) an epitope  
 CC cluster comprising the polypeptide of (a); (c) a polypeptide having  
 CC substantial similarity to (a) or (b); (d) a polypeptide having functional  
 CC similarity to any of (a)-(c); or (e) a nucleic acid encoding the  
 CC polypeptide of (a)-(d). (I) has virucide and cytostatic activities, and  
 CC can be used in vaccines. The methods and compositions of the present  
 CC invention are useful for the diagnosis and/or treatment of viral  
 CC infections, cancers and tumors. The present sequence is used in the  
 CC exemplification of the present invention.

XX SQ Sequence 10 AA;

Query Match 40.8%; Score 29; DB 8; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 2e+02;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 IIVAMMON 14

Db 2 ILWLLMNN 9

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 Job time : 41.5106 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:04:13 ; Search time 23.3333 Seconds  
(without alignments)  
42.633 Million cell updates/sec

Title: US-09-831-253F-9  
Perfect score: 77  
Sequence: 1 LBSLSFQLGLYLSPH 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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4: /cgn2\_6/prodata/1/iaa/6B COMB.pcp.\*  
5: /cgn2\_6/prodata/1/iaa/6C COMB.pcp.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pcp.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	39.0	15	4	US-09-514-245-55
2	30	39.0	15	4	US-09-514-245-98
3	29	37.7	13	4	US-08-753-750B-64
4	28	36.4	15	4	US-09-514-245-99
5	27	35.1	7	4	US-09-463-239-29
6	27	35.1	9	4	US-09-239-043D-1855
7	27	35.1	10	3	US-08-159-339A-458
8	27	35.1	10	4	US-09-239-043D-620
9	27	35.1	11	4	US-09-239-043D-1944
10	27	35.1	10	4	US-09-239-043D-467
11	27	35.1	11	4	US-09-239-043D-580
12	27	35.1	11	4	US-09-239-043D-1867
13	27	35.1	15	1	US-08-102-738-20
14	27	35.1	15	4	US-09-009-953-264
15	27	35.1	15	4	US-09-239-043D-2188
16	26.5	34.4	12	3	US-09-298-924-19
17	26	33.8	8	3	US-08-913-842-28
18	26	33.8	9	4	US-09-311-784A-271
19	26	33.8	9	4	US-09-601-729-70
20	26	33.8	10	3	US-08-159-339A-472
21	26	33.8	10	3	US-08-159-339A-503
22	26	33.8	12	4	US-09-407-687-34
23	26	33.8	14	1	US-07-914-280-14
24	26	33.8	14	5	PCT-US93-06625-14
25	26	33.8	15	4	US-09-148-712-7
26	25	32.5	8	3	US-08-444-818-557
27	25	32.5	9	1	US-08-336-618-2

28	25	32.5	12	4	US-09-389-956-52	Sequence 52, Appl
29	25	32.5	15	1	US-08-049-783-11	Sequence 11, Appl
30	25	32.5	15	1	US-08-158-232-22	Sequence 22, Appl
31	25	32.5	15	1	US-08-304-626-22	Sequence 22, Appl
32	25	32.5	15	1	US-08-316-301A-23	Sequence 23, Appl
33	25	32.5	15	2	US-08-611-928-22	Sequence 22, Appl
34	25	32.5	15	3	US-09-224-024-5	Sequence 5, Appl
35	25	32.5	15	3	US-09-173-891-22	Sequence 22, Appl
36	25	32.5	15	3	US-09-076-137-23	Sequence 23, Appl
37	25	32.5	15	4	US-09-738-363-23	Sequence 23, Appl
38	25	32.5	15	4	US-09-514-245-151	Sequence 151, App
39	25	32.5	15	4	US-09-514-245-152	Sequence 152, App
40	25	32.5	15	5	PCT-US92-03624-23	Sequence 23, Appl
41	25	32.5	15	5	PCT-US94-07902-5	Sequence 5, Appl
42	24	31.2	8	3	US-08-444-818-558	Sequence 558, App
43	24	31.2	13	1	US-08-290-919-15	Sequence 15, Appl
44	24	31.2	14	1	US-08-798-897-14	Sequence 14, Appl
45	24	31.2	14	2	US-08-978-523-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-514-245-55  
; Sequence 55, Application US/09514245  
; Patent No. 6703023  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre  
; APPLICANT: BLANCHARD, Philippe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire  
; APPLICANT: TRUONG, Catherine  
; APPLICANT: MAHE, Dominique  
; APPLICANT: CAROLET, Roland  
; APPLICANT: MADSC, Francois  
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASES  
; FILE REFERENCE: 065691/0176  
; CURRENT APPLICATION NUMBER: US/09/514,245  
; CURRENT FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: FR 97/15396  
; PRIOR FILING DATE: 1997-12-05  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 55  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Type B PWD circovirus  
US-09-514-245-55

Query Match 39.0%; Score 30; DB 4; Length 15;  
Best Local Similarity 35.7%; Pred. No. 23;  
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LBSLSFQLGLYLSP 14

Db 2 VNELRFNIGQLPFP 15

RESULT 2

US-09-514-245-98  
; Sequence 98, Application US/09514245  
; Patent No. 6703023  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre  
; APPLICANT: BLANCHARD, Philippe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire  
; APPLICANT: TRUONG, Catherine

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; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-98

Query Match 39.0%; Score 30; DB 4; Length 15;
Best Local Similarity 35.7%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LBSLSFQLGLYLSP 14
   :|:|:|:|:|
Db 2 VNELRFNIGQFLPP 15

RESULT 3
US-08-753-750B-64
; Sequence 64, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: LO, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; FILE REFERENCE: PASTERELLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Escherichia coli
US-08-753-750B-64

Query Match 37.7%; Score 29; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQLGLY 11
   |:|:|:|
Db 4 SESWELGY 12

RESULT 4
US-09-514-245-99
; Sequence 99, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
```

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; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 99
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-99

Query Match 36.4%; Score 28; DB 4; Length 15;
Best Local Similarity 45.5%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSP 14
   ||:|:|:|
Db 1 LRFNIGQFLPP 11

RESULT 5
US-09-463-239-29
; Sequence 29, Application US/09463239
; Patent No. 6700039
; GENERAL INFORMATION:
; APPLICANT: Jepson, Ian
; APPLICANT: Ebneeth, Marcus
; APPLICANT: Sonnewald, Uwe
; TITLE OF INVENTION: Genetic Method for Controlling Sprouting
; FILE REFERENCE: 109846.178
; CURRENT APPLICATION NUMBER: US/09/463,239
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: PCT/GB98/02023
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: EP 97113118.0
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence encoding MOT isolated from potato.
US-09-463-239-29

Query Match 35.1%; Score 27; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 3.8e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FQLGLYL 12
   |||||
Db 1 FQLGLNL 7

RESULT 6
US-09-239-043D-1855
; Sequence 1855, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
```



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; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1855
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-1855

Query Match 35.1%; Score 27; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 8 LGLYLSPH 15
DB 1 LGIHLNPN 8

RESULT 7
US-08-159-339A-458
; Sequence 458, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 458:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-458

Query Match 35.1%; Score 27; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 8 LGLYLSPH 15
DB 2 LGIHLNPN 9

RESULT 8
US-09-239-043D-620
; Sequence 620, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16

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; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2579  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 620

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Orthohepadnaviridae hepatitis B virus

US-09-239-043D-620

Query Match 35.1%; Score 27; DB 4; Length 10;

Best Local Similarity 50.0%; Pred. No. 55;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LGLYLSPH 15

||:|:|:

Db 2 LGLHLNPN 9

RESULT 9

US-09-239-043D-1944

; Sequence 1944, Application US/09239043D

; Patent No. 6689363

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Vitiello, Maria A.

; APPLICANT: Livingston, Brian D.

; APPLICANT: Celis, Esteban

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Chesnut, Robert

; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus

; FILE REFERENCE: 2060.0060007

; CURRENT FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: US/09/239,043D

; PRIOR FILING DATE: 1999-01-27

; PRIOR FILING DATE: 1998-11-10

; PRIOR FILING DATE: 1997-11-25

; PRIOR FILING DATE: 1997-11-25

; PRIOR FILING DATE: 1997-03-12

; PRIOR FILING DATE: 1996-03-13

; PRIOR FILING DATE: 1995-06-05

; PRIOR FILING DATE: 1994-12-01

; PRIOR FILING DATE: 1994-11-23

; PRIOR FILING DATE: 1994-07-21

; PRIOR FILING DATE: 1994-03-04

; PRIOR FILING DATE: 1994-02-16

; PRIOR FILING DATE: 1994-02-16

; NUMBER OF SEQ ID NOS: 2579

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1944

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Orthohepadnaviridae hepatitis B virus

US-09-239-043D-1944

Query Match 35.1%; Score 27; DB 4; Length 10;

Best Local Similarity 50.0%; Pred. No. 55;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LGLYLSPH 15

||:|:|:

Db 2 LGLHLNPN 9

RESULT 10

US-09-239-043D-467

; Sequence 467, Application US/09239043D

; Patent No. 6689363

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Vitiello, Maria A.

; APPLICANT: Livingston, Brian D.

; APPLICANT: Celis, Esteban

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Chesnut, Robert

; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus

; FILE REFERENCE: 2060.0060007

; CURRENT FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: US/09/239,043D

; PRIOR FILING DATE: 1999-01-27

; PRIOR FILING DATE: 1998-11-10

; PRIOR FILING DATE: 1997-11-25

; PRIOR FILING DATE: 1997-03-12

; PRIOR FILING DATE: 1996-03-13

; PRIOR FILING DATE: 1995-06-05

; PRIOR FILING DATE: 1994-12-01

; PRIOR FILING DATE: 1994-11-23

; PRIOR FILING DATE: 1994-07-21

; PRIOR FILING DATE: 1994-03-04

; PRIOR FILING DATE: 1994-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 2579

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 467

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Orthohepadnaviridae hepatitis B virus

US-09-239-043D-467

Query Match 35.1%; Score 27; DB 4; Length 11;

Best Local Similarity 50.0%; Pred. No. 62;

Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 8 LGLYLSPH 15

||:|:|:

Db 2 LGLHLNPN 9

RESULT 11

US-09-239-043D-580

; Sequence 580, Application US/09239043D

; Patent No. 6689363

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Vitiello, Maria A.

; APPLICANT: Livingston, Brian D.

; APPLICANT: Celis, Esteban

; APPLICANT: Kubo, Ralph T.

```

; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 580
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
; US-09-239-043D-580

Query Match      35.1%; Score 27; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0

Qy      8 LGLYLSPH 15
Db      3 LGTHLNP 10
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RESULT 12
US-09-239-043D-1867
; Sequence 1867, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363

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Qy 8 LGLYLSPH 15  
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Db 7 LGIHLNPN 14

Search completed: November 14, 2004, 13:18:39  
Job time : 24.3333 secs

Qy 8 LGLYLSPH 15  
||::||::  
Db 7 LGIHLNPN 14

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 13:16:33 ; Search time 79.6667 Seconds  
(without alignments)  
66.619 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77

Sequence: 1 LPSLSFQLGLYLSPH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 238011

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	40.3	10	10	US-09-572-270A-102
2	30	39.0	15	15	US-10-682-420-55
3	30	39.0	15	15	US-10-682-420-98
4	30	39.0	15	15	US-10-409-613-55
5	30	39.0	15	15	US-10-409-613-55
6	30	39.0	15	15	US-10-442-180-55
7	30	39.0	15	15	US-10-442-180-98
8	29	37.7	11	14	US-10-197-954-26
9	28	36.4	9	14	US-10-119-536A-101
10	28	36.4	10	15	US-10-462-452-757
11	28	36.4	10	15	US-10-601-953-60
12	28	36.4	10	16	US-10-322-266-758
13	28	36.4	14	10	US-09-820-649-319

14	28	36.4	14	14	US-10-160-162-319	Sequence 319, Appl
15	28	36.4	15	15	US-10-682-420-99	Sequence 99, Appl
16	28	36.4	15	15	US-10-409-613-99	Sequence 99, Appl
17	28	36.4	15	15	US-10-442-180-99	Sequence 99, Appl
18	27	35.1	9	14	US-10-163-499-12	Sequence 12, Appl
19	27	35.1	10	10	US-09-572-404B-1179	Sequence 1179, Ap
20	27	35.1	10	10	US-09-572-270A-100	Sequence 100, Appl
21	27	35.1	13	13	US-10-103-395-264	Sequence 264, Appl
22	27	35.1	15	15	US-10-163-499-31	Sequence 31, Appl
23	27	35.1	15	15	US-10-296-734-808	Sequence 808, Appl
24	26.5	34.4	12	16	US-10-688-276-19	Sequence 19, Appl
25	26	33.8	9	14	US-10-371-525-271	Sequence 271, Appl
26	26	33.8	9	14	US-10-371-645-271	Sequence 271, Appl
27	26	33.8	9	14	US-10-371-645-271	Sequence 271, Appl
28	26	33.8	9	14	US-10-371-260-271	Sequence 271, Appl
29	26	33.8	9	16	US-10-415-014-19	Sequence 19, Appl
30	26	33.8	9	16	US-10-415-014-49	Sequence 49, Appl
31	26	33.8	9	16	US-10-415-014-202	Sequence 202, Appl
32	26	33.8	9	16	US-10-415-014-301	Sequence 301, Appl
33	26	33.8	10	16	US-10-415-014-64	Sequence 64, Appl
34	26	33.8	10	16	US-10-415-014-165	Sequence 89, Appl
35	26	33.8	10	16	US-10-415-014-165	Sequence 165, Appl
36	26	33.8	10	16	US-10-415-014-253	Sequence 253, Appl
37	26	33.8	10	16	US-10-415-014-364	Sequence 364, Appl
38	26	33.8	11	14	US-10-369-736-26	Sequence 26, Appl
39	26	33.8	11	14	US-10-369-738-26	Sequence 26, Appl
40	26	33.8	12	14	US-10-075-869-40	Sequence 40, Appl
41	26	33.8	12	14	US-10-366-493-40	Sequence 40, Appl
42	26	33.8	12	14	US-10-191-540-154	Sequence 154, Appl
43	26	33.8	12	15	US-10-302-100B-34	Sequence 34, Appl
44	26	33.8	13	14	US-10-199-820-274	Sequence 274, Appl
45	26	33.8	14	14	US-10-081-119-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-572-270A-102  
; Sequence 102, Application US/09572270A  
; Publication No. US20030148368A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Inter- complementary peptide listing  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/572,270A  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 1144  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 102  
; LENGTH: 10  
; TYPE: PPT  
; ORGANISM: Arabidopsis Thaliana  
; OTHER INFORMATION: Sequence located in ILI2. at 8-17 and may interact with  
US-09-572-270A-102

Query Match 40.3%; Score 31; DB 10; Length 10;  
Best Local Similarity 70.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12

Db 1 SLTFQLLLFL 10  
|||:|:  
|||:|:

RESULT 2

US-10-682-420-55  
; Sequence 55, Application US/10682420  
; Publication No. US20040062775A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre

```
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-682-420-55

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 LDSLSFOLGLYLSP 14
       ::|||::|:|:|
DB      2 VNELRFNIGQFLPP 15

RESULT 3
US-10-682-420-98
; Sequence 98, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-682-420-98

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
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QY      1 LDSLSFOLGLYLSP 14
       ::|||::|:|:|
DB      2 VNELRFNIGQFLPP 15

RESULT 4
US-10-409-613-55
; Sequence 55, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-409-613-55

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY      1 LDSLSFOLGLYLSP 14
       ::|||::|:|:|
DB      2 VNELRFNIGQFLPP 15

RESULT 5
US-10-409-613-98
; Sequence 98, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
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; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-409-613-98

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYLSP 14
   :|:|:|:|:|
Db 2 VNELRFNIGQFLPP 15

RESULT 6
US-10-442-180-55
; Sequence 55, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-442-180-55

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYLSP 14
   :|:|:|:|:|
Db 2 VNELRFNIGQFLPP 15

RESULT 7
US-10-442-180-98
; Sequence 98, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
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; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-442-180-98

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYLSP 14
   :|:|:|:|:|
Db 2 VNELRFNIGQFLPP 15

RESULT 8
US-10-197-954-26
; Sequence 26, Application US/10197954
; Publication No. US20030119021A1
; GENERAL INFORMATION:
; APPLICANT: K'ster, Hubert
; APPLICANT: Siddiqi, Suhaib
; APPLICANT: Little, Daniel
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: 24743-2305
; CURRENT APPLICATION NUMBER: US/10/197,954
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 60/306,019
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 60/314,123
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/363,433
; PRIOR FILING DATE: 2002-03-11
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo Sapien
; NAME/KEY: AMIDATION
; FEATURE:
; LOCATION: 11
US-10-197-954-26

Query Match      37.7%; Score 29; DB 14; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10
   :|:|:|:|
Db 2 MDLAFSGGL 11

RESULT 9
US-10-119-536A-101
; Sequence 101, Application US/10119536A
; Publication No. US20030199438A1
; GENERAL INFORMATION:
; APPLICANT: Shaw, Allan Christian
; APPLICANT: Vandahl, Brian Berg
; TITLE OF INVENTION: Method for Identification of Proteins from Intracellular Bacteri.
; FILE REFERENCE: 4305/U091US1
; CURRENT APPLICATION NUMBER: US/10/119,536A
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; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: DK PA 200100581  
; PRIOR FILING DATE: 2001-04-09  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 101  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Chlamydia pneumoniae  
; FEATURE:  
; NAME/KEY: BINDING  
; LOCATION: (1)..(9)  
; OTHER INFORMATION: CPN0998 immunogenic peptide  
US-10-119-536A-101

Query Match 36.4%; Score 28; DB 14; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 LGLYLSP 14  
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Db 2 IGYLSP 8

RESULT 10  
US-10-462-452-757  
; Sequence 757, Application US/10462452  
; Publication No. US20040037809A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven  
; APPLICANT: Gupta, Mohammed Abd  
; APPLICANT: de Meireles, Jorge  
; TITLE OF INVENTION: Compositions and Methods for Enhanced  
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta  
; FILE REFERENCE: 02-02US  
; CURRENT APPLICATION NUMBER: US/10/462,452  
; CURRENT FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: 60/393,066  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 790  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 757  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-462-452-757

Query Match 36.4%; Score 28; DB 15; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSLSPQLG 9  
|||  
Db 3 DSMKFEIG 10

RESULT 11  
US-10-601-953-60  
; Sequence 60, Application US/10601953  
; Publication No. US2004007540A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven C.  
; TITLE OF INVENTION: Compositions and Methods For Modulating Physiology of Epithelial  
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of  
; TITLE OF INVENTION: Therapeutic Compounds  
; FILE REFERENCE: 02-03US  
; CURRENT APPLICATION NUMBER: US/10/601,953  
; CURRENT FILING DATE: 2003-06-24  
; PRIOR APPLICATION NUMBER: 60/392,512  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 900  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 60  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-601-953-60

Query Match 36.4%; Score 28; DB 15; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSLSPQLG 9  
|||  
Db 3 DSMKFEIG 10

RESULT 12  
US-10-322-266-758  
; Sequence 758, Application US/10322266  
; Publication No. US20040115135A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven C.  
; TITLE OF INVENTION: Compositions and Methods For Enhanced Mucosal Delivery Of Peptide  
; FILE REFERENCE: NPCI0567  
; CURRENT APPLICATION NUMBER: US/10/322,266  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 797  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 758  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-322-266-758

Query Match 36.4%; Score 28; DB 16; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 DSLSPQLG 9  
|||  
Db 3 DSMKFEIG 10

RESULT 13  
US-09-820-649-319  
; Sequence 319, Application US/09820649  
; Publication No. US20030199683A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 83 Human Secreted Proteins  
; FILE REFERENCE: P2012P1  
; CURRENT APPLICATION NUMBER: US/09/820,649  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US/09/236,557  
; PRIOR FILING DATE: 1999-01-26  
; PRIOR APPLICATION NUMBER: PCT/US98/15949  
; PRIOR FILING DATE: 1998-07-29  
; PRIOR APPLICATION NUMBER: 60/054,212  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,209  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,234  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,218  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,214  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,236  
; PRIOR FILING DATE: 1997-07-30



; PRIOR APPLICATION NUMBER: 60/054,215  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,211  
; PRIOR FILING DATE: 1997-07-30  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 353  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 319  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-820-649-319

Query Match 36.4%; Score 28; DB 10; Length 14;  
Best Local Similarity 50.0%; Pred. No. 5.7e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12  
|:|:|:|  
Db 5 SISYISGLVL 14

RESULT 14  
US-10-160-162-319  
; Sequence 319, Application US/10160162  
; Publication No. US20030166541A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 83 Human Secreted Proteins  
; FILE REFERENCE: P2012P2  
; CURRENT APPLICATION NUMBER: US/10/160,162  
; CURRENT FILING DATE: 2002-06-04  
; PRIOR APPLICATION NUMBER: 60/295,558  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 09/236,557  
; PRIOR FILING DATE: 1999-01-26  
; PRIOR APPLICATION NUMBER: PCT/US98/15949  
; PRIOR FILING DATE: 1998-07-29  
; PRIOR APPLICATION NUMBER: 60/054,212  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,209  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,234  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,218  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,214  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,236  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,215  
; PRIOR FILING DATE: 1997-07-30  
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; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/054,213  
; PRIOR FILING DATE: 1997-07-30  
; PRIOR APPLICATION NUMBER: 60/055,968  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,969  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/055,972  
; PRIOR FILING DATE: 1997-08-18  
; PRIOR APPLICATION NUMBER: 60/056,561  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,534  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,729  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,543  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,727

; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,554  
; PRIOR FILING DATE: 1997-08-19  
; PRIOR APPLICATION NUMBER: 60/056,730  
; PRIOR FILING DATE: 1997-08-19  
; NUMBER OF SEQ ID NOS: 353  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 319  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-160-162-319

Query Match 36.4%; Score 28; DB 14; Length 14;  
Best Local Similarity 50.0%; Pred. No. 5.7e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12  
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Db 5 SISYISGLVL 14

RESULT 15  
US-10-682-420-99  
; Sequence 99, Application US/10682420  
; Publication No. US20040062775A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre  
; APPLICANT: BLANCHARD, Philippe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire  
; APPLICANT: TRUONG, Catherine  
; APPLICANT: MAHE, Dominique  
; APPLICANT: CARIOLET, Roland  
; APPLICANT: MADEC, Francois  
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS  
; FILE REFERENCE: 065691/0176  
; CURRENT APPLICATION NUMBER: US/10/682,420  
; CURRENT FILING DATE: 2003-10-10  
; PRIOR APPLICATION NUMBER: US/10/637,011  
; PRIOR FILING DATE: 2003-08-08  
; PRIOR APPLICATION NUMBER: US/09/514,245B  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: FR 97/15396  
; PRIOR FILING DATE: 1997-12-05  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 99  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Type A PWD circovirus  
US-10-682-420-99

Query Match 36.4%; Score 28; DB 15; Length 15;  
Best Local Similarity 45.5%; Pred. No. 6.2e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSLP 14  
|:|:|:|  
Db 1 LRFNIGQLP 11

Search completed: November 14, 2004, 13:37:00  
Job time : 80.6667 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:55:26 ; Search time 93.3333 Seconds  
(without alignments)  
57.653 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77

Sequence: 1 LBSLSFQLGLYLSPH 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	77	100.0	15	3 AAY92953	Aay92953 Transform
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4	31	40.3	15	5 ABP58975	Abp58975 Human I k
5	30	39.0	15	5 AAM47809	Aam47809 Miniature
6	29	37.7	11	8 ADN03302	Adn03302 Exemplary
7	29	37.7	12	3 AAB07274	Aab07274 Human pep
8	29	37.7	12	6 ABR00682	Abr00682 HCV nonst
9	29	37.7	13	6 ABR00699	Abr00699 HCV nonst
10	29	37.7	13	6 ABR00693	Abr00693 HCV nonst
11	29	37.7	14	4 AAM37619	Aam37619 Human pep
12	29	37.7	14	6 ABR00703	Abr00703 HCV nonst
13	29	37.7	14	6 ABR00706	Abr00706 HCV nonst
14	29	37.7	15	6 ABR00715	Abr00715 HCV nonst
15	29	37.7	15	6 ABR00714	Abr00714 HCV nonst
16	28	36.4	9	6 ABP75290	Abp75290 Chlamydia
17	28	36.4	10	8 ADI46351	Adi46351 Permeabil
18	28	36.4	10	8 ADP87353	Adp87353 Human cla
19	28	36.4	11	1 AAP50351	Aap50351 Antigenic
20	28	36.4	11	1 AAP50388	Aap50388 Adult T-c
21	28	36.4	13	3 AAB34406	Aab34406 Gene 33 h
22	28	36.4	14	7 ADD90504	Add90504 Novel hum
23	28	36.4	14	7 ADG90323	Adg90323 Human sec
24	27	35.1	9	4 AAE03688	Aae03688 Pytho re
25	27	35.1	9	5 ABJ08453	Abj08453 Hepatitis

ALIGNMENTS

RESULT 1  
AAY93106  
ID AAY93106 standard; peptide; 15 AA.  
XX  
AC AAY93106;  
XX  
DT 08-NOV-2000 (first entry)  
XX  
DE Transforming growth factor inhibitory peptide P152.  
XX  
KW Hepatotrophic; antagonist; transforming growth factor beta1; TGF-beta1;  
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200031135-A1.  
XX  
PD 02-JUN-2000.  
XX  
PF 23-NOV-1999; 99WO-ES000375.  
XX  
PR 24-NOV-1998; 98ES-00002465.  
(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
Borras Cuesta F;  
WPI; 2000-411935/35.  
Peptides that antagonize binding of transforming growth factor beta1,  
useful for treatment of liver disease, especially cirrhosis, are partial  
sequences of the factor or its receptors.  
Disclosure; Page 33; 86pp; Spanish.  
The invention relates to synthetic peptides that antagonise the binding  
of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in  
vivo which have partial amino acid sequences identical, or similar, with  
those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent  
examples of the peptides of the invention. The peptides act by  
competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.  
they are inhibitors of stimulation of collagen synthesis in liver cells  
and inhibitors of synthesis of proteolytic enzymes able to degrade the  
extracellular matrix. The peptides, their mimetopes and/or DNA (or  
expression systems) encoding the peptides are used for treatment of liver  
disease, specifically cirrhosis

```
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDSLSPQLGLYLSPPH 15
Db 1 LDSLSPQLGLYLSPPH 15

RESULT 2
AAY2953
ID AAY2953 standard; peptide; 15 AA.
XX
XX AAY2953;
XX
XX 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide #9.
XX
XX Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX extracellular matrix degradation inhibitor; mimotope; cirrhosis.
XX
XX Homo sapiens.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Segastibelza JJ, Prieto Valtuena J;
XX Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor beta1,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Claim 10; Page 82; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-beta1 and/or its receptors. Peptides AAY2945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis.
XX
XX Sequence 15 AA;
Query Match 100.0%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDSLSPQLGLYLSPPH 15
Db 1 LDSLSPQLGLYLSPPH 15

RESULT 3
AAG83462
ID AAG83462 standard; peptide; 10 AA.
XX
XX AAG83462;
XX
XX 11-SEP-2001 (first entry)
XX
XX Arabidopsis thaliana peptide ligand #102.
XX
XX Plant; peptide pesticide; peptide herbicide; agricultural research.
XX
XX Arabidopsis thaliana.
XX
XX WO200142279-A2.
XX
XX 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB004781.
XX
XX 13-DEC-1999; 99GB-00029469.
XX
XX (PROT-) PROTEOM LTD.
XX
XX Roberts GW, Heal JR;
XX
XX WPI; 2001-381629/40.
XX
XX A set of peptide ligands for agricultural research and development of
XX therapeutic agents comprise specific complementary peptides to proteins
XX encoded by genes of plant genomes.
XX
XX Example 4; Page 45; 201pp; English.
XX
XX The present invention relates to a set of peptide ligands consisting of
XX specific complementary peptides to proteins encoded by genes of plant
XX genomes. The present sequence is one such peptide from Arabidopsis
XX thaliana. The peptides of the present invention are useful in an assay to
XX identify a peptide, especially a peptide pesticide or herbicide. The
XX peptides are also useful for tools for agricultural research and
XX development
XX
XX Sequence 10 AA;
Query Match 40.3%; Score 31; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 98;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12
Db 1 SLTFQLLLFL 10

RESULT 4
ABP58975
ID ABP58975 standard; peptide; 15 AA.
XX
XX ABP58975;
XX
XX 14-APR-2003 (first entry)
XX
XX Human I kappa B kinase inhibitor 37.40 N-terminal peptide.
XX
XX Human; I kappa B kinase inhibitor 37.40; recombinant production;
XX gene therapy; cancer; tumour; angiodysplasia; cardiovascular disorder;
XX neurological disorder; immune disorder; inflammatory condition;
XX cytostatic; antineoplastic; immunomodulator; N-terminal peptide;
XX enzyme linked immunosorbent assay; ELISA.
XX
XX Homo sapiens.
XX
XX CN1361264-A.
XX
XX 31-JUL-2002.
```

XX	26-DEC-2000; 2000CN-00136306.
PF	
XX	26-DEC-2000; 2000CN-00136306.
XX	
XX	(BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA	
XX	
PI	Mao Y, Xie Y;
XX	
XX	WPI; 2002-751595/82.
DR	
XX	
PT	Human inhibitor molecule I kappa B kinase 37.40 polypeptides and
PT	polynucleotides encoding this polypeptide.
XX	
XX	Example 5; Page 18 (Disclosure); 33pp; Chinese.
PS	
XX	The invention relates to human I kappa B kinase inhibitor 37.40
XX	(ABP58974) and nucleic acids encoding it (ABZ70827). The protein has a
CC	molecular weight of 37.4 kD. The invention also relates to a method for
CC	the recombinant production of the protein, an antagonist of the protein,
CC	and the use of the protein, gene and antagonist in therapeutic
CC	applications. I kappa B kinase inhibitor 37.40 can be used in the
CC	treatment of a variety of diseases such as cancer, angiocardiopathy,
CC	neurological disorders, immune disorders and inflammatory conditions. The
CC	present sequence represents the 15 N-terminal amino acids of human I
CC	kappa B kinase inhibitor 37.40 used in ELISA (enzyme linked immunosorbent
CC	assay) in an exemplification of the invention
XX	
XX	Sequence 15 AA;
SQ	
Query Match	40.3%; Score 31; DB 5; Length 15;
Best Local Similarity	75.0%; Pred. NO. 1.5e+02;
Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy	6 FQLGLYLS 13
Db	5 FLGLYIS 12
RESULT 5	
AAM47809	
ID	AAM47809 standard; peptide; 15 AA.
XX	
AC	AAM47809;
XX	
DT	15-FEB-2002 (first entry)
XX	
DE	Miniature protein 9.
XX	
KW	Avian pancreatic polypeptide; alpha helix domain; modulate transcription;
KW	miniature protein.
XX	
OS	Synthetic.
XX	
XX	WO200181375-A2.
PN	
XX	
PD	01-NOV-2001.
XX	
PF	24-APR-2001; 2001WO-US013023.
XX	
XX	24-APR-2000; 2000US-0199408P.
PR	16-OCT-2000; 2000US-0240566P.
PR	30-JAN-2001; 2001US-0265099P.
PR	23-FEB-2001; 2001US-0271368P.
XX	
XX	(UYUA ) UNIV YALE.
PA	
XX	
PI	Schepartz Shrader A, Chin JWK, Zutshi R, Rutledge SE;
PI	Kehlbeck Martin JD, Zondlo NJ;
XX	
XX	WPI; 2002-041395/05.
DR	
XX	
PT	Polypeptide scaffold e.g. an avian pancreatic polypeptide that comprises

modification by substitution of an amino acid residue, that is exposed on the alpha helix domain of the polypeptide is useful for screening for drugs.

Example 17; Fig 5; 8lpp; English.

The invention relates to an avian pancreatic polypeptide, modified by substitution of at least one amino acid residue, where the residue is being exposed on the alpha helix domain of the polypeptide when the polypeptide is in a tertiary form. The polypeptide is useful for screening drugs to identify agents capable of binding to the same binding site as the avian pancreatic polypeptide. It is also useful for diagnostic purposes to identify the presence and/or detect the levels of DNA or protein that binds to the polypeptide, in treatment of diseases associated with the presence of a particular DNA or protein, where the polypeptide can be used to bind to DNA to promote or inhibit transcription and for identifying binding partners. The present sequence is that of a miniature protein of the invention used to modulate the interaction between a known protein and another molecule

Sequence 15 AA;

Query Match 39.0%; Score 30; DB 5; Length 15;  
Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FQLGLYL 12  
|||  
DB 6 FQLGWYL 12

RESULT 6  
ADN03302  
ID ADN03302 standard; peptide; 11 AA.  
XX ADN03302;  
XX 17-JUN-2004 (first entry)  
XX Exemplary peptide ligand for proteome analysis #26.  
XX Peptide ligand; proteome; capture compound; mass spectrometry;  
KW protein separation;  
KW matrix assisted laser desorption ionisation-time of flight; MALDI-TOF.  
XX Unidentified.  
XX US2003119021-A1.  
XX  
XX 26-JUN-2003.  
XX  
XX 16-JUL-2002; 2002US-00197954.  
XX  
XX 16-JUL-2001; 2001US-0306019P.  
XX 21-AUG-2001; 2001US-0314123P.  
XX 11-MAR-2002; 2002US-0363433P.  
XX  
XX (KOST/) KOSTER H.  
XX (SIDD/) SIDDIQI S.  
XX (LITT/) LITTLE D P.  
XX  
XX Koster H, Siddiqi S, Little DP;  
XX WPI; 2004-059185/06.  
XX  
XX Collection of capture compounds capable of binding to biomolecules to form complexes that are stable under mass spectrometry conditions, useful for analysis of biomolecules, especially proteins.  
XX Disclosure; SEQ ID NO 26; 165pp; English.  
XX  
XX The invention relates to a collection of capture compounds capable of binding to biomolecules to form complexes that are stable under mass

CC spectrometry conditions. The formulae for the capture compounds comprises  
 CC sets of compounds of formula (I)-(III) given in the specification. Also  
 CC included are analysis of biomolecules (by contacting a composition  
 CC comprising a biomolecule with the above collection and identifying or  
 CC detecting bound biomolecules), separating protein conformers (by  
 CC contacting a composition comprising a biomolecule with the above  
 CC collection, separating the members of a complex mixture of biomolecules  
 CC bound proteins), reducing diversity of a complex mixture of biomolecules  
 CC (by contacting the mixture with the above collection and separating each  
 CC set of complexes of capture compounds with biomolecules from the other  
 CC sets) and identifying phenotype-specific biomolecules (by sorting cells  
 CC from a single subject into sets according to a phenotype, contacting  
 CC mixtures of biomolecules from each set with the above collection and  
 CC comparing the patterns of biomolecule binding from each set). The  
 CC collection of capture compounds is useful for the analysis of  
 CC biomolecules, especially proteins (e.g. analysis of a proteome), using  
 CC mass spectrometry, especially matrix assisted laser desorption ionisation  
 CC -time of flight (MALDI-TOF) mass spectrometry. The present sequence is an  
 CC exemplary peptide ligand which may be incorporated into a capture  
 CC compound of the invention.

XX SQ Sequence 11 AA;

Query Match 37.7%; Score 29; DB 8; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSPQLGL 10  
 :|||:| ||  
 Db 2 MDLAFSGGL 11

RESULT 7

AB07274  
 ID AAB07274 standard; peptide; 12 AA.

XX AC

XX AAB07274;

XX 17-OCT-2000 (first entry)

XX Human peptide-mimetic # 108.

XX Human; peptide-mimetic; tumour metastasis; E-selectin; adhesion molecule;  
 KW Lewis antigen; anti-adhesion therapy.

XX Homo sapiens.

XX WO200027420-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-US026277.

XX 06-NOV-1998; 98US-0107478P.

XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.

XX (UYPE-) UNIV PENNSYLVANIA.

XX Blaszczyk-Thurin M, Kieber-Emmons T;

XX WPI; 2000-376309/32.

XX Peptidomimetics of carbohydrate Lewis ligands useful for modulating  
 PT inflammation, metastasis and angiogenesis.

XX Claim 8; Page 58; 107pp; English.

XX Tumour metastasis requires detachment of malignant cells from the primary  
 CC tumour, penetration of blood or lymph vessels and attachment to the  
 CC endothelium of distant organs, ultimately resulting in the formation of  
 CC new tumours. The selectin family of adhesion molecules is implicated in  
 CC this process. E-selectin is a calcium-dependent molecule expressed by  
 CC activated vascular endothelium. E-selectins bind to glycoconjugates

CC carrying a terminal tetraasaccharide Lewis antigen, which are found on  
 CC tumour cell surfaces. One such Lewis antigen is sialyl (SA)-Lea. The  
 CC binding of selectin molecules to their ligands is thought to be an  
 CC important step in metastasis. Therefore, inhibition of E-selectin-  
 CC dependent carbohydrate-mediated interactions is thought to be a target  
 CC for anti-cancer therapy. The present sequence is a Human Family II  
 CC peptido-mimetic of E-selectin-SA-Lea binding. This sequence blocks E-  
 CC selectin-SA-Lea binding and therefore blocks adhesion of tumour cells and  
 CC leukocytes to endothelial cells and hence metastasis. This sequence is  
 CC therefore an E-selectin antagonist

XX SQ Sequence 12 AA;

Query Match 37.7%; Score 29; DB 3; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DSLSPQLGLY 11  
 :|||:| ||  
 Db 1 DKETFELGLF 10

RESULT 8

ABR00682

ID ABR00682 standard; peptide; 12 AA.

XX AC ABR00682;

XX 01-APR-2003 (first entry)

XX HCV nonstructural protein NS5A complementary peptide 88.

XX HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;  
 KW non-structural protein; virucide; gene therapy; immunological; NS5A;  
 KW complementary peptide.

XX Hepatitis C virus.

XX WO200289731-A2.

XX 14-NOV-2002.

XX 03-MAY-2002; 2002WO-US013951.

XX 03-MAY-2001; 2001US-0288687P.

XX 31-AUG-2001; 2001US-0316805P.

XX (STRD ) UNIV STANFORD.

XX (ELIL ) LILLY & CO ELI.

XX Glenn JS, Myers TM, Glass JI;

XX WPI; 2003-201229/19.

XX Identifying a compound for treating Hepatitis C virus (HCV) infection by  
 PT assessing the ability of a compound to interfere the binding of an  
 PT amphipathic helix of an HCV nonstructural protein with cytoplasmic  
 PT membranes of eukaryotic cell.

XX Claim 44; Page 13; 43pp; English.

XX The invention relates to a novel method for identifying a compound useful  
 CC for treating Hepatitis C virus (HCV) infection. The method comprises  
 CC assessing the ability of a candidate compound to interfere with the  
 CC binding of an amphipathic helix present in the N-terminal region of an  
 CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic  
 CC cell, where a compound that interferes with the binding is useful for  
 CC treating the infection. The compounds of the invention have virucide, and  
 CC hepatotropic activity. The peptides may have a use in gene therapy. The  
 CC methods and compounds are useful for treating Hepatitis C virus (HCV)  
 CC infection. The composition is useful for eliciting an immunological  
 CC response against HCV. The peptides are useful for the preparation of a  
 CC medicament for the prevention or treatment of HCV infection in a human.

CC The sequences shown in ABR00595-ABR00746 represent complementary peptides  
CC of varying lengths to the amphipathic helix of the HCV nonstructural  
CC protein NS5A  
XX  
SQ Sequence 12 AA;

Query Match 37.7%; Score 29; DB 6; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15  
| | | | | : : :  
DB 1 LGFQPLGLKVAQH 12

## RESULT 9

ABR00699  
ID ABR00699 standard; peptide; 13 AA.

XX  
AC ABR00699;  
XX  
DT 01-APR-2003 (first entry)  
XX  
DE HCV nonstructural protein NS5A complementary peptide 105.  
XX  
KW HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;  
KW non-structural protein; virucide; gene therapy; immunological; NS5A;  
KW complementary peptide.  
XX  
OS Hepatitis C virus.

XX  
PN WO200289731-A2.

XX  
PD 14-NOV-2002.

XX  
PF 03-MAY-2002; 2002WO-US013951.

XX  
PR 03-MAY-2001; 2001US-0288687P.

XX  
PR 31-AUG-2001; 2001US-0316805P.

XX  
PA (STRD ) UNIV STANFORD.

XX  
PA (ELIL ) LILLY & CO ELI.

XX  
PI Glenn JS, Myers TM, Glass JI;

XX  
WPI; 2003-201229/19.

XX  
PT Identifying a compound for treating Hepatitis C virus (HCV) infection by  
PT assessing the ability of a compound to interfere the binding of an  
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic  
PT membranes of eukaryotic cell.  
XX  
PS Claim 44; Page 14; 43pp; English.

XX  
CC The invention relates to a novel method for identifying a compound useful  
CC for treating Hepatitis C virus (HCV) infection. The method comprises  
CC assessing the ability of a candidate compound to interfere with the  
CC binding of an amphipathic helix present in the N-terminal region of an  
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic  
CC cell, where a compound that interferes with the binding is useful for  
CC treating the infection. The compounds of the invention have virucide, and  
CC hepatotropic activity. The peptides may have a use in gene therapy. The  
CC methods and compounds are useful for treating Hepatitis C virus (HCV)  
CC infection. The composition is useful for eliciting an immunological  
CC response against HCV. The peptides are useful for the preparation of a  
CC medicament for the prevention or treatment of HCV infection in a human.  
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides  
CC of varying lengths to the amphipathic helix of the HCV nonstructural  
CC protein NS5A

XX  
SQ Sequence 13 AA;

Query Match 37.7%; Score 29; DB 6; Length 13;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15  
| | | | | : : :  
DB 2 LGFQPLGLKVAQH 13

## RESULT 10

ABR00693  
ID ABR00693 standard; peptide; 13 AA.

XX  
AC ABR00693;

XX  
DT 01-APR-2003 (first entry)

XX  
DE HCV nonstructural protein NS5A complementary peptide 99.

XX  
KW HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;  
KW non-structural protein; virucide; gene therapy; immunological; NS5A;  
KW complementary peptide.

XX  
OS Hepatitis C virus.

XX  
PN WO200289731-A2.

XX  
PD 14-NOV-2002.

XX  
PF 03-MAY-2002; 2002WO-US013951.

XX  
PR 03-MAY-2001; 2001US-0288687P.

XX  
PR 31-AUG-2001; 2001US-0316805P.

XX  
PA (STRD ) UNIV STANFORD.

XX  
PA (ELIL ) LILLY & CO ELI.

XX  
PI Glenn JS, Myers TM, Glass JI;

XX  
WPI; 2003-201229/19.

XX  
PT Identifying a compound for treating Hepatitis C virus (HCV) infection by  
PT assessing the ability of a compound to interfere the binding of an  
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic  
PT membranes of eukaryotic cell.

XX  
PS Claim 44; Page 14; 43pp; English.

XX  
CC The invention relates to a novel method for identifying a compound useful  
CC for treating Hepatitis C virus (HCV) infection. The method comprises  
CC assessing the ability of a candidate compound to interfere with the  
CC binding of an amphipathic helix present in the N-terminal region of an  
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic  
CC cell, where a compound that interferes with the binding is useful for  
CC treating the infection. The compounds of the invention have virucide, and  
CC hepatotropic activity. The peptides may have a use in gene therapy. The  
CC methods and compounds are useful for treating Hepatitis C virus (HCV)  
CC infection. The composition is useful for eliciting an immunological  
CC response against HCV. The peptides are useful for the preparation of a  
CC medicament for the prevention or treatment of HCV infection in a human.  
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides  
CC of varying lengths to the amphipathic helix of the HCV nonstructural  
CC protein NS5A

XX  
SQ Sequence 13 AA;

Query Match 37.7%; Score 29; DB 6; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3.1e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15  
| | | | | : : :  
DB 1 LGFQPLGLKVAQH 12

```
RESULT 11
AAM97619
ID AAM97619 standard; peptide; 14 AA.
XX
AC AAM97619;
XX
AC AAM97619;
XX
DT 24-JAN-2002 (first entry)
XX
XX
DE Human peptide #894 encoded by a SNP oligonucleotide.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.
XX
XX Homo sapiens.
OS
XX
XX WO200147944-A2.
PN
XX
XX 05-JUL-2001.
PD
XX
XX 28-DEC-2000; 2000WO-US035498.
PF
XX
XX 28-DEC-1999; 99US-0173419F.
PR
XX 27-DEC-2000; 2000US-00173419.
PR
XX (CURA-) CUPAGEN CORP.
PA
XX
XX Shinkets RA, Leach M;
PI
XX
XX WPI; 2001-465210/50.
DR
XX
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
PT
XX
XX Disclosure; Page 3863; 4143pp; English.
PS
XX
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
CC
XX
XX Sequence 14 AA;
SQ
Query Match 37.7%; Score 29; DB 4; Length 14;
Best Local Similarity 46.2%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 3 SLSFQGLGLVLSPH 15
DB 2 SLSFRTGCKVKKH 14
RESULT 12
ABR00703
ID ABR00703 standard; peptide; 14 AA.
XX
AC ABR00703;
XX
DT 01-APR-2003 (first entry)
XX
XX
DE HCV nonstructural protein NS5A complementary peptide 109.
XX
XX HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;
KW non-structural protein; virucide; gene therapy; immunological; NS5A;
KW complementary peptide.
XX
XX Hepatitis C virus.
OS
XX WO200289731-A2.
PN
XX 14-NOV-2002.
PD
XX 03-MAY-2002; 2002WO-US013951.
PF
XX 03-MAY-2001; 2001US-0288687P.
PR
XX 31-AUG-2001; 2001US-0316805P.
PR
XX (STRD ) UNIV STANFORD.
PA (ELIL ) LILLY & CO ELI.
XX
XX Glenn JS, Myers TM, Glass JI;
PI
XX WPI; 2003-201229/19.
DR
XX
XX Identifying a compound for treating Hepatitis C virus (HCV) infection by
PT assessing the ability of a compound to interfere the binding of an
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic
PT membranes of eukaryotic cell.
PT
XX
XX Claim 44; Page 14; 43pp; English.
PS
XX
XX The invention relates to a novel method for identifying a compound useful
CC for treating Hepatitis C virus (HCV) infection. The method comprises
CC assessing the ability of a candidate compound to interfere with the
CC binding of an amphipathic helix present in the N-terminal region of an
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic
CC cell, where a compound that interferes with the binding is useful for
CC treating the infection. The compounds of the invention have virucide, and
CC hepatotropic activity. The peptides may have a use in gene therapy. The
CC methods and compounds are useful for treating Hepatitis C virus (HCV)
CC infection. The composition is useful for eliciting an immunological
CC response against HCV. The peptides are useful for the preparation of a
CC medicament for the prevention or treatment of HCV infection in a human.
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides
CC of varying lengths to the amphipathic helix of the HCV nonstructural
CC protein NS5A
XX
XX Sequence 14 AA;
SQ
Query Match 37.7%; Score 29; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 4 LSFQGLGLVLSPH 15
DB 2 LGFQGLKVAQH 13
RESULT 13
ABR00706
ID ABR00706 standard; peptide; 14 AA.
XX
AC ABR00706;
XX
DT 01-APR-2003 (first entry)
XX
XX
DE HCV nonstructural protein NS5A complementary peptide 112.
```



XX HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;  
 KW non-structural protein; virucide; gene therapy; immunological; NS5A;  
 KW complementary peptide.  
 XX Hepatitis C virus.  
 OS  
 XX WO200289731-A2.  
 PN 14-NOV-2002.  
 XX  
 PD 03-MAY-2002; 2002WO-US013951.  
 XX  
 PF 03-MAY-2001; 2001US-0288687P.  
 XX  
 PR 31-AUG-2001; 2001US-0316805P.  
 XX  
 XX (STRD ) UNIV STANFORD.  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Glenn JS, Myers TM, Glass JI;  
 XX WPI; 2003-201229/19.  
 DR  
 XX Identifying a compound for treating Hepatitis C virus (HCV) infection by  
 PT assessing the ability of a compound to interfere the binding of an  
 PT amphipathic helix of an HCV nonstructural protein with cytoplasmic  
 PT membranes of eukaryotic cell.  
 XX  
 XX Claim 44; Page 14; 43pp; English.  
 PS  
 XX The invention relates to a novel method for identifying a compound useful  
 CC for treating Hepatitis C virus (HCV) infection. The method comprises  
 CC assessing the ability of a candidate compound to interfere with the  
 CC binding of an amphipathic helix present in the N-terminal region of an  
 CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic  
 CC cell, where a compound that interferes with the binding is useful for  
 CC treating the infection. The compounds of the invention have virucide, and  
 CC hepatotropic activity. The peptides may have a use in gene therapy. The  
 CC methods and compounds are useful for treating Hepatitis C virus (HCV)  
 CC infection. The composition is useful for eliciting an immunological  
 CC response against HCV. The peptides are useful for the preparation of a  
 CC medicament for the prevention or treatment of HCV infection in a human.  
 CC The sequences shown in ABR00595-ABR00746 represent complementary peptides  
 CC of varying lengths to the amphipathic helix of the HCV nonstructural  
 CC protein NS5A  
 XX  
 SQ Sequence 14 AA;  
 Query Match 37.7%; Score 29; DB 6; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 3.3e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 LSFQLGLYLSPH 15  
 DB 1 LGFQPLKVAQH 12  
 RESULT 14  
 ABR00715  
 ID ABR00715 standard; peptide; 15 AA.  
 XX  
 AC ABR00715;  
 XX  
 DT 01-APR-2003 (first entry)  
 XX  
 DE HCV nonstructural protein NS5A complementary peptide 121.  
 XX  
 KW HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;  
 KW non-structural protein; virucide; gene therapy; immunological; NS5A;  
 KW complementary peptide.  
 XX  
 OS Hepatitis C virus.  
 XX

PN WO200289731-A2.  
 XX 14-NOV-2002.  
 XX  
 PF 03-MAY-2002; 2002WO-US013951.  
 XX  
 PR 03-MAY-2001; 2001US-0288687P.  
 PR 31-AUG-2001; 2001US-0316805P.  
 XX  
 XX (STRD ) UNIV STANFORD.  
 PA (ELIL ) LILLY & CO ELI.  
 XX  
 PI Glenn JS, Myers TM, Glass JI;  
 XX WPI; 2003-201229/19.  
 DR  
 XX Identifying a compound for treating Hepatitis C virus (HCV) infection by  
 PT assessing the ability of a compound to interfere the binding of an  
 PT amphipathic helix of an HCV nonstructural protein with cytoplasmic  
 PT membranes of eukaryotic cell.  
 XX  
 XX Claim 44; Page 14; 43pp; English.  
 PS  
 XX The invention relates to a novel method for identifying a compound useful  
 CC for treating Hepatitis C virus (HCV) infection. The method comprises  
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 CC binding of an amphipathic helix present in the N-terminal region of an  
 CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic  
 CC cell, where a compound that interferes with the binding is useful for  
 CC treating the infection. The compounds of the invention have virucide, and  
 CC hepatotropic activity. The peptides may have a use in gene therapy. The  
 CC methods and compounds are useful for treating Hepatitis C virus (HCV)  
 CC infection. The composition is useful for eliciting an immunological  
 CC response against HCV. The peptides are useful for the preparation of a  
 CC medicament for the prevention or treatment of HCV infection in a human.  
 CC The sequences shown in ABR00595-ABR00746 represent complementary peptides  
 CC of varying lengths to the amphipathic helix of the HCV nonstructural  
 CC protein NS5A  
 XX  
 SQ Sequence 15 AA;  
 Query Match 37.7%; Score 29; DB 6; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 3.6e+02;  
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 4 LSFQLGLYLSPH 15  
 DB 1 LGFQPLKVAQH 12  
 RESULT 15  
 ABR00714  
 ID ABR00714 standard; peptide; 15 AA.  
 XX  
 AC ABR00714;  
 XX  
 DT 01-APR-2003 (first entry)  
 XX  
 DE HCV nonstructural protein NS5A complementary peptide 120.  
 XX  
 KW HCV; hepatitis C virus; amphipathic helix; N-terminal; hepatotropic;  
 KW non-structural protein; virucide; gene therapy; immunological; NS5A;  
 KW complementary peptide.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO200289731-A2.  
 XX  
 PD 14-NOV-2002.  
 XX  
 PF 03-MAY-2002; 2002WO-US013951.  
 XX  
 PR 03-MAY-2001; 2001US-0288687P.  
 XX

PR 31-AUG-2001; 2001US-031680SP.  
XX (STED ) UNIV STANFORD.  
PA (ELIL ) LILLY & CO ELI.  
XX  
XX Glenn JS, Myers TM, Glass JI;  
XX WPI; 2003-201229/19.  
XX  
XX Identifying a compound for treating Hepatitis C virus (HCV) infection by  
PT assessing the ability of a compound to interfere the binding of an  
PT amphipathic helix of an HCV nonstructural protein with cytoplasmic  
PT membranes of eukaryotic cell.  
XX  
XX Claim 44; Page 14; 43pp; English.  
XX  
XX The invention relates to a novel method for identifying a compound useful  
CC for treating Hepatitis C virus (HCV) infection. The method comprises  
CC assessing the ability of a candidate compound to interfere with the  
CC binding of an amphipathic helix present in the N-terminal region of an  
CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic  
CC cell, where a compound that interferes with the binding is useful for  
CC treating the infection. The compounds of the invention have virucide, and  
CC hepatotropic activity. The peptides may have a use in gene therapy. The  
CC methods and compounds are useful for treating Hepatitis C virus (HCV)  
CC infection. The composition is useful for eliciting an immunological  
CC response against HCV. The peptides are useful for the preparation of a  
CC medicament for the prevention or treatment of HCV infection in a human.  
CC The sequences shown in ABR00595-ABR00746 represent complementary peptides  
CC of varying lengths to the amphipathic helix of the HCV nonstructural  
CC protein NS5A  
XX  
XX Sequence 15 AA;  
SQ

Query Match 37.7%; Score 29; DB 6; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.6e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 4 LSFQLGLYLSPH 15  
| | | | | : :  
Db 2 LGFQFGLKVAQH 13

Search completed: November 14, 2004, 13:11:18  
Job time : 94.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:56:07 ; Search time 100 Seconds  
(without alignments)  
86.306 Million cell updates/sec

Title: US-09-831-253F-9  
Perfect score: 77  
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	27	35.1	12	1	FRE1_LITIN	P82021 litoria inf
2	26	33.8	15	1	ASPI_LACSN	P82648 lactobacill
3	25	32.5	15	2	Q9R470	Q9r4t0 rhodobacter
4	24	31.2	15	2	Q7M3G3	Q7m3g3 bos taurus
5	23	29.9	9	2	P92072	P92072 euhadra her
6	23	29.9	15	2	Q9TR52	Q9tr52 bos taurus
7	22	28.6	12	1	CD11_LITCH	P62567 litoria chl
8	22	28.6	12	1	CD11_LITGI	P62566 litoria gil
9	22	28.6	12	1	CD11_LITSP	P62565 litoria spl
10	22	28.6	12	1	CD11_LITXA	P62564 litoria xan
11	22	28.6	15	1	TRPA_LEUMA	P81753 leucophaea
12	22	28.6	15	2	Q9MYT7	Q9myt7 sus scrofa
13	21	27.3	8	2	Q6LDP8	Q6ldp8 pseudomonas
14	21	27.3	8	2	AAA26011	Aaa26011 pseudomon
15	21	27.3	8	2	AAA26012	Aaa26012 pseudomon
16	21	27.3	12	1	CD14_LITCH	P62581 litoria chl
17	21	27.3	12	1	CD14_LITXA	P62582 litoria xan
18	21	27.3	13	1	RAN7_RANCA	P82822 rana catesb
19	20	26.0	8	2	P92211	P92211 agropyron c
20	20	26.0	8	2	P92215	P92215 amblyopyrum
21	20	26.0	8	2	P92219	P92219 australopyr
22	20	26.0	8	2	P92222	P92222 bromus iner
23	20	26.0	8	2	P92227	P92227 crithopsis
24	20	26.0	8	2	P92373	P92373 haynaldia v
25	20	26.0	8	2	P92382	P92382 hordeum bra
26	20	26.0	8	2	P92384	P92384 hordeum mur
27	20	26.0	8	2	P92388	P92388 henrardia p
28	20	26.0	8	2	P92391	P92391 heteranthe
29	20	26.0	8	2	P92394	P92394 hordeum vul
30	20	26.0	8	2	P92404	P92404 lophopyrum
31	20	26.0	8	2	P92422	P92422 psathyrosta

32	20	26.0	8	2	P92426	P92426 pseudoroegn
33	20	26.0	8	2	P92428	P92428 peridictyon
34	20	26.0	8	2	P92431	P92431 aegilops ta
35	20	26.0	8	2	P92441	P92441 thinopyrum
36	20	26.0	8	2	P92443	P92443 taeniatheru
37	20	26.0	8	2	P93955	P93955 festucopsis
38	20	26.0	8	2	P93957	P93957 festucopsis
39	20	26.0	8	2	P93959	P93959 hordeum ere
40	20	26.0	8	2	P93961	P93961 psathyrosta
41	20	26.0	8	2	P93963	P93963 psathyrosta
42	20	26.0	8	2	P93965	P93965 secale stri
43	20	26.0	8	2	P93966	P93966 aegilops ep
44	20	26.0	8	2	P93970	P93970 eremopyrum
45	20	26.0	8	2	P93973	P93973 eremopyrum

ALIGNMENTS

RESULT 1  
FRE1\_LITIN STANDARD; PRT; 12 AA.  
AC P82021;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Frenatin 1.  
OS Litoria infrenata (Giant tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=61195;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=97368637; PubMed=9225251;  
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "The structures of the frenatin peptides from the skin secretion of  
the giant tree frog Litoria infrenata.";  
RL J. Pept. Sci. 2:117-124(1996).  
CC -!- FUNCTION: Wide spectrum antimicrobial peptide.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral  
glands.  
CC -!- MASS SPECTROMETRY: MW=1140; METHOD=PAB; RANGE=1-12; NOTE=Ref.1.  
KW Amidation; Amphibian defense peptide; Antibiotic;  
KW Direct protein sequencing.  
FT MOD\_RES 12 12 Leucine amide.  
SQ SEQUENCE 12 AA; 1141 MW; C622550BC365B72D CRC64;  
Query Match 35.1%; Score 27; DB 1; Length 12;  
Best Local Similarity 70.0%; Pred. No. 8.9e+02; Mismatches 2; Indels 0; Gaps 0;  
Matches 7; Conservative 1;  
QY 1 LDSLSFQLGL 10  
||:|||||  
Db 3 LDALSGILGL 12  
RESULT 2  
ASPI\_LACSN STANDARD; PRT; 15 AA.  
ID ASPI\_LACSN  
AC P82648;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Acid shock protein 1 (Fragment).  
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=16295;  
RN [1]  
RP SEQUENCE.

```

RC STRAIN=CB1;
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Coconcelli P.S., Gobbetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CB1.";
RL Microbiology 147:1863-1873(2001).
CC -I- INDUCTION: Overexpressed in acid environments.
KW Direct protein sequencing.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Query Match 33.8%; Score 26; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFQLGLYL 12
DB 1 SPKGLFL 8

RESULT 3
Q9R4T0 PRELIMINARY; PRT; 15 AA.
AC Q9R4T0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Periplasmic protein 5 (Fragment).
OS Rhodobacter sphaeroides (Rhodospirillum rubrum sphaeroides).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1063;
RN [1]_
RP SEQUENCE.
RX MEDLINE=95160605; PubMed=7857198;
RA Sabaty M., Gagnon J., Vermeglio A.;
RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the
RT photodinitrifier Rhodobacter sphaeroides forma sp. denitrificans under
RT anaerobic or aerobic condition.";
RL Arch. Microbiol. 162:335-343(1994).
SQ SEQUENCE 15 AA; 1718 MW; DA5BF4BD9AEBE157 CRC64;

Query Match 32.5%; Score 25; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.6e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DSLSFQLGL 10
DB 4 DSETFQSGM 12

RESULT 4
Q7M3G3 PRELIMINARY; PRT; 15 AA.
AC Q7M3G3
DT 01-WAR-2004 (TrEMBLrel. 26, Created)
DT 01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 28K serine proteinase homolog (fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE.
RX MEDLINE=90343797; PubMed=2200404;
RA Ho P.L., Carpenter M.R., Smillie L.B., Gambarini A.G.;
RT "Co-purification of proteases with basic fibroblast growth factor
RT (FGF).";
RL Biochem. Biophys. Res. Commun. 170:769-774(1990).
DR PIR; A35417; A35417.
FT NON_TER 1 1
FT NON_TER 15 15

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SQ SEQUENCE 15 AA; 1710 MW; 6358BCB0D3627321 CRC64;

Query Match 31.2%; Score 24; DB 2; Length 15;
Best Local Similarity 30.8%; Pred. No. 4e+03;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 DSLSFQLGLYLSP 14
DB 3 DSIDYRKKGVTTP 15

RESULT 5
P92072 PRELIMINARY; PRT; 9 AA.
AC P92072
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ATPase subunit 8 (Fragment).
OS Euhadra herklotsi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Helicoidea; Bradybaenidae; Euhadra.
OX NCBI_TaxID=58912;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Hepatopancreas;
RA Yamazaki N., Ueshima R., Terrett J.A., Yokobori S., Kaifu M.,
RA Segawa R., Kobayashi T., Numachi K., Ueda T., Nishikawa K.,
RA Watanabe K., Thomas R.H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; 271697; CRA96373.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1009 MW; 380CB1F775B736C7 CRC64;

Query Match 29.9%; Score 23; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LSPH 15
DB 4 LSPH 7

RESULT 6
Q9TR52 PRELIMINARY; PRT; 15 AA.
AC Q9TR52
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE LMP7 multicatalytic proteinase complex subunit (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_
RP SEQUENCE.
RX MEDLINE=95403474; PubMed=7673255;
RA Cardozo C., Eleuteri A.M., Orłowski M.;
RT "Differences in catalytic activities and subunit pattern of
RT multicatalytic proteinase complexes (proteasomes) isolated from bovine
RT pituitary, lung, and liver. Changes in LMP7 and the component
RT necessary for expression of the chymotrypsin-like activity.";
RL J. Biol. Chem. 270:22645-22651(1995).
SQ SEQUENCE 15 AA; 1640 MW; DB334789F42EB2DD CRC64;

Query Match 29.9%; Score 23; DB 2; Length 15;
Best Local Similarity 27.3%; Pred. No. 6.1e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

```

QY 3 SLSFQLGLYL 13  
: ||| :  
Db 5 AKFKQGVFA 15

## RESULT 7

CD11 LITX  
ID -CD11 LITX STANDARD; PRT; 12 AA.  
AC P62567; P56245; P81253;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Caeridin 1.1/1.2/1.3.  
OS Litoria chloris (Blue-thighed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=86064;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Skin secretion.  
RX MEDLINE=98175802; PubMed=9516047;  
RA Steinboerner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "New antibiotic caerin 1 peptides from the skin secretion of the  
RT Australian tree frog Litoria chloris. Comparison of the activities of  
RT the caerin 1 peptides from the genus Litoria.";  
RL J. Pept. Res. 51:121-126(1998).  
RC -!- FUNCTION: Caeridins show neither neuropeptide activity nor  
CC antibiotic activity.  
CC -!- TISSUE SPECIFICITY: Secreted by the skin.  
CC -!- PTM: Isomerization alpha-beta of the Asp-4 residue in caeridin  
CC 1.2; a cyclic succinimide may be formed between Asp-4 and Gly-5  
CC residues in caeridin 1.3 (By similarity).  
CC Amidation; Amphibian defense peptide; Direct protein sequencing.  
KW MOD RES 12 12  
FT MOD RES 12 12 Leucine amide.  
SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;

Query Match 28.6%; Score 22; DB 1; Length 12;  
Best Local Similarity 60.0%; Pred. No. 7.3e+03;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10  
: ||| :  
Db 3 LDGLLGLTGL 12

## RESULT 8

CD11 LITX  
ID -CD11 LITX STANDARD; PRT; 12 AA.  
AC P62566; P56245; P81253;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Caeridin 1.1/1.2/1.3.  
OS Litoria gilleni (Centralian tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=39405;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Parotoid gland;  
RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "Peptides from Australian frogs. The structures of the caerins and  
RT caeridins from Litoria gilleni.";  
RL J. Chem. Res. 139:937-961(1993).  
RN [2]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RA Waugh R.J., Steinboerner S.T., Bowie J.H., Wallace J.C., Tyler M.J.,  
RA Hu P., Gross M.L.;  
RT "Two isomeric alpha and beta aspartyl dodecapeptides and their cyclic  
RT amino succinyl analogue from the Australian tree frog Litoria

RT gilleni.";  
RL Aust. J. Chem. 48:1981-1987(1995).  
CC -!- FUNCTION: Caeridins show neither neuropeptide activity nor  
CC antibiotic activity.  
CC -!- TISSUE SPECIFICITY: Specifically secreted by the skin parotoid  
CC and/or rostral glands.  
CC -!- PTM: Isomerization alpha-beta of the Asp-4 residue in caeridin  
CC 1.2; a cyclic succinimide may be formed between Asp-4 and Gly-5  
CC residues in caeridin 1.3.  
CC -!- MASS SPECTROMETRY: MW=1140; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing.  
FT MOD RES 12 12 Leucine amide.  
SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;

Query Match 28.6%; Score 22; DB 1; Length 12;

Best Local Similarity 60.0%; Pred. No. 7.3e+03;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10  
: ||| :  
Db 3 LDGLLGLTGL 12

## RESULT 9

CD11 LITSP  
ID -CD11 LITSP STANDARD; PRT; 12 AA.  
AC P62565; P56245; P81253;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Caeridin 1.1/1.2/1.3.  
OS Litoria splendida (Magnificent tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=30345;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Parotoid gland;  
RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "Peptides from Australian frogs. Structures of the caerins and  
RT caeridin 1 from Litoria splendida.";  
RL J. Chem. Soc. Perkin Trans. I 1:3173-3178(1992).  
CC -!- FUNCTION: Caeridins show neither neuropeptide activity nor  
CC antibiotic activity.  
CC -!- TISSUE SPECIFICITY: Specifically secreted by the skin parotoid  
CC and/or rostral glands.  
CC -!- PTM: Isomerization alpha-beta of the Asp-4 residue in caeridin  
CC 1.2; a cyclic succinimide may be formed between Asp-4 and Gly-5  
CC residues in caeridin 1.3 (By similarity).  
CC -!- MASS SPECTROMETRY: MW=1139; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing.  
FT MOD RES 12 12 Leucine amide.  
SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;

Query Match 28.6%; Score 22; DB 1; Length 12;

Best Local Similarity 60.0%; Pred. No. 7.3e+03;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10  
: ||| :  
Db 3 LDGLLGLTGL 12

## RESULT 10

CD11 LITXA  
ID -CD11 LITXA STANDARD; PRT; 12 AA.  
AC P62564; P56245; P81253;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Caeridin 1.1/1.2/1.3.  
OS Litoria xanthomera (Orange-thighed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=79697;  
 RN [1]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RX MEDLINE=97374000; PubMed=9230483;  
 RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,  
 RA Ramsey S.L.;  
 RT "New caerin antibacterial peptides from the skin glands of the  
 RT Australian tree frog *Litoria xanthomera*.";  
 RL J. Pept. Sci. 3:181-185(1997).  
 CC -|- FUNCTION: Caeridins show neither neuropeptide activity nor  
 CC antibiotic activity.  
 CC -|- TISSUE SPECIFICITY: Secreted by the skin dorsal glands.  
 CC -|- PTM: Isomerization alpha-beta of the Asp-4 residue in caerin  
 CC 1.2; a cyclic succinimide may be formed between Asp-4 and Gly-5  
 CC residues in caerin 1.3 (By similarity).  
 CC -|- MASS SPECTROMETRY: MW=1140; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.  
 KW Amidation; Amphibian defense peptide; Direct protein sequencing.  
 FT MOD\_RES 12 12 Leucine amide.  
 FT SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;  
 SQ  
 Query Match 28.6%; Score 22; DB 1; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 7.3e+03;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 LDSLFSQGL 10  
 |||||  
 Db 3 LDGLLGLGL 12  
 RESULT 11  
 TRPA\_LEUMA STANDARD; PRT; 15 AA.  
 AC P81753;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tachykinin-related peptide 10 (leuTRP 10).  
 OS Leucophaea madecae (Madeira cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OX NCBI\_TaxID=6988;  
 RN [1]  
 RN SEQUENCE, AND MASS SPECTROMETRY.  
 RX TISSUE=Brain;  
 RX MEDLINE=9726266; PubMed=9114447;  
 RA Muren J.E., Nessel D.R.;  
 RT "Seven tachykinin-related peptides isolated from the brain of the  
 RT Madeira cockroach; evidence for tissue-specific expression of  
 RT isoforms.";  
 RL Peptides 18:7-15(1997).  
 CC -|- FUNCTION: Myoactive peptide. Increases the amplitude and frequency  
 CC of spontaneous contractions and tonus of hindgut muscle.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Brain.  
 CC -|- MASS SPECTROMETRY: MW=1436.0; METHOD=MALDI; RANGE=1-15;  
 CC NOTE=Ref.1.  
 KW Direct protein sequencing; Neuropeptide; Tachykinin.  
 FT SEQUENCE 15 AA; 1438 MW; 298572F373FA7007 CRC64;  
 SQ  
 Query Match 28.6%; Score 22; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.2e+03;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LDSL 5  
 |||||  
 Db 3 LDSL 7

RESULT 12

Q9MYT7  
 ID Q9MYT7 PRELIMINARY; PRT; 15 AA.  
 AC Q9MYT7;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Type I collagen alpha 1 chain (Fragment).  
 GN Name=collagen;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Intestine;  
 RC MEDLINE=21560060; PubMed=11704606;  
 RA Alho H.S., Inkinen K.A., Salminen U.S., Maasilta P.K., Taskinen E.I.,  
 RA Glumoff V., Vuorio E.I., Ikonen T.S., Harjula A.L.J.;  
 RT "Collagens I and III in a porcine bronchial model of obliterative  
 RT bronchiolitis.";  
 RL Am. J. Respir. Crit. Care Med. 164:1519-1525(2001).  
 DR EMBL; AJ289757; CAB94729.1; -.  
 KW Collagen.  
 FT NON\_TER 1 1  
 FT SEQUENCE 15 AA; 1680 MW; 895303298274A63A CRC64;  
 SQ  
 Query Match 28.6%; Score 22; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 9.2e+03;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 7 OLGLYLSP 14  
 :|||  
 Db 4 EFGIDLSP 11  
 RESULT 13  
 Q6LDP8  
 ID Q6LDP8 PRELIMINARY; PRT; 8 AA.  
 AC Q6LDP8;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE (strain Pa388) toxA gene encoding exotoxin A, 5' end ((strain PA103)  
 DE toxA gene encoding exotoxin A, 5' end (Fragment).  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RA Pritchard A.E., Vasil M.L.;  
 RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=90202723; PubMed=2156808;  
 RA Pritchard A.E., Vasil M.L.;  
 RT "Possible insertion sequences in a mosaic genome organization upstream  
 RT of the exotoxin A gene in *Pseudomonas aeruginosa*.";  
 RL J. Bacteriol. 172:2020-2028(1990).  
 DR EMBL; M27186; AAA26012.1; -.  
 DR EMBL; M27175; AAA26011.1; -.  
 FT NON\_TER 8 8  
 FT SEQUENCE 8 AA; 1046 MW; F94371F7605721E6 CRC64;  
 SQ  
 Query Match 27.3%; Score 21; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 10 LYLSPH 15  
 :|||  
 Db 1 MHLIPH 6

```
RESULT 14
AAA26011 PRELIMINARY; PRT; 8 AA.
AC AAA26011;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE (STRAIN PA103) TOXA GENE ENCODING EXOTOXIN A, 5' END
DE (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90202723; PubMed=2156808;
RA Pritchard A.E., Vasil M.L.;
RT "Possible insertion sequences in a mosaic genome organization upstream
RT of the exotoxin A gene in Pseudomonas aeruginosa.";
RL J. Bacteriol. 172:2020-2028(1990).
DR EMBL; M27175; AAA26011.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; F94371F7605721E6 CRC64;

Query Match 27.3%; Score 21; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 LYLSPH 15
Db 1 MHLIPH 6

RESULT 15
AAA26012 PRELIMINARY; PRT; 8 AA.
AC AAA26012;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE (STRAIN PS388) TOXA GENE ENCODING EXOTOXIN A, 5' END
DE (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RA Pritchard A.E., Vasil M.L.;
RT "A mosaic genome organization upstream of the exotoxin A gene in
RT Pseudomonas aeruginosa: Possible insertion sequences.";
RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; M27186; AAA26012.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 1046 MW; F94371F7605721E6 CRC64;

Query Match 27.3%; Score 21; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 LYLSPH 15
Db 1 MHLIPH 6
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Search completed: November 14, 2004, 13:16:24  
Job time : 101 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:03:52 ; Search time 18.3333 Seconds  
(without alignments)  
78.723 Million cell updates/sec

Title: US-09-831-253F-9  
Perfect score: 77  
Sequence: 1 LDSLSFQLGLYLSPH 15  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 2523  
Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	29	37.7	11	2 A35594	buccalin - Califor
2	24	31.2	15	2 A35417	28K serine protein
3	24	31.2	15	4 I38335	hypothetical REL/M
4	23	29.9	11	2 PH0914	T-cell receptor be
5	23	29.9	12	2 C36201	1-aminocyclopropan
6	21	27.3	15	2 A47628	FC gamma receptor
7	20	26.0	11	4 PC2124	aminotransferase c
8	20	26.0	12	2 B61497	seed protein ws-17
9	20	26.0	14	2 B61597	cytochrome P450 AL
10	19	24.7	7	2 A11483	aspartate transami
11	19	24.7	10	2 A30823	bothropatoxin - ja
12	19	24.7	10	2 D60787	sperm-activating p
13	19	24.7	14	2 A28018	very late antigen-
14	19	24.7	15	2 T46625	hypothetical prote
15	19	24.7	15	2 PC1317	large granule L4 c
16	19	24.7	15	2 B45115	peptidylprolyl iso
17	19	24.7	15	2 C32521	hexokinase (EC 2.7
18	18.5	24.0	11	2 PT0301	Ig heavy chain CRD
19	18	23.4	6	2 JN0861	peptidyl-dipeptida
20	18	23.4	8	2 PC4131	hypothetical prote
21	18	23.4	10	2 PC2044	beta-Kirilowin - M
22	18	23.4	12	2 S01749	collagen alpha 1(I
23	18	23.4	12	2 S01122	photosystem II 3.7
24	18	23.4	12	2 H41946	T-cell receptor ga
25	18	23.4	13	2 B61620	locustamyotropin I
26	17	22.1	8	2 A37521	R-phycosythrins ga
27	17	22.1	8	2 T13818	cytochrome oxidase
28	17	22.1	9	2 PS0253	glycine cleavage s
29	17	22.1	10	1 ECLQ3M	tachykinin III - m

30	17	22.1	10	2 A47364	placental lactogen
31	17	22.1	11	2 S19775	wound-induced prot
32	17	22.1	12	2 PH0771	T-cell receptor be
33	17	22.1	13	2 PH1596	Ig H chain V-D-J r
34	17	22.1	14	2 PA0109	porin por 1B - Ara
35	17	22.1	14	2 PA0045	porin por1 - Arabi
36	17	22.1	15	2 S08209	hypothetical prote
37	17	22.1	15	2 A49252	T-cell receptor be
38	17	22.1	15	2 PH1616	Ig H chain V-D-J r
39	17	22.1	15	2 PH0782	T-cell receptor al
40	16.5	21.4	13	4 I70075	glycophorin B (mis
41	16.5	21.4	14	2 PH1758	T cell receptor al
42	16.5	21.4	14	2 PH1758	T cell receptor al
43	16	20.8	9	4 I57650	hemoglobin alpha c
44	16	20.8	10	1 SPFGNK	neuromedin K - pig
45	16	20.8	10	2 S65432	angiotensin I - ho

ALIGNMENTS

RESULT 1

A35594  
buccalin - California sea hare  
C;Species: Aplysia californica (California sea hare)  
C;Date: 14-Sep-1990 #sequence\_revision 14-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: A35594  
R;Cropper, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.  
Proc. Natl. Acad. Sci. U.S.A. 85: 6177-6181, 1988  
A;Title: Structure and action of buccalin: a modulatory neuropeptide localized to an id  
A;Reference number: A35594; MUID:88320404; PMID:3413086  
A;Accession: A35594  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <CRO>  
A;Cross-references: UNIPROT:P20481

Query Match 37.7%; Score 29; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 56;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10  
:|:|:|:|:|  
Db 2 MDSLAFSGGL 11

RESULT 2

A35417  
28K serine proteinase homolog - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004  
C;Accession: A35417  
R;Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambarini, A.G.  
Biochem. Biophys. Res. Commun. 170, 769-774, 1990  
A;Title: Co-purification of proteases with basic fibroblast growth factor (FGF).  
A;Reference number: A35417; MUID:90343797; PMID:2200404  
A;Accession: A35417  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <HOA>  
A;Cross-references: UNIPROT:Q7M3G3

Query Match 31.2%; Score 24; DB 2; Length 15;  
Best Local Similarity 30.8%; Pred. No. 6.2e+02;  
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 DSLSFQLGLYLS 14  
|:|:|:|:|:|  
Db 3 DSIDYRKGVT 15

RESULT 3

I38335

hypothetical TEL/MNI mutant fusion protein type II - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Apr-2000  
C:Accession: I38335  
R:Buijjs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.  
Oncogene 10, 1511-1519, 1995  
A:Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion  
A:Reference number: I38031; MUID:95249265; PMID:7731705  
A:Accession: I38335  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-15 <BUI>  
A:Cross-references: EMBL:X85024; NID:g971471; PIDN:CAA59397.1; PID:g971472  
C:Comment: This sequence is the chimeric product of a translocation mutation.  
C:Genetics:  
A:Gene: ETV6/MNI; TEL/MNI  
A:Map position: 22q11/12p13  
C:Keywords: fusion protein

Query Match 31.2%; Score 24; DB 4; Length 15;  
Best Local Similarity 80.0%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YLSPH 15  
| | | | |  
Db 2 YRSPH 6

RESULT 4  
PH0914  
T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0914  
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0914  
A:Molecule type: mRNA  
A:Residues: 1-11 <GOL>  
A:Experimental source: myelin basic protein-immunized lymph node  
C:Keywords: T-cell receptor

Query Match 29.9%; Score 23; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 6.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLSLFO 7  
| | | | |  
Db 5 DLSLYE 10

RESULT 5  
C36201  
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment)  
C:Species: Malus domestica (apple tree)  
C>Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 09-Jul-2004  
C:Accession: C36201; C33103  
R:Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990  
A:Title: Characterization and sequencing of the active site of 1-aminocyclopropane-1-car  
A:Reference number: A36201; MUID:91045911; PMID:2122449  
A:Accession: C36201  
A:Molecule type: protein  
A:Residues: 1-12 <YIP>  
A:Cross-references: UNIPROT:Q9SFB01; UNIPROT:Q9SB94; UNIPROT:O24062  
A:Experimental source: strain Golden delicious  
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase  
A:Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph  
F:4/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental

Query Match 29.9%; Score 23; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 7.3e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFOLGL 10  
| | | | |  
Db 1 SLSKDLGL 8

RESULT 6  
A47628  
Fc gamma receptor II (CD32) - human (fragments)  
C:Species: Homo sapiens (man)  
C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C:Accession: A47628  
R:Warmerdam, P.A.M.; van de Winkel, J.G.J.; Gosselin, E.J.; Capel, P.J.A.  
J. Exp. Med. 172, 19-25, 1990  
A:Title: Molecular basis for a polymorphism of human Fc gamma receptor II (CD32).  
A:Reference number: A47628; MUID:90293679; PMID:2141627  
A:Accession: A47628  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-15 <WAR>  
C:Keywords: immunoglobulin receptor

Query Match 27.3%; Score 21; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 GLYLSP 14  
| | | | |  
Db 9 GSHLSP 14

RESULT 7  
PC2124  
aminotransferase chimera DY376 - synthetic (fragment)  
C:Species: synthetic  
C>Date: 28-May-1999 #sequence\_revision 28-May-1999 #text\_change 28-May-1999  
C:Accession: PC2124  
R:Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.  
J. Biochem. 115, 568-577, 1994  
A:Title: Construction of aminotransferase chimeras and analysis of their substrate speci  
A:Reference number: JX0315; MUID:94334304; PMID:8056774  
A:Accession: PC2124  
A:Molecule type: DNA  
A:Residues: 1-11 <MIY>  
A:Comment: This is a chimeric enzyme of Escherichia coli aspartate aminotransferase (EC  
C:Comment: The parental enzymes catalyze the reversible amino group transfer reaction be  
C:Genetics:  
A:Gene: aspC; tyrB  
C:Keywords: aminotransferase

Query Match 26.0%; Score 20; DB 4; Length 11;  
Best Local Similarity 50.0%; Pred. No. 2.3e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 QLGLYL 12  
| | | | |  
Db 6 BFGVYL 11

RESULT 8  
B61497  
seed protein ws-17 - winged bean (fragment)  
C:Species: Psophocarpus tetragonolobus (winged bean)  
C>Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: B61497  
R:Hiirano, H.  
J. Protein Chem. 8, 115-130, 1989  
A:Title: Microsequence analysis of winged bean seed proteins electroblooded from two-di  
A:Reference number: A61491; MUID:89351606; PMID:2765119  
A:Accession: B61497  
A:Status: preliminary

A:Molecule type: protein  
A:Residues: 1-12 <HIR>  
A:Cross-references: UNIPROT:Q7M1H9  
C:Keywords: seed

Query Match 26.0%; Score 20; DB 2; Length 12;  
Best Local Similarity 30.0%; Pred. No. 2.5e+03;  
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 DLSLFGGLY 11  
|:|:|:  
Db 1 DTISFNFNQF 10

## RESULT 9

B61597  
cytochrome P450 AL-2 - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: B61597  
R:Shimeno, H.; Toda, A.; Ogata, S.; Nagamatsu, A.  
Drug Metab. Dispos. 19, 291-297, 1991  
A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cytochrome P450  
A:Reference number: A61597; MUID:91292910; PMID:1676625  
A:Accession: B61597  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <SHI>  
A:Cross-references: UNIPROT:Q7M047

Query Match 26.0%; Score 20; DB 2; Length 14;  
Best Local Similarity 83.3%; Pred. No. 3e+03;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQL 8  
|:|:|:  
Db 6 SLSFLL 11

## RESULT 10

A11483  
aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)  
N:Alternate names: aspartate aminotransferase, mitochondrial  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 20-Aug-1999  
C:Accession: A11483  
R:Campos-Cavieles, M.; Milstein, C.P.  
Biochem. J. 147, 275-281, 1975  
A:Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mitochondrial  
A:Reference number: A11483; MUID:76039441; PMID:1180894  
A:Accession: A11483  
A:Molecule type: protein  
A:Residues: 1-7 <CAM>  
A:Experimental source: liver  
C:Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate  
F:2/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental

Query Match 24.7%; Score 19; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 LGLY 11  
|:|:|:  
Db 4 MGLY 7

## RESULT 11

A30823  
bothropstoxin - jararacussu (fragment)  
C:Species: Bothrops jararacussu (jararacussu)  
C:Date: 01-Dec-1989 #sequence\_revision 01-Dec-1989 #text\_change 09-Jul-2004  
C:Accession: A30823  
R:Homsí-Brandeburgo, M.I.; Queiroz, L.S.; Santo-Neto, H.; Rodrigues-Simioni, L.; Giglio,

Toxicon 26, 615-627, 1988

A:Title: Fractionation of Bothrops jararacussu snake venom: partial chemical characterization  
A:Reference number: A30823; MUID:89020120; PMID:3176051  
A:Accession: A30823  
A:Molecule type: protein  
A:Residues: 1-10 <HOM>  
A:Cross-references: UNIPROT:Q7L225

Query Match 24.7%; Score 19; DB 2; Length 10;  
Best Local Similarity 75.0%; Pred. No. 3.1e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FQLG 9  
|:|:  
Db 3 FZLG 6

## RESULT 12

D60787  
sperm-activating peptide (Ser-1, Ala-3, Gly-5 speract) - sea urchin (Hemicentrotus pulcherrimus)  
C:Species: Hemicentrotus pulcherrimus  
C:Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 16-Aug-2004  
C:Accession: D60787  
R:Suzuki, N.; Kajitara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, K.  
Comp. Biochem. Physiol. B 89, 687-693, 1988  
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus  
A:Reference number: A60787; MUID:88242184; PMID:3378407  
A:Accession: D60787  
A:Molecule type: protein  
A:Residues: 1-10 <SUZ>  
A:Cross-references: UNIPROT:Q7M4D1  
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of  
at shows some, but not absolute, species restriction.

Query Match 24.7%; Score 19; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 3.1e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFOLG 9  
|:|:|:  
Db 1 SFALG 5

## RESULT 13

A28018  
very late antigen-1 alpha chain - human (fragment)  
N:Alternate names: VLA-1 alpha chain  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 12-May-1994  
C:Accession: A28018  
R:Takada, Y.; Strominger, J.L.; Hemler, M.E.  
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987  
A:Title: The very late antigen family of heterodimers is part of a superfamily of molecules  
A:Reference number: A94151; MUID:87204112; PMID:3033641  
A:Accession: A28018  
A:Molecule type: protein  
A:Residues: 1-14 <TAK>  
C:Keywords: duplication; heterodimer; membrane protein

Query Match 24.7%; Score 19; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 4.5e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLSLF 6  
|:|:|:  
Db 7 DSWTF 11

## RESULT 14

T46625  
hypothetical protein c3 - loblolly pine  
C:Species: Pinus taeda (loblolly pine)  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000

C:Accession: T46625  
R:Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.  
submitted to the EMBL Data Library, July 1995  
A:Description: Cloning of a chitinase homolog which lacks chitin binding sites and is d  
A:Reference number: Z23105  
A:Accession: T46625  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-15 <CHA>  
A:Cross-references: EMBL:U31309; NID:G974285; PID:G974290  
A:Experimental source: strain sePT2xs6PT3; 8 month seedlings

Query Match 24.7%; Score 19; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 4.8e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QLGL 10  
Db 6 QLGL 9

## RESULT 15

PCI317  
large granule L4 chain - horseshoe crab (Tachypleus tridentatus) (fragment)  
C:Species: Tachypleus tridentatus  
C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
C:Accession: PCI317  
R:Shigenaga, T.; Takayenoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa  
J. Biochem. 114, 307-316, 1993  
A>Title: Separation of large and small granules from horseshoe crab (Tachypleus tridenta  
A:Reference number: PCI309; MUID:94110249; PMID:8282718  
A:Accession: PCI317  
A:Molecule type: protein  
A:Residues: 1-15 <SHI>  
C:Comment: This protein participates in immobilization of invading microbes.

Query Match 24.7%; Score 19; DB 2; Length 15;  
Best Local Similarity 38.5%; Pred. No. 4.8e+03;  
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 2 DSLSPQLGLYLSP 14  
Db 3 DEIFHLKXKASP 15

Search completed: November 14, 2004, 13:17:23  
Job time : 18.3333 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 40.0532 Seconds  
(without alignments)  
215.479 Million cell updates/sec

Title: US-09-831-253F-9  
Perfect score: 77  
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	35.1	12	1	FREI_LITIN
2	27	35.1	18	2	Q38573
3	27	35.1	23	2	Q91CX2
4	27	35.1	23	2	Q91CX8
5	26	33.8	15	1	ASPI_LACSN
6	26	33.8	16	2	Q91CX7
7	26	33.8	17	2	Q9PRU8
8	26	33.8	18	2	Q9QUX0
9	26	33.8	19	2	Q8UVW4
10	26	33.8	23	2	Q9SC61
11	25	32.5	22	2	Q9R4T0
12	25	32.5	22	2	Q6ZXI6
13	25	32.5	22	2	CAG27598
14	25	32.5	22	2	CAG27600
15	25	32.5	22	2	CAG27725
16	25	32.5	22	2	Q64065
17	24	31.2	15	2	Q7M3G3
18	24	31.2	18	2	Q9ZYV9
19	24	31.2	18	2	Q6RJY6
20	24	31.2	18	2	AAR83863
21	24	31.2	22	2	Q37112
22	24	31.2	22	2	Q9ZYX8
23	24	31.2	22	2	Q45654
24	23	29.9	9	2	P92072
25	23	29.9	15	2	Q9TR52
26	23	29.9	16	2	Q6LBM5
27	23	29.9	16	2	Q7L216
28	23	29.9	16	2	CAA40176
29	23	29.9	20	1	UCRQ_EQUAR
30	23	29.9	20	2	Q9TRA1
31	23	29.9	21	2	Q9TRA9

32	23	29.9	22	2	Q9RLW6	Q9rlw6 mus musculu
33	23	29.9	23	1	PQQA_PSEAE	Q9zaa0 pseudomonas
34	23	29.9	23	2	Q7RDE9	Q7rde9 plasmodium
35	23	29.9	23	2	Q9T2J3	Q9t2j3 nicotiana s
36	23	29.9	23	2	Q39633	Q39633 cucumis sat
37	23	29.9	23	2	Q53469	Q53469 mycobacteri
38	22.5	29.2	19	2	Q9TWQ6	Q9twq6 tachypleus
39	22.5	29.2	22	2	Q82520	Q82520 influenza a
40	22.5	29.2	23	1	SODM_RANCA	P36215 rana catesb
41	22	28.6	12	1	CD11_LITGH	P62567 litoria chl
42	22	28.6	12	1	CD11_LITGI	P62566 litoria gil
43	22	28.6	12	1	CD11_LITSP	P62565 litoria spl
44	22	28.6	12	1	CD11_LITXA	P62564 litoria xan
45	22	28.6	15	1	TRPA_LEUMA	P81753 leucophaea

ALIGNMENTS

RESULT 1

FREI\_LITIN STANDARD; PRT; 12 AA.  
AC P82021;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Prenatin 1.  
OS Litoria infrafrenata (Giant tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=61195;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Skin secretion;  
RX MEDLINE=97368637; PubMed=9225251;  
RA Raftery M.J., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;  
RT "The structures of the frenatin peptides from the skin secretion of  
the giant tree frog Litoria infrafrenata.";  
RL J. Pept. Sci. 2:117-124(1996).  
CC -!- FUNCTION: Wide spectrum antimicrobial peptide.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the skin parotoid and/or rostral  
glands.  
CC -!- MASS SPECTROMETRY: MW=1140; METHOD=FAB; RANGE=1-12; NOTE=Ref.1.  
KW Amidation; Amphibian defense peptide; Antibiotic;  
KW Direct protein sequencing.  
FT MOD RES 12 12 Leucine amide.  
SQ SEQUENCE 12 AA; 1141 MW; C622550BC365B72D CRC64;

Query Match 35.1%; Score 27; DB 1; Length 12;  
Best Local Similarity 70.0%; Pred. No. 8.9e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10  
||:|||||  
DB 3 LDALSGLGL 12

RESULT 2

Q38573  
ID Q38573 PRELIMINARY; PRT; 18 AA.  
AC Q38573;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Coat protein (Fragment).  
OS Bacteriophage Kuf.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;  
OC Levivirus.  
OX NCBI\_TaxID=12021;  
RN [1]  
RP SEQUENCE FROM N.A.

```

RX MEDLINE=96207403; PubMed=8615017;
RA Groeneveld H., Oudot F., van Duin J.V.;
RT "RNA phage KGI has an insertion of 18 nucleotides in the start codon
of its lysis gene.";
RL Virology 218:141-147(1996).
DR EMBL; S81763; AAD14371.1; -.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
KW Coat protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 1825 MW; 2D4092DC226D8904 CRC64;

Query Match 35.1%; Score 27; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DLSLFQGLGYL 11
Db 8 DAISSQSGFY 17

RESULT 3
Q91CX2
ID Q91CX2 PRELIMINARY; PRT; 23 AA.
AC Q91CX2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 (Fragment).
GN Names=ORF1;
OS TT virus.
OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488921; PubMed=11601907;
RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
RA Yoshikawa A.;
RT "Heterogeneous distribution of TT virus of distinct genotypes in
multiple tissues from infected humans.";
RL Virology 288:358-368(2001).
DR EMBL; AB060623; BAB69943.1; -.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2710 MW; 51246068099E107F CRC64;

Query Match 35.1%; Score 27; DB 2; Length 23;
Best Local Similarity 45.5%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSFQGLGYLSP 14
Db 7 LKTAQGVHLNP 17

RESULT 4
Q91CX8
ID Q91CX8 PRELIMINARY; PRT; 23 AA.
AC Q91CX8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 (Fragment).
GN Names=ORF1;
OS TT virus.
OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488921; PubMed=11601907;
RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
RA Yoshikawa A.;
RT "Heterogeneous distribution of TT virus of distinct genotypes in
multiple tissues from infected humans.";

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RL Virology 288:358-368(2001).
DR EMBL; AB060605; BAB69928.1; -.
FT NON_TER 1
SQ SEQUENCE 23 AA; 2710 MW; 51246068099E107F CRC64;

Query Match 35.1%; Score 27; DB 2; Length 23;
Best Local Similarity 45.5%; Pred. No. 1.8e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSFQGLGYLSP 14
Db 7 LKTAQGVHLNP 17

RESULT 5
ASPI_LACSN
ID ASPI_LACSN STANDARD; PRT; 15 AA.
AC P82648;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Acid shock protein 1 (Fragment).
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1625;
RN [1]
RP SEQUENCE.
RX MEDLINE=21322712; PubMed=11429463;
RA De Angelis M., Bini L., Pallini V., Coconcelli P.S., Gobetti M.;
RT "The acid-stress response in Lactobacillus sanfranciscensis CBL.";
RL Microbiology 147:1863-1873(2001).
KW Direct protein sequencing.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1509 MW; 575853B4DFB030A8 CRC64;

Query Match 33.8%; Score 26; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFQGLGYL 12
Db 1 SPKGLFL 8

RESULT 6
Q91CX7
ID Q91CX7 PRELIMINARY; PRT; 16 AA.
AC Q91CX7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 (Fragment).
GN Name=ORF1;
OS TT virus.
OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21488921; PubMed=11601907;
RA Okamoto H., Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
RA Yoshikawa A.;
RT "Heterogeneous distribution of TT virus of distinct genotypes in
multiple tissues from infected humans.";
RL Virology 288:358-368(2001).
DR EMBL; AB060615; BAB69936.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1793 MW; E152327E7C679238 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;

```

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 QLGLYLSP 14

Db 3 QAGLHNP 10

RESULT 7

ID Q9PR8 PRELIMINARY; PRT; 17 AA.  
AC Q9PR8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=95105151; PubMed=7806494;  
RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,  
RA Yazaki Y., Hirai H.;  
RT "Characterization, partial purification, and peptide sequencing of  
RT P130, the main phosphoprotein associated with v-Crk oncoprotein.";  
RL J. Biol. Chem. 269:32740-32746(1994).  
FT NON\_TER 1  
FT NON\_TER 17  
SQ SEQUENCE 17 AA; 1861 MW; 379058CDE44F8879 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 17;  
Best Local Similarity 62.5%; Pred. No. 2e+03;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 QLGLYLSP 14

Db 2 QOGLYQAP 9

RESULT 8

ID Q9QUX0 PRELIMINARY; PRT; 18 AA.  
AC Q9QUX0;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE TUMORLYTIC factor (Fragment).  
OS Mus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10095;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=96078161; PubMed=7590903;  
RA Kita E., Matsui N., Sawaki M., Mikasa K., Katsui N.;  
RT "Murine tumorigenic factor, immunologically distinct from tumor  
RT necrosis factor-alpha and -beta, induced in the serum of mice treated  
RT with a T-cell mitogen of Corynebacterium kutscheri.";  
RL Immunol. Lett. 46:101-106(1995).  
SQ SEQUENCE 18 AA; 2049 MW; 3544227DA4EFD1D0 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 LGLYLSP 15

Db 8 MGLYMLTH 15

RESULT 9

Q8UVW4 PRELIMINARY; PRT; 19 AA.  
AC Q8UVW4;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE AMPA receptor subunit 2 (Fragment).  
GN Name=gria2.1; Synonyms=glur2a;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21617183; PubMed=11741603;  
RA Kung S.-S., Chen Y.-C., Lin W.-H., Chen C.-C., Chow W.-Y.;  
RT "q/R RNA editing of the AMPA receptor subunit 2 (GRIA2) transcript  
RT evolves no later than the appearance of cartilaginous fishes.";  
RL FEBS Lett. 509:277-281(2001).  
DR EMBL; AF350048; AAL57190.1; -.  
DR ZFIN; ZDB-GENE-020125-3; gria2.1.  
DR GO; GO:0004872; F:receptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1  
FT NON\_TER 19  
SQ SEQUENCE 19 AA; 2101 MW; 19490444CB82EF5B CRC64;

Query Match 33.8%; Score 26; DB 2; Length 19;  
Best Local Similarity 45.5%; Pred. No. 2.2e+03;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DLSFOLGLYL 12

Db 1 NSLWFLGAFM 11

RESULT 10

ID Q9SC61 PRELIMINARY; PRT; 23 AA.  
AC Q9SC61;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Ribonuclease H (Fragment).  
GN Name=RNaseH;  
OS Picea abies (Norway spruce) (Picea excelsa).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.  
OX NCBI\_TaxID=3329;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20040041; PubMed=10571856;  
RA Pearce S.R., Stuart-Rogers C.M., Knox M.R., Kumar A., Ellis N.T.,  
RA Flavell A.J.;  
RT "Rapid isolation of plant Tyl-copia group retrotransposon LTR  
RT sequences for molecular marker studies.";  
RL Plant J. 19:711-717(1999).  
DR EMBL; AJ243314; CAB65328.1; -.  
FT NON\_TER 1  
FT NON\_TER 23  
SQ SEQUENCE 23 AA; 2678 MW; 6C9FD7957DCFAB64 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 2.7e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LSFOLGLY 11

Db 16 IQFMLGVY 23

## RESULT 11

Q9R4T0 PRELIMINARY; PRT; 15 AA.  
 AC Q9R4T0; DB 2; Length 15;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Periplasmic protein 5 (Fragment).  
 OS Rhodospirillum rubrum (Rhodospirillum rubrum).  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;  
 OC Rhodospirillaceae; Rhodospirillum.  
 NCBI\_TaxID=1063;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=95160605; PubMed=7857198;  
 RA Sabaty M., Gagnon J., Vermeglio A.;  
 RT "Induction by nitrate of cytoplasmic and periplasmic proteins in the  
 RT photodinitrifier Rhodospirillum rubrum forma sp. denitrificans under  
 RT anaerobic or aerobic condition.";  
 RL Arch. Microbiol. 162:335-343(1994).  
 SQ SEQUENCE 15 AA; 1718 MW; DA5BF4BD9AEBE157 CRC64;

Query Match 32.5%; Score 25; DB 2; Length 15;  
 Best Local Similarity 55.6%; Pred. No. 2.6e+03;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DLSFQGL 10

DB 4 DSETFQSGM 12

## RESULT 12

Q6ZXI6 PRELIMINARY; PRT; 22 AA.  
 AC Q6ZXI6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Harpin (Fragment).  
 GN Name-hrpW;  
 OS Erwinia amylovora.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Erwinia.  
 NCBI\_TaxID=552;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCPBP 2293;  
 RA Giorgi S., Scottichini M.;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ698835; CAG27600.1;  
 DR EMBL; AJ698835; CAG27600.1;  
 DR EMBL; AJ698835; CAG27600.1;  
 FT NON\_TER 22  
 SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;

Query Match 32.5%; Score 25; DB 2; Length 22;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFQGLGLYL 13

DB 11 SSSGLGLYQS 19

## RESULT 13

CAG27598  
 ID CAG27598 PRELIMINARY; PRT; 22 AA.  
 AC CAG27598;  
 DT 10-MAY-2004 (TrEMBLrel. 27, Created)  
 DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Harpin (Fragment).  
 GN HRPW.

OS Erwinia amylovora.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Erwinia.  
 NCBI\_TaxID=552;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCPBP 2292;  
 RA Giorgi S., Scottichini M.;  
 RT "Molecular characterization of Erwinia amylovora strains isolated from  
 RT different host plants through genomic fingerprinting and RFLP analysis  
 RT and sequencing of hrpN and dspA genes.";  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ698834; CAG27598.1;  
 FT NON\_TER 22  
 SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;

Query Match 32.5%; Score 25; DB 2; Length 22;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFQGLGLYL 13

DB 11 SSSGLGLYQS 19

## RESULT 14

CAG27600 PRELIMINARY; PRT; 22 AA.  
 AC CAG27600;  
 DT 10-MAY-2004 (TrEMBLrel. 27, Created)  
 DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Harpin (Fragment).  
 GN HRPW.  
 OS Erwinia amylovora.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Erwinia.  
 NCBI\_TaxID=552;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCPBP 2293;  
 RA Giorgi S., Scottichini M.;  
 RT "Molecular characterization of Erwinia amylovora strains isolated from  
 RT different host plants through genomic fingerprinting and RFLP analysis  
 RT and sequencing of hrpN and dspA genes.";  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ698835; CAG27600.1;  
 FT NON\_TER 22  
 SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;

Query Match 32.5%; Score 25; DB 2; Length 22;  
 Best Local Similarity 66.7%; Pred. No. 3.9e+03;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 SFQGLGLYL 13

DB 11 SSSGLGLYQS 19

## RESULT 15

CAG27725 PRELIMINARY; PRT; 22 AA.  
 ID CAG27725;  
 DT 10-MAY-2004 (TrEMBLrel. 27, Created)  
 DT 10-MAY-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Harpin (Fragment).  
 GN HRPW.  
 OS Erwinia amylovora.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Erwinia.  
 NCBI\_TaxID=552;  
 RN [1]



RP SEQUENCE FROM N.A.  
RC STRAIN=PD 2915;  
RA Giorgi S., Scortichini M.;  
RT "Molecular characterization of Erwinia amylovora strains isolated from  
RT different host plants through genomic fingerprinting and RFLP analysis  
RT and sequencing of hrpN and dspA genes.";  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ698952; CAG27725.1; -.  
FT NON TER 22 22  
SQ SEQUENCE 22 AA; 2245 MW; CC34D82FCC1BC69B CRC64;  
  
Query Match 32.5%; Score 25; DB 2; Length 22;  
Best Local Similarity 66.7%; Pred. No. 3.9e+03;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 5 SFQLGLYLS 13  
| | | | |  
Db 11 SSSLGLYQS 19

Search completed: November 14, 2004, 12:07:38  
Job time : 42.0532 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 9.25532 Seconds  
(without alignments)  
155.938 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77  
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*

- 1: pir1:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	39.0	20	2 S10876	hypothetical prote
2	29	37.7	11	2 A35594	buccalin - Califor
3	27	35.1	19	2 B53145	high conductance c
4	25	32.5	16	2 PH1634	Ig H chain V-D-J r
5	24	31.2	15	2 A35417	28K serine protein
6	24	31.2	15	4 I38335	hypothetical TEL/M
7	24	31.2	22	2 S29326	hypothetical prote
8	23	29.9	11	2 PH0914	T-cell receptor be
9	23	29.9	12	2 C36201	1-aminocyclopropan
10	23	29.9	16	2 A42411	myosin light chain
11	23	29.9	17	2 A58946	formylmethanofuran
12	23	29.9	23	2 PQ0690	photosystem I 8.0K
13	23	29.9	23	2 A83397	pyrroloquinoline q
14	23	29.9	23	2 T10123	probable catalase
15	22.5	29.2	19	2 FC1309	small granule S2 c
16	22	28.6	19	2 A39729	amylase (EC 3.2.1.1
17	22	28.6	19	2 I52721	gene hMLH1 protein
18	22	28.6	23	1 S20453	pyrroloquinoline q
19	21	27.3	15	2 A47628	Pc gamma receptor
20	21	27.3	18	2 S55501	thrombospondin pre
21	21	27.3	18	4 I39461	anti-angiotensin,
22	21	27.3	20	2 A61576	insulin-like growt
23	21	27.3	21	2 S03504	T-cell receptor al
24	20	26.0	11	4 PC2124	aminotransferase c
25	20	26.0	12	2 B61497	seed protein ws-17
26	20	26.0	14	2 B61597	cytochrome P450 AL
27	20	26.0	16	2 S11290	matrix protein M1
28	20	26.0	16	2 S51057	ribosomal protein
29	20	26.0	17	2 JH0785	DNA-directed RNA p

30	20	26.0	18	2 S09087	proteasome chain 6
31	20	26.0	19	2 PS0332	phospholipase A2 (
32	20	26.0	20	2 S00774	kinase-related tra
33	20	26.0	20	2 A56900	chymotrypsin I (EC
34	20	26.0	20	2 S03505	T-cell receptor al
35	20	26.0	21	2 JQ2196	hypothetical 2.5K
36	20	26.0	22	2 S09021	carboxylesterase (
37	20	26.0	22	2 T45268	hypothetical prote
38	19	24.7	7	2 A11483	aspartate transami
39	19	24.7	10	2 A30823	bothropstoxin - ja
40	19	24.7	10	2 D60787	sperm-activating p
41	19	24.7	14	2 A28018	very late antigen-
42	19	24.7	15	2 T46625	hypothetical prote
43	19	24.7	15	2 PC1317	large granule L4 c
44	19	24.7	15	2 B45115	peptidylprolyl iso
45	19	24.7	15	2 C32521	hexokinase (EC 2.7

ALIGNMENTS

RESULT 1

S10876

hypothetical protein - human

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 18-Nov-1994

C;Accession: S10876

R;Assouline, Z.; Kerbirou-Nabias, D.M.; Pietu, G.; Thomas, N.; Bahnak, B.R.; Meyer, D.

Biochem. Biophys. Res. Commun. 153, 1159-1166, 1988

A;Title: The human gene for von Willebrand factor. Identification of repetitive Alu seq

A;Reference number: S10876; MUID:88268889; PMID:3260493

A;Accession: S10876

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-20 <ASS>

A;Cross-references: EMBL:X07258

Query Match 39.0%; Score 30; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 70;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QLGLYL 12

DB 3 QLGLYL 8

RESULT 2

A35594

buccalin - California sea hare

C;Species: Aplysia californica (California sea hare)

C;Date: 14-Sep-1990 #sequence\_revision 14-Sep-1990 #text\_change 09-Jul-2004

C;Accession: A35594

R;Cropper, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.

Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988

A;Title: Structure and action of buccalin: a modulatory neuropeptide localized to an id

A;Reference number: A35594; MUID:88320404; PMID:3413086

A;Accession: A35594

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CRO>

A;Cross-references: UNIPROT:P20481

Query Match 37.7%; Score 29; DB 2; Length 11;

Best Local Similarity 60.0%; Pred. No. 56;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10

DB 2 MDSLAFSGGL 11

RESULT 3

B53145

high conductance calcium-activated potassium channel, maxi-K channel - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 06-Oct-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: B53145

R:Knaus, H.G.; Garcia-Calvo, M.; Kaczorowski, G.J.; Garcia, M.L.  
 J. Biol. Chem. 269, 3921-3924, 1994  
 A>Title: Subunit composition of the high conductance calcium-activated potassium channel  
 A:Reference number: A35145; MUID:94140798; PMID:7508434

A:Accession: B53145  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-19 <KNA>

A:Cross-references: UNIPROT:Q28204; UNIPROT:Q9TS86  
 A>Note: sequence extracted from NCBI backbone (NCBIP:144547)  
 C:Superfamily: fruit fly calcium-activated potassium channel slo

Query Match 35.1%; Score 27; DB 2; Length 19;  
 Best Local Similarity 41.7%; Pred. No. 2.3e+02;  
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15  
 : : : : :  
 DB 5 VEFYQGSVLNPH 16

RESULT 4  
 PH1634  
 Ig H chain V-D-J region (clone B-less 213) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1634  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993

A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A:Reference number: PH1580; MUID:93301609; PMID:8315387  
 A:Accession: PH1634  
 A:Molecule type: DNA  
 A:Residues: 1-16 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 32.5%; Score 25; DB 2; Length 16;  
 Best Local Similarity 80.0%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YLSPH 15  
 : : : : :  
 DB 6 YVSPH 10

RESULT 5  
 A35417  
 28K serine proteinase homolog - bovine (fragment)  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 18-Jan-1991 #sequence\_revision 18-Jan-1991 #text\_change 09-Jul-2004  
 C:Accession: A35417  
 R:Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambarini, A.G.  
 Biochem. Biophys. Res. Commun. 170, 769-774, 1990  
 A>Title: Co-purification of proteases with basic fibroblast growth factor (FGF).  
 A:Reference number: A35417; MUID:90343797; PMID:2200404

A:Accession: A35417  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <HOA>  
 A:Cross-references: UNIPROT:Q7M3G3

Query Match 31.2%; Score 24; DB 2; Length 15;  
 Best Local Similarity 30.8%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 DLSLSFQLGLYLSP 14  
 : : : : :  
 DB 3 DSIDYRKGYVTP 15

RESULT 6  
 I38335

hypothetical TEL/MNI mutant fusion protein type II - human (fragment)  
 C:Species: Homo sapiens (man)

C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Apr-2000

C:Accession: I38335

R:Buyls, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.

Oncogene 10, 1511-1519, 1995

A>Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fus;

A:Reference number: I38031; MUID:95249265; PMID:7731705

A:Accession: I38335

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-15 <BUI>

A:Cross-references: EMBL:X85024; NID:G971471; PIDN:CAA59397.1; PID:G971472

C:Comment: This sequence is the chimeric product of a translocation mutation.

C:Genetics:

A:Gene: ETV6/MNI; TEL/MNI

A:Map position: 22q11/12p13

C:Keywords: fusion protein

Query Match 31.2%; Score 24; DB 4; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 6.2e+02;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YLSPH 15  
 : : : : :  
 DB 2 YRSPH 6

RESULT 7  
 S29326

hypothetical protein 22, psbA 5'-region - Japanese black pine chloroplast

C:Species: chloroplast Pinus thunbergiana (Japanese black pine)

C>Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004

C:Accession: S29326; T07427

R:Tsudzuki, J.; Nakashima, K.; Tsudzuki, T.; Hirtatsuka, J.; Shibata, M.; Wakasugi, T.; S

Mol. Gen. Genet. 232, 206-214, 1992

A>Title: Chloroplast DNA of black pine retains a residual inverted repeat lacking rRNA

A:Reference number: S20449; MUID:92212283; PMID:1557027

A:Accession: S29326

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-22 <TSU>

A:Cross-references: UNIPROT:Q37112; EMBL:D11467; NID:G344007; PIDN:BAA02023.1; PID:G3440

R:Wakasugi, T.; Tsudzuki, J.; Ito, S.; Nakashima, K.; Taudzuki, T.; Sugiura, M.

Proc. Natl. Acad. Sci. U.S.A. 91, 9794-9798, 1994

A>Title: Loss of all ndh genes as determined by sequencing the entire chloroplast genom

A:Reference number: Z16030; MUID:95024047; PMID:7937893

A:Accession: T07427

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-22 <WAK>

A:Cross-references: EMBL:D17510; NID:G529643; PIDN:BAA04307.1; PID:G1262588

A:Genome: chloroplast

C:Keywords: chloroplast

Query Match 31.2%; Score 24; DB 2; Length 22;  
 Best Local Similarity 50.0%; Pred. No. 9.3e+02;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SFQLGLYL 12  
 : : : : :  
 DB 9 STECGIYL 16

RESULT 8

PH0914

T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C;Accession: PH0914  
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
A;Reference number: PH0891; MUID:92078857; PMID:1836012  
A;Accession: PH0914  
A;Molecule type: mRNA  
A;Residues: 1-11 <GO>  
A;Experimental source: myelin basic protein-immunized lymph node  
C;Keywords: T-cell receptor

Query Match 29.9%; Score 23; DB 2; Length 11;  
Best Local Similarity 66.7%; Pred. No. 6.7e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 DLSLFQ 7  
|||:  
5 DLSLYE 10

Db

RESULT 9  
C36201  
l-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment)  
C;Species: Malus domestica (apple tree)  
C;Date: 28-Mar-1991 #sequence\_revision 28-Mar-1991 #text\_change 09-Jul-2004  
C;Accession: C36201; C33103  
R;Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.  
Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990  
A;Title: Characterization and sequencing of the active site of l-aminocyclopropane-1-car  
A;Reference number: A36201; MUID:91045911; PMID:2122449  
A;Accession: C36201  
A;Molecule type: protein  
A;Residues: 1-12 <YIP>  
A;Cross-references: UNIPROT:Q9PUC3; UNIPROT:Q9SB01; UNIPROT:Q9SB94; UNIPROT:Q24062  
C;Experimental source: strain Golden delicious  
C;Superfamily: l-aminocyclopropane-1-carboxylate synthase  
C;Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph  
F;4/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 29.9%; Score 23; DB 2; Length 12;  
Best Local Similarity 75.0%; Pred. No. 7.3e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFQLGL 10  
|||:  
1 SLSKDLGL 8

Db

RESULT 10  
A42411  
myosin light chain kinase - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A42411  
R;Leachman, S.A.; Gallagher, P.J.; Herring, B.P.; McPhaul, M.J.; Stull, J.T.  
J. Biol. Chem. 267, 4930-4938, 1992  
A;Title: Biochemical properties of chimeric skeletal and smooth muscle myosin light chain  
A;Reference number: A42411; MUID:92165861; PMID:1371510  
A;Accession: A42411  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid; protein  
A;Residues: 1-16 <LEA>  
A;Cross-references: UNIPROT:Q7LZ16  
A;Experimental source: skeletal muscle  
A;Note: sequence extracted from NCBI backbone (NCBIP:84332)

Query Match 29.9%; Score 23; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LSPH 15  
|||

Db 13 LSPH 16

RESULT 11  
A58946  
formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum) chain C - Methanobacterium  
N;Alternate names: formylmethanofuran dehydrogenase (molybdenum) chain B [misidentifica  
C;Species: Methanobacterium thermoautotrophicum  
C;Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 04-Feb-2000  
C;Accession: A58946  
R;Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.  
Eur. J. Biochem. 234, 910-920, 1995  
A;Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoauto  
A;Reference number: S63519; MUID:96163477; PMID:8575452  
A;Accession: A58946  
A;Molecule type: protein  
A;Residues: 1-17 <HOC>  
A;Note: the authors identify this peptide as the amino terminus of chain B, but it appe  
C;Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin; oxidoreduct

Query Match 29.9%; Score 23; DB 2; Length 17;  
Best Local Similarity 80.0%; Pred. No. 1.1e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FQLGL 10  
|||:  
10 FQIGL 14

Db

RESULT 12  
PQ0690  
photosystem I 8.0 K chain - common tobacco (fragment)  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 17-Mar-1999  
C;Accession: PQ0690  
R;Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugiyama, M.  
Plant Physiol. 102, 1259-1267, 1993  
A;Title: Molecular heterogeneity of photosystem I. psaD, psaE, psaF, psaH and psaL are  
A;Reference number: PQ0667; MUID:94105345; PMID:8278548  
A;Accession: PQ0690  
A;Molecule type: protein  
A;Residues: 1-23 <ORO>  
C;Superfamily: photosystem I chain V  
C;Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 29.9%; Score 23; DB 2; Length 23;  
Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12  
|||:  
9 SLSTGLSLFL 18

Db

RESULT 13  
A83397  
pyrroloquinoline quinone biosynthesis protein A PA1985 [imported] - Pseudomonas aerugin  
C;Species: Pseudomonas aeruginosa  
C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C;Accession: A83397  
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path  
A;Reference number: A82950; MUID:20437337; PMID:10984043  
A;Accession: A83397  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-23 <STO>  
A;Cross-references: UNIPROT:Q9ZAA0; GB:AE004625; GB:AE0047983; PIDN:AG053  
A;Experimental source: strain PA01  
C;Genetics:

A;Gene: pqQA; PA1985

Query Match 29.9%; Score 23; DB 2; Length 23;  
Best Local Similarity 40.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSFQLGLYLS 13  
| | | | |  
Db 12 LGFEVTLYFA 21

#### RESULT 14

T10123  
probable catalase (EC 1.11.1.6) - cucumber (fragment)  
C;Species: Cucumis sativus (cucumber)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T10123  
R;Toyama, T.; Teramoto, H.; Takeba, G.; Tsuji, H.  
Plant Cell Physiol. 36, 1349-1359, 1995  
A;Title: Cytokinin induces a rapid decrease in the levels of mRNAs for catalase, 3-hydroxyisovaleryl-CoA synthetase, and isochlorogenic acid synthase  
A;Reference number: Z16946; MUID:96104306; PMID:8564304  
A;Accession: T10123  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-23 <TOY>  
A;Cross-references: UNIPROT:Q39633; EMBL:D63385; NID:g1199475; PIDN:BAA09701.1; PID:g1199475  
A;Experimental source: seedling; cotyledons  
C;Keywords: oxidoreductase

Query Match 29.9%; Score 23; DB 2; Length 23;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 LGLYLSPH 15  
| | | | |  
Db 9 VGQKLAPH 16

#### RESULT 15

PC1309  
small granule S2 chain - horseshoe crab (Tachypleus tridentatus) (fragment)  
C;Species: Tachypleus tridentatus  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
C;Accession: PC1309  
R;Shigenaga, T.; Takayanoki, Y.; Kawasaki, S.; Seki, N.; Muta, T.; Toh, Y.; Ito, A.; Iwa  
J. Biochem. 114, 307-316, 1993  
A;Title: Separation of large and small granules from horseshoe crab (Tachypleus tridentatus) and their protein composition  
A;Reference number: PC1309; MUID:94110249; PMID:8282718  
A;Accession: PC1309  
A;Molecule type: protein  
A;Residues: 1-19 <SHI>  
A;Cross-references: UNIPROT:Q9TW06  
C;Comment: This protein contributes to a self-defense system against invaders.

Query Match 29.2%; Score 22.5; DB 2; Length 19;  
Best Local Similarity 54.5%; Pred. No. 1.5e+03;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 4 LSFQLGLYLS 14  
| | | | |  
Db 2 LAFKXGRY-SP 11

Search completed: November 14, 2004, 12:03:15  
Job time : 10.2553 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 43.4043 Seconds  
(without alignments)  
123.973 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77  
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	15	3 AAY93106	Aay93106 Transform
2	77	100.0	15	3 AAY92953	Aay92953 Transform
3	33	42.9	20	8 ADM29169	Adm29169 Hepatitis
4	32	41.6	16	4 AAB68433	Aab68433 Peptide d
5	32	41.6	20	2 AAR82557	Aar82557 Bovine PL
6	31	40.3	10	4 AAG83462	Aag83462 Arabidops
7	31	40.3	15	5 ABP58975	Abp58975 Human I k
8	30	39.0	15	5 AAM47809	Aam47809 Miniature
9	30	39.0	17	6 ABP82548	Abp82548 G protein
10	30	39.0	21	2 AAW17133	Aaw17133 Rabbit 3-
11	30	39.0	23	4 AAE09350	Aae09350 Human ion
12	30	39.0	23	4 AAE10097	Aae10097 Human ion
13	30	39.0	23	6 ABU97358	Abu97358 Amino aci
14	30	39.0	23	6 ABO12018	Abol12018 Human zin
15	30	39.0	23	7 ADE92976	Ade92976 Novel hum
16	29.5	38.3	16	5 ABP46134	Abp46134 Human Bly
17	29.5	38.3	16	7 ADG96961	Adg96961 scFV VHCD
18	29	37.7	11	8 ADN03302	Adn03302 Exemplary
19	29	37.7	12	3 AAB07274	Aab07274 Human pep
20	29	37.7	12	6 ABR00682	Abr00682 HCV nonst
21	29	37.7	13	6 ABR00699	Abr00699 HCV nonst
22	29	37.7	13	6 ABR00693	Abr00693 HCV nonst
23	29	37.7	14	4 AAM97619	Aam97619 Human pep
24	29	37.7	14	6 ABR00703	Abr00703 HCV nonst
25	29	37.7	14	6 ABR00706	Abr00706 HCV nonst

26	29	37.7	15	6 ABR00715	Abr00715 HCV nonst
27	29	37.7	15	6 ABR00714	Abr00714 HCV nonst
28	29	37.7	16	6 ABR00725	Abr00725 HCV nonst
29	29	37.7	16	6 ABR00726	Abr00726 HCV nonst
30	29	37.7	17	2 AAR91038	Aar91038 V8 protea
31	29	37.7	17	6 ABR00732	Abr00732 HCV nonst
32	29	37.7	17	6 ABR00731	Abr00731 HCV nonst
33	29	37.7	18	6 ABR00733	Abr00733 HCV nonst
34	29	37.7	18	6 ABR00735	Abr00735 HCV nonst
35	29	37.7	19	6 ABR00739	Abr00739 HCV nonst
36	29	37.7	19	6 ABR00741	Abr00741 HCV nonst
37	29	37.7	20	6 ABR00742	Abr00742 HCV nonst
38	29	37.7	20	6 ABR00743	Abr00743 HCV nonst
39	29	37.7	21	6 ABR00745	Abr00745 HCV nonst
40	29	37.7	21	6 ABR00746	Abr00746 HCV nonst
41	29	37.7	22	6 ABR00594	Abr00594 HCV nonst
42	29	37.7	23	2 AAY27698	Aay27698 Human sec
43	29	37.7	23	6 ABO14129	Abol14129 Novel hum
44	29	37.7	23	8 ADG78536	Adg78536 Human sec
45	29	37.7	23	8 ADN60827	Adn60827 Human sec

ALIGNMENTS

RESULT 1  
AAY93106  
ID AAY93106 standard; peptide; 15 AA.  
XX AC AAY93106;  
XX  
DT 08-NOV-2000 (first entry)  
XX  
DE Transforming growth factor inhibitory peptide P152.  
XX  
KW Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;  
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200031135-A1.  
XX  
PD 02-JUN-2000.  
XX  
PF 23-NOV-1999; 99WO-ES000375.  
XX  
PR 24-NOV-1998; 98ES-00002465.  
XX  
(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
XX  
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
PI Borras Cuesta F;  
XX  
WPI; 2000-411935/35.  
XX  
PT Peptides that antagonize binding of transforming growth factor betal,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.  
XX  
PS Disclosure; Page 33; 86pp; Spanish.  
XX  
CC The invention relates to synthetic peptides that antagonise the binding  
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
CC vivo which have partial amino acid sequences identical, or similar, with  
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
CC examples of the peptides of the invention. The peptides act by  
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis

```

XX SQ Sequence 15 AA;
Query Match 100.0%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. NO. 5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYLSPH 15
Db 1 LDSLSFQLGLYLSPH 15

RESULT 2
AAY92953
ID AAY92953 standard; peptide; 15 AA.
XX AC AAY92953;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide #9.
XX KW Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX OS Homo sapiens.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX PI Borrás Cuesta F;
XX DR WPI; 2000-411935/35.
XX PT Peptides that antagonize binding of transforming growth factor betaf,
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.
XX PS Claim 10; Page 82; 86pp; Spanish.
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis
XX SQ Sequence 15 AA;
Query Match 100.0%; Score 77; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. NO. 5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYLSPH 15
Db 1 LDSLSFQLGLYLSPH 15

RESULT 3

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ADM29169
ID ADM29169 standard; peptide; 20 AA.
XX AC ADM29169;
XX DT 01-JUL-2004 (first entry)
XX DE Hepatitis C virus cellular immune response related peptide.
XX KW DNA vaccine; vaccine; antigen gene; antigen; hepatitis C virus; HCV;
XX KW recombinant adenovirus vaccine; adenovirus; HCV infection;
XX KW hepatitis C virus infection; infection; virucide.
XX OS Hepatitis C virus.
XX OS Synthetic.
XX PN WO2004028563-A1.
XX PD 08-APR-2004.
XX PF 24-SEP-2003; 2003WO-KR001951.
XX PR 27-SEP-2002; 2002KR-00058712.
XX PR 06-NOV-2002; 2002KR-00068496.
XX PA (GENE-) GENEXINE INC.
XX PA (POST-) POSTECH FOUND.
XX PA (DONG-) DONG-A PHARM CO LTD.
XX PA (DAEW-) DAEWONG CO LTD.
XX PA (POSC-) POSCO.
XX PI Sung YC, Youn J, Yang S, Park S, Lee CG;
XX DR WPI; 2004-305120/28.
XX PT New DNA vaccine comprising plasmid containing 2-6 kb of the total antigen
XX PT gene of hepatitis C virus (HCV), useful in treating or preventing HCV
XX PT infection.
XX PS Disclosure; Fig 20e; 165pp; English.
XX CC The present invention describes a DNA vaccine which comprises a plasmid
XX CC containing 2-6 kb of the total antigen gene of hepatitis C virus (HCV).
XX CC Also described: (1) a recombinant adenovirus vaccine including an
XX CC adenovirus containing 2-6 kb of total antigen gene of HCV; (2) a vaccine
XX CC administering method; and (3) a method for treating or preventing HCV
XX CC infection. The DNA vaccine has virucide activity. The DNA vaccine is
XX CC useful in treating or preventing HCV infection. The present sequence
XX CC represents a peptide from the HCV peptide pool used for the investigation
XX CC of cellular immune response in the exemplification of the present
XX CC invention.
XX SQ Sequence 20 AA;
Query Match 42.9%; Score 33; DB 8; Length 20;
Best Local Similarity 66.7%; Pred. NO. 90;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LDSLSFQLGL 10
Db 11 DEVSFQVGL 19

RESULT 4
AAB68433
ID AAB68433 standard; peptide; 16 AA.
XX AC AAB68433;
XX DT 23-JUL-2001 (first entry)
XX DE Peptide derived from human G-protein coupled receptor HG67.
XX

```



KW G-protein coupled receptor; HG67; MCH-R2; weight loss; obesity; stress;  
 KW melanin concentrating hormone receptor; cancer; pain; sexual dysfunction;  
 KW weight gain; hypertension; dyslipidemia; cardiovascular disease;  
 KW gall stone; osteoarthritis; cancer; diabetes; anorexia; AIDS; wasting;  
 KW cachexia.

XX Synthetic.  
 OS Homo sapiens.  
 XX WO200136479-A1.  
 XX 25-MAY-2001.  
 XX 14-NOV-2000; 2000WO-US031240.  
 XX 16-NOV-1999; 99US-0165871P.  
 XX 13-MAR-2000; 2000US-0188977P.  
 XX 18-APR-2000; 2000US-0198029P.  
 XX (MERI ) MERCK & CO INC.  
 XX (BANY ) BANYU PHARM CO LTD.

XX Liu Q, McDonald TP, Howard AD, Iwaasa H, Sano H;

XX WPI; 2001-355618/37.

XX New G-protein coupled receptor, designated MCH-R2, is a receptor for  
 PT melanin-concentrating hormone and is useful to provide treatment for  
 PT weight disorders including obesity.

XX Claim 3; Page 32; 32pp; English.

XX AAB68429-33 represent peptides derived from a human G-protein coupled  
 CC receptor, designated HG67 or MCH-R2. HG67 is a melanin concentrating  
 CC hormone receptor. Modulators of HG67 can be used to treat a patient,  
 CC particularly to reduce weight, particularly in obesity, or to treat  
 CC stress. These modulators can also be used to treat cancer, reduce pain,  
 CC treat sexual dysfunction or to produce weight gain. Bringing about weight  
 CC loss can be used to reduce the likelihood of hypertension, diabetes,  
 CC dyslipidemia, cardiovascular disease, gall stones, osteoarthritis or  
 CC certain forms of cancers. Increasing weight can be useful in the  
 CC treatment of anorexia, AIDS, wasting, cachexia and frail elderly  
 CC patients, or those undergoing chemotherapy or radiation therapy

XX Sequence 16 AA;

Query Match 41.6%; Score 32; DB 4; Length 16;  
 Best Local Similarity 54.5%; Pred. No. 1.1e+02;  
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SLSFQLGLYLS 13  
 :|:|:|  
 Db 5 TLAFYGVGYLS 15

RESULT 5

AAR82557  
 ID AAR82557 standard; peptide; 20 AA.

XX AAR82557;

DT 17-MAY-1996 (first entry)

XX Bovine PVP peptide 71-90.

XX Myelin basic protein; MBP; multiple sclerosis; MS; bystander antigen;  
 KW non-interferon polypeptide; Th2-enhancing cytokine activity.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "Indicated in the specification as COOH-Pro"

FT Modified-site 20  
 /note= "Indicated in the specification as Cys-NH2"

XX WO9527500-A1.

XX 19-OCT-1995.

XX 07-APR-1995; 95WO-US004512.

XX 08-APR-1994; 94US-00225372.

XX 31-OCT-1994; 94US-00332524.

XX (BGHM ) BRIGHAM & WOMENS HOSPITAL.

XX Weiner HL, Chen Y;

XX WPI; 1995-366229/47.

XX Use of oral tolerisation and/or Th2-enhancing cytokine(s) - to treat  
 PT auto-immune diseases such as multiple sclerosis.

XX Example 1; Page 33; 49pp; English.

XX The sequences given in AAR82556-57 are myelin basic protein (MBP) derived  
 CC peptides which were used in the method of the invention for the treatment  
 CC of multiple sclerosis. These peptides act as bystander antigens and act  
 CC in combination with an amount of a non- interferon polypeptide having Th2  
 CC -enhancing cytokine activity

XX Sequence 20 AA;

Query Match 41.6%; Score 32; DB 2; Length 20;

Best Local Similarity 33.3%; Pred. No. 1.4e+02;

Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSFQLGLYLSPH 15

|:|:|:|

Db 2 LAYTIGVFKDPH 13

RESULT 6

AAG83462

ID AAG83462 standard; peptide; 10 AA.

XX AAG83462;

DT 11-SEP-2001 (first entry)

XX Arabidopsis thaliana peptide ligand #102.

XX Plant; peptide pesticide; peptide herbicide; agricultural research.

XX Arabidopsis thaliana.

XX WO200142279-A2.

XX 14-JUN-2001.

XX 13-DEC-2000; 2000WO-GB004781.

XX 13-DEC-1999; 99GB-00029469.

XX (PROT-) PROTEOM LTD.

XX Roberts GW, Heal JR;

XX WPI; 2001-381629/40.

XX A set of peptide ligands for agricultural research and development of  
 PT therapeutic agents comprise specific complementary peptides to proteins  
 PT encoded by genes of plant genomes.

XX Example 4; Page 45; 201pp; English.

XX The present invention relates to a set of peptide ligands consisting of  
 CC specific complementary peptides to proteins encoded by genes of plant  
 CC genomes. The present sequence is one such peptide from Arabidopsis  
 CC thaliana. The peptides of the present invention are useful in an assay to  
 CC identify a peptide, especially a peptide pesticide or herbicide. The  
 CC peptides are also useful for tools for agricultural research and  
 CC development  
 XX  
 SQ Sequence 10 AA;

Query Match 40.3%; Score 31; DB 4; Length 10;  
 Best Local Similarity 70.0%; Pred. No. 98;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQLGLYL 12  
 DB 1 SLTFQLLFL 10  
 ||||| |

RESULT 7  
 ABP58975  
 ID ABP58975 standard; peptide; 15 AA.  
 XX  
 AC ABP58975;  
 XX

DT 14-APR-2003 (first entry)  
 XX

DE Human I kappa B kinase inhibitor 37.40 N-terminal peptide.  
 XX

XX Human; I kappa B kinase inhibitor 37.40; recombinant production;  
 KW gene therapy; cancer; tumor; angiocardiopathy; cardiovascular disorder;  
 KW neurological disorder; immune disorder; inflammatory condition;  
 KW cytostatic; antiinflammatory; immunomodulator; N-terminal peptide;  
 KW enzyme linked immunosorbent assay; ELISA.

XX Homo sapiens.  
 XX

XX CN1361264-A.  
 PN

XX 31-JUL-2002.  
 PD

XX 26-DEC-2000; 2000CN-00136306.  
 PF

XX 26-DEC-2000; 2000CN-00136306.  
 PR

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 PA

XX Mao Y, Xie Y;  
 PI

XX WPI; 2002-751595/82.  
 DR

XX Human inhibitor molecule I kappa B kinase 37.40 polypeptides and  
 PT polynucleotides encoding this polypeptide.  
 XX

XX Example 5; Page 18 (disclosure); 33pp; Chinese.  
 PS

XX The invention relates to human I kappa B kinase inhibitor 37.40  
 CC (ABP58974) and nucleic acids encoding it (ABZ70827). The protein has a  
 CC molecular weight of 37.4 kD. The invention also relates to a method for  
 CC the recombinant production of the protein, an antagonist of the protein,  
 CC and the use of the protein, gene and antagonist in therapeutic  
 CC applications. I kappa B kinase inhibitor 37.40 can be used in the  
 CC treatment of a variety of diseases such as cancer, angiocardiopathy,  
 CC neurological disorders, immune disorders and inflammatory conditions. The  
 CC present sequence represents the 15 N-terminal amino acids of human I  
 CC kappa B kinase inhibitor 37.40 used in ELISA (enzyme linked immunosorbent  
 CC assay) in an exemplification of the invention  
 XX

XX Sequence 15 AA;

Query Match 40.3%; Score 31; DB 5; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FOLGLYLS 13  
 DB 5 FLLGLYIS 12  
 ||||| |

RESULT 8  
 AAM47809  
 ID AAM47809 standard; peptide; 15 AA.  
 XX

XX AAM47809;  
 AC

DT 15-FEB-2002 (first entry)  
 XX

DE Miniature protein 9.  
 XX

XX Avian pancreatic polypeptide; alpha helix domain; modulate transcription;  
 KW miniature protein.  
 KW

XX Synthetic.  
 OS

XX WO200181375-A2.  
 PN

XX 01-NOV-2001.  
 PD

XX 24-APR-2001; 2001WO-US013023.  
 PF

XX 24-APR-2000; 2000US-0199408P.  
 PR

XX 16-OCT-2000; 2000US-0240566P.  
 PR

XX 30-JAN-2001; 2001US-0265099P.  
 PR

XX 23-FEB-2001; 2001US-0271368P.  
 PR

XX (UYVA ) UNIV YALE.  
 PA

XX Schepartz Shrader A, Chin JWK, Zutshi R, Rutledge SE;  
 PI Kehlbek Martin JD, Zondlo NJ;  
 PI

XX WPI; 2002-041395/05.  
 DR

XX Polypeptide scaffold e.g. an avian pancreatic polypeptide that comprises  
 PT modification by substitution of an amino acid residue, that is exposed on  
 PT the alpha helix domain of the polypeptide is useful for screening for  
 PT drugs.  
 XX

XX Example 17; Fig 5; 81pp; English.  
 PS

XX The invention relates to an avian pancreatic polypeptide, modified by  
 CC substitution of at least one amino acid residue, where the residue is  
 CC being exposed on the alpha helix domain of the polypeptide when the  
 CC polypeptide is in a tertiary form. The polypeptide is useful for  
 CC screening drugs to identify agents capable of binding to the same binding  
 CC site as the avian pancreatic polypeptide. It is also useful for  
 CC diagnostic purposes to identify the presence and/or detect the levels of  
 CC DNA or protein that binds to the polypeptide, in treatment of diseases  
 CC associated with the presence of a particular DNA or protein, where the  
 CC polypeptide can be used to bind to DNA to promote or inhibit  
 CC transcription and for identifying binding partners. The present sequence  
 CC is that of a miniature protein of the invention used to modulate the  
 CC interaction between a known protein and another molecule  
 XX

XX Sequence 15 AA;

Query Match 39.0%; Score 30; DB 5; Length 15;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+02;

- Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 FOLGLYL 12  
 DB 6 FOLGWYL 12  
 ||||| |

RESULT 9

ABP82548  
ID ABP82548 standard; peptide; 17 AA.  
XX AC  
XX ABP82548;  
XX DT  
XX 04-MAR-2003 (first entry)  
XX DE  
XX G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1221.  
XX KW  
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.  
XX OS  
XX Homo sapiens.  
XX KW  
XX WO200261087-A2.  
XX PN  
XX  
XX PD  
XX 08-AUG-2002.  
XX PF  
XX 19-DEC-2001; 2001WO-US050107.  
XX PR  
XX 19-DEC-2000; 2000US-0257144P.  
XX PA  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX KW  
XX Burner GC, Roush CL, Brown JP;  
XX PI  
XX WPI; 2003-046718/04.  
XX DR  
XX  
XX PT  
XX New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
XX  
XX Claim 1; Fig 2; 523pp; English.  
XX  
XX The present invention describes antigenic peptides (I) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related disease, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. ABP82523 to ABP82869 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 17 AA;

Query Match 39.0%; Score 30; DB 6; Length 17;

Best Local Similarity 45.5%; Pred. No. 2.7e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 5 SFOLGLYLSPH 15  
||| |:  
DB 2 SFOKSPYINAH 12  
RESULT 10  
AAW71733  
ID AAW71733 standard; peptide; 21 AA.  
XX AC  
XX AAW71733;  
XX DT  
XX 10-DEC-1998 (first entry)  
XX DE  
XX Rabbit 3-phosphoinositide dependent protein kinase peptide #5.  
XX KW  
XX Protein kinase B-alpha; 3-phosphoinositide-dependent protein kinase;  
KW diabetes; cancer; cell proliferation; phosphorylation.  
XX OS  
XX Oryctolagus cuniculus.  
XX PN  
XX WO9841638-A1.  
XX PD  
XX 24-SEP-1998.  
XX PF  
XX 16-MAR-1998; 98WO-GB000777.  
XX PR  
XX 17-MAR-1997; 97GB-00005462.  
XX PR  
XX 19-JUN-1997; 97GB-00012826.  
XX PR  
XX 15-AUG-1997; 97GB-00017253.  
XX PR  
XX 03-OCT-1997; 97US-00943667.  
XX PA  
XX (WEDI-) MEDICAL RES COUNCIL.  
XX PI  
XX Alessi DR;  
XX WPI; 1998-531572/45.  
XX PT  
XX New isolated 3-phosphoinositide-dependent protein kinase - which  
PT phosphorylates and activates protein kinase B-alpha, used to develop  
PT products for treating diabetes or cancers or for enhancing cell  
PT proliferation.  
XX PS  
XX Example 2; Page 57; 120pp; English.  
XX CC  
XX A pure 3-phosphoinositide-dependent protein kinase (3PDPK) that  
CC phosphorylates and activates PK B-alpha has been isolated. The present  
CC sequence represents a rabbit 3-phosphoinositide dependent protein kinase  
CC peptide. Products from the present invention (e.g. 3PDPK, nucleotide  
CC sequence encoding 3PDPK, antibodies against 3PDPK) can be used to  
CC identify compounds which modulate the PK activity e.g. for treating  
CC diabetes or cancers or for enhancing cell proliferation in the  
CC regeneration of nerves or in wound healing  
XX SQ  
XX Sequence 21 AA;  
Query Match 39.0%; Score 30; DB 2; Length 21;  
Best Local Similarity 70.0%; Pred. No. 3.4e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LDSLSFQLGL 10  
||| |:  
DB 12 LDSNSFELD 21  
RESULT 11  
AAE09350  
ID AAE09350 standard; protein; 23 AA.  
XX AC  
XX AAE09350;  
XX

DT 19-NOV-2001 (first entry)  
XX Human ion-10 protein.  
XX Human; ion channel-10; ion-10; schizophrenia; depression; anxiety;  
XX attention deficit hyperactivity disorder; ADHD; migraine; stroke;  
KW ischaemia; respiratory disease; asthma; neurodegenerative disease;  
KW Alzheimer's disease; Parkinson's disease; arrhythmia; cancer;  
KW macular degeneration; cardiovascular disease; endocrine disorder;  
KW congestive heart failure; thyroid disorder; inflammatory condition;  
KW epilepsy; muscular disorder; autoimmune disorder; mood disorder;  
XX Gene therapy.  
XX Homo sapiens.  
XX OS  
XX WO200160864-A2.  
PN  
XX  
XX  
PD 23-AUG-2001.  
XX  
XX 14-FEB-2001; 2001WO-US004644.  
XX  
XX 14-FEB-2000; 2000US-0182325P.  
PR  
XX (PHAA ) PHARMACIA & UPJOHN CO.  
PA  
XX  
XX Roberds SL, Karnovsky AM, Ruble CL;  
PI  
XX WPI: 2001-536567/59.  
DR  
XX N-PSDB; AAD16151.  
XX  
XX New ion channel polypeptides and polynucleotides encoding them, for  
PT treating e.g. schizophrenia, depression, anxiety, attention deficit  
PT hyperactivity disorder, migraine, stroke, ischemia, respiratory diseases.  
XX  
XX Claim 35; Page 67; 108pp; English.  
XX  
XX The present sequence is human ion channel-10 (ion-10) protein. The  
CC invention relates to human ion channel polypeptides and nucleic acid  
CC molecules encoding such polypeptides. The ion channel proteins are useful  
CC targets for discovering ligands or drugs to treat disorders or defects,  
CC including schizophrenia, depression, anxiety, attention deficit  
CC hyperactivity disorder (ADHD), migraine, stroke, ischaemia, respiratory  
CC diseases (e.g. asthma), brain injury, neurodegenerative diseases such as  
CC Alzheimer's disease, Parkinson's disease, glaucoma and macular  
CC degeneration. Compounds which modulate ion channel proteins are used in  
CC the treatment of cardiovascular diseases including congestive heart  
CC failure, arrhythmia, high blood pressure, restenosis, endocrine disorders  
CC (e.g. thyroid disorder), epilepsy, proliferative disorders (e.g. cancer),  
CC bipolar and other mood disorders, inflammatory conditions, autoimmune  
CC disorders, muscular disorders, obesity and retinal degeneration. The ion  
CC channel proteins are used as research tools for identification. The ion  
CC characterisation and purification of interacting regulatory proteins. Ion  
CC channel cDNAs are used in gene therapy  
XX  
SQ Sequence 23 AA;  
Query Match 39.0%; Score 30; DB 4; Length 23;  
Best Local Similarity 50.0%; Pred. No. 3.8e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LBSLSFQLGLYL 12  
Db |||:|:|:|:  
9 LDLVSCVLGIYI 20  
RESULT 12  
AAE10097  
ID AAE10097 standard; protein; 23 AA.  
XX  
XX AAE10097;  
AC  
XX  
XX 29-NOV-2001 (first entry)  
DT  
XX

DE Human ion channel-72 (ion72) protein.  
XX  
XX Human; ion channel-72; ion72; antiinflammatory; immunosuppressive;  
KW analgesic; nootropic; neuroprotective; antidepressant; cardiant;  
KW cytostatic; antiviral; human immunodeficiency virus; HIV; anorectic;  
KW antitaxial; thyroid disorder; thyrotoxicosis; myxoedema; renal failure;  
KW Crohn's disease; rheumatoid arthritis; autoimmune disorder; pain; stroke;  
KW Crohn's disease; rheumatoid arthritis; autoimmune disorder; pain; stroke;  
KW psychotic disorder; neurological disorder; anxiety; dyskinesia;  
KW Huntington's disease; degenerative disorder; Parkinson's disease;  
KW schizophrenia; Alzheimer's disease; cardiovascular disease; cancer;  
KW metabolic disorder; anorexia; obesity; mental disorder.  
XX  
XX Homo sapiens.  
XX OS  
XX WO200168849-A2.  
PN  
XX  
XX 20-SEP-2001.  
PD  
XX 09-MAR-2001; 2001WO-US007503.  
XX  
XX 10-MAR-2000; 2000US-0188400P.  
PR  
XX 10-MAR-2000; 2000US-0188517P.  
PR  
XX 10-MAR-2000; 2000US-0188518P.  
PR  
XX 10-MAR-2000; 2000US-0188519P.  
PR  
XX 05-JUL-2000; 2000US-0215815P.  
PR  
XX 06-JUL-2000; 2000US-0216481P.  
XX  
XX (PHAA ) PHARMACIA & UPJOHN CO.  
PA  
XX  
XX Wood LS, Vogeli G, Karnovsky AM, Ruble CL, Linske-O'connell LI;  
PI Wang J, Liu D;  
XX  
XX WPI: 2001-565795/63.  
DR  
XX N-PSDB; AAD17149.  
XX  
XX New ion channel polynucleotides and polypeptides, useful for  
PT identification of ion channel modulators and treatment of mental  
PT disorders, infections, cancer and autoimmune diseases.  
XX  
XX Claim 31; Page 93; 188pp; English.  
XX  
XX The patent discloses novel human ion channel polypeptides and their  
CC corresponding polynucleotides. The ion channel sequences and their  
CC modulators are used for the treatment of viral infections (e.g. human  
CC immunodeficiency virus (HIV)) thyroid disorders (e.g., Crohn's  
CC myxoedema), renal failure, inflammatory conditions (e.g., Crohn's  
CC disease), rheumatoid arthritis, autoimmune disorders, pain, stroke,  
CC psychotic and neurological disorders (e.g. anxiety, depression and  
CC schizophrenia), dyskinesias (e.g. Huntington's disease), degenerative  
CC disorders (e.g., Parkinson's disease, Alzheimer's disease), cardio-  
CC vascular diseases, cancer, metabolic disorders (e.g. anorexia, obesity)  
CC and mental disorders. The present sequence is ion channel-72 (ion72)  
CC protein from human  
XX  
SQ Sequence 23 AA;  
Query Match 39.0%; Score 30; DB 4; Length 23;  
Best Local Similarity 50.0%; Pred. No. 3.8e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LBSLSFQLGLYL 12  
Db |||:|:|:|:  
9 LDLVSCVLGIYI 20  
RESULT 13  
ABU97358  
ID ABU97358 standard; peptide; 23 AA.  
XX  
XX ABU97358;  
AC  
XX  
XX 29-JUL-2003 (first entry)  
DT  
XX



KW antiarteriosclerotic; antiinflammatory; antidepressant; antiarthritic;  
KW ophthalmological; cytostatic; hypertensive; hypotensive; vasotropic;  
KW antimigraine; analgesic; antiparkinsonian; thrombolytic; antithyroid;  
KW ion channel; ion-x; brain disorder; mental disorder; schizophrenia;  
KW depression; anxiety; attention deficit hyperactivity disorder; migraine;  
KW stroke; neurodegenerative disease; Alzheimer's disease;  
KW Parkinson's disease; glaucoma; macular degeneration;  
KW cardiovascular disease; ischaemia; congestive heart failure; arrhythmia;  
KW high blood pressure; retinosis; thyroid disorder; renal failure;  
KW inflammatory condition; autoimmune disorder; rheumatoid arthritis;  
KW movement disorder; central nervous system disorder; infection;  
KW eating disorder; cardiovascular disorder; thrombosis; atherosclerosis;  
KW proliferative disorder; cancer; hormonal disorder; sexual dysfunction.  
XX  
OS Homo sapiens.  
XX  
XX US2003190714-A1.  
XX  
XX  
XX 09-OCT-2003.  
XX  
XX  
XX 09-MAR-2001; 2001US-00802668.  
XX  
XX 10-MAR-2000; 2000US-0188400P.  
XX 10-MAR-2000; 2000US-0188484P.  
XX 10-MAR-2000; 2000US-0188517P.  
XX 10-MAR-2000; 2000US-0188518P.  
XX 10-MAR-2000; 2000US-0188519P.  
XX 05-JUL-2000; 2000US-0215815P.  
XX 06-JUL-2000; 2000US-0216481P.  
XX  
XX (ROBE/) ROBERTS S L.  
XX (BENJ/) BENJAMIN C W.  
XX (KARN/) KARNOVSKY A M.  
XX (RUBL/) RUBLE C L.  
XX (LINS/) LINSKE-O'CONNELL L I.  
XX (WANG/) WANG.  
XX (LIUD/) LIU D.  
XX  
XX Roberts SL, Benjamin CW, Karnovsky AM, Ruble CL;  
PI Linske-O'connell LI, Wang J, Liu D;  
PI  
XX  
XX WPI; 2003-875311/81.  
XX N-PSDB; ADE29225.  
XX  
XX New nucleic acid sequences encoding ion channels are useful to detect and  
PT treat human diseases and conditions, particularly of the brain,  
PT especially mental disorders.  
XX  
XX Claim 31; SEQ ID NO 79; 105pp; English.  
XX  
XX The invention describes an isolated nucleic acid comprising a sequence  
CC encoding at least a portion of an ion channel (ion-x). The invention is  
CC useful to detect and treat diseases and conditions of the brain,  
CC particularly mental disorders, including schizophrenia, depression,  
CC anxiety, attention deficit hyperactivity disorder, migraine, stroke, and  
CC neurodegenerative diseases such as Alzheimer's disease, Parkinson's  
CC disease, glaucoma and macular degeneration, cardiovascular diseases such  
CC as ischaemia, congestive heart failure, arrhythmia, high blood pressure  
CC and retinosis. The invention may also be used to detect or treat thyroid  
CC disorders, renal failure, inflammatory conditions, autoimmune disorders  
CC including rheumatoid arthritis, movement disorders, central nervous  
CC system disorders, infections, eating disorders, cardiovascular disorders  
CC including thrombosis and atherosclerosis, and proliferative disorders such  
CC as cancers, hormonal disorders and sexual dysfunction. This is the amino  
CC acid sequence of a novel ion channel.  
XX  
SQ Sequence 23 AA;

Query Match 39.0%; Score 30; DB 7; Length 23;  
Best Local Similarity 50.0%; Pred. No. 3.8e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 1 LBSLSFQLGLYL 12

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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 35.4255 Seconds  
(without alignments)  
149.815 Million cell updates/sec

Title: US-09-831-253F-9  
Perfect score: 77  
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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10: /cgn2\_6/ptodata/1/pubppa/US09B\_PUBCOMB.pep.\*  
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19: /cgn2\_6/ptodata/1/pubppa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	40.3	10	10	US-09-572-270A-102
2	30	39.0	15	15	US-10-682-420-55
3	30	39.0	15	15	US-10-682-420-98
4	30	39.0	15	15	US-10-409-613-55
5	30	39.0	15	15	US-10-409-613-98
6	30	39.0	15	15	US-10-442-180-55
7	30	39.0	15	15	US-10-442-180-98
8	30	39.0	17	14	US-10-225-567A-1221
9	30	39.0	21	14	US-10-150-012-12
10	30	39.0	23	10	US-09-802-668-79
11	30	39.0	23	14	US-10-243-475-79
12	29.5	38.3	16	10	US-09-880-748-2145
13	29.5	38.3	16	14	US-10-293-418-2145

14	29	37.7	11	14	US-10-197-954-26	Sequence 26, Appl
15	29	37.7	23	10	US-09-974-879-297	Sequence 297, App
16	29	37.7	23	10	US-09-305-736-297	Sequence 297, App
17	29	37.7	23	10	US-09-818-683-297	Sequence 297, App
18	29	37.7	23	11	US-09-818-683-297	Sequence 297, App
19	29	37.7	23	15	US-10-424-599-180905	Sequence 180905
20	29	37.7	23	15	US-10-621-401-297	Sequence 297, App
21	28	36.4	9	14	US-10-119-536A-101	Sequence 101, App
22	28	36.4	10	15	US-10-462-452-757	Sequence 757, App
23	28	36.4	10	15	US-10-601-953-60	Sequence 60, Appl
24	28	36.4	10	16	US-10-322-266-758	Sequence 758, App
25	28	36.4	14	10	US-09-820-649-319	Sequence 319, App
26	28	36.4	14	14	US-10-160-162-319	Sequence 319, App
27	28	36.4	15	15	US-10-682-420-99	Sequence 99, Appl
28	28	36.4	15	15	US-10-409-613-99	Sequence 99, Appl
29	28	36.4	15	15	US-10-442-180-99	Sequence 2058, Ap
30	28	36.4	20	14	US-10-225-567A-2058	Sequence 2062, Ap
31	28	36.4	23	14	US-10-225-567A-2062	Sequence 12, Appl
32	27	35.1	9	14	US-10-163-499-12	Sequence 1179, Ap
33	27	35.1	10	10	US-09-572-404B-1179	Sequence 100, App
34	27	35.1	10	10	US-09-572-270A-100	Sequence 264, App
35	27	35.1	15	13	US-10-103-395-264	Sequence 31, Appl
36	27	35.1	15	14	US-10-163-499-31	Sequence 808, App
37	27	35.1	15	15	US-10-296-734-808	Sequence 49, Appl
38	27	35.1	19	14	US-10-237-852-49	Sequence 326, App
39	27	35.1	20	14	US-10-280-066-326	Sequence 28, Appl
40	27	35.1	20	15	US-10-186-229-28	Sequence 611, App
41	27	35.1	21	10	US-09-962-756-611	Sequence 3, Appli
42	27	35.1	21	14	US-10-097-896-3	Sequence 611, App
43	27	35.1	21	14	US-10-253-471-611	Sequence 611, App
44	27	35.1	21	15	US-10-253-493-611	Sequence 1, Appli
45	27	35.1	21	16	US-10-685-105-1	

ALIGNMENTS

RESULT 1

US-09-572-270A-102  
; Sequence 102, Application US/09572270A  
; Publication No. US20030148368A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Inter- complementary peptide listing  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/09/572,270A  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 1144  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 102  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Arabidopsis Thaliana  
; OTHER INFORMATION: Sequence located in ILL2. at 8-17 and may interact with  
US-09-572-270A-102

Query Match 40.3%; Score 31; DB 10; Length 10;  
Best Local Similarity 70.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SLSFQLGLYL 12  
Db 1 SLTFQLLLFL 10  
||:|||||:  
||:|||||:

RESULT 2

US-10-682-420-55  
; Sequence 55, Application US/10682420  
; Publication No. US20040062775A1  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre

```

; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-682-420-55

Query Match          39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLSFQGLGYLSP 14
Db 2 VNELRFNIGQFLPP 15

RESULT 3
US-10-682-420-98
; Sequence 98, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-682-420-98

Query Match          39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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QY 1 LDLSFQGLGYLSP 14
Db 2 VNELRFNIGQFLPP 15

RESULT 4
US-10-409-613-55
; Sequence 55, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-409-613-55

Query Match          39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLSFQGLGYLSP 14
Db 2 VNELRFNIGQFLPP 15

RESULT 5
US-10-409-613-98
; Sequence 98, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98

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; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-409-613-98

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQGLGLSP 14
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Db 2 VNELRFNIGQLP 15

RESULT 6
US-10-442-180-55
; Sequence 55, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-442-180-55

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQGLGLSP 14
   ::|||::|
Db 2 VNELRFNIGQLP 15

RESULT 7
US-10-442-180-98
; Sequence 98, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
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; CURRENT APPLICATION NUMBER: US/10/442,180
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US/09/514,245
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-442-180-98

Query Match      39.0%; Score 30; DB 15; Length 15;
Best Local Similarity 35.7%; Pred. No. 2.8e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSFQGLGLSP 14
   ::|||::|
Db 2 VNELRFNIGQLP 15

RESULT 8
US-10-225-567A-1221
; Sequence 1221, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1221
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1221

Query Match      39.0%; Score 30; DB 14; Length 17;
Best Local Similarity 45.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 SFQGLGLSPH 15
   |||||::|
Db 2 SFQKSFYNH 12

RESULT 9
US-10-190-012-12
; Sequence 12, Application US/10190012
; Publication No. US20030108971A1
; GENERAL INFORMATION:
; APPLICANT: Alessi, Dario R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaeckle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/10/190,012  
FILING DATE: 05-JUL-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,667  
FILING DATE: 03-OCT-1997  
APPLICATION NUMBER: GB 9705462.1  
FILING DATE: 17-MAR-1997  
APPLICATION NUMBER: GB 9712826.8  
FILING DATE: 19-JUN-1997  
APPLICATION NUMBER: GB 9717253.0  
FILING DATE: 15-AUG-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Braman, Susan J  
REGISTRATION NUMBER: 34,103  
REFERENCE/DOCKET NUMBER: 87792.97R421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 716-262-3640  
TELEFAX: 716-262-4133  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 12:  
US-10-190-012-12

Query Match 39.0%; Score 30; DB 14; Length 21;  
Best Local Similarity 70.0%; Pred. No. 4e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSFQLGL 10  
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DB 12 LDSNSPELDL 21

RESULT 10  
US-09-802-668-79  
; Sequence 79, Application US/09802668  
; Publication No. US20030190714A1  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Linda  
; APPLICANT: Vogel, Gabriel  
; APPLICANT: Karnovsky, Alla  
; APPLICANT: Linske-O'Connell, Lisa I.  
; APPLICANT: Wang, Jun  
; APPLICANT: Liu, Derong  
; TITLE OF INVENTION: Human Ion Channels  
; FILE REFERENCE: 00069US1  
; CURRENT APPLICATION NUMBER: US/09/802,668  
; CURRENT FILING DATE: 2001-03-09  
; PRIOR APPLICATION NUMBER: 60/188,517  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 79  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-802-668-79

Query Match 39.0%; Score 30; DB 10; Length 23;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYL 12  
|||:|:|:  
DB 9 LDLVSCVLGIYI 20

RESULT 11  
US-10-243-475-79  
; Sequence 79, Application US/10243475  
; Publication No. US20030194720A1  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, Steven L.  
; APPLICANT: Benjamin, Christopher W.  
; APPLICANT: Karnovsky, Alla M.  
; APPLICANT: Ruble, Cara L.  
; TITLE OF INVENTION: Human Ion Channels  
; FILE REFERENCE: PHRM0039-100  
; CURRENT APPLICATION NUMBER: US/10/243,475  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: 60/403,254  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 60/318,733  
; PRIOR FILING DATE: 2001-09-12  
; NUMBER OF SEQ ID NOS: 138  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 79  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-243-475-79

Query Match 39.0%; Score 30; DB 14; Length 23;  
Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYL 12  
|||:|:|:  
DB 9 LDLVSCVLGIYI 20

RESULT 12  
US-09-880-748-2145  
; Sequence 2145, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2145  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2145

Query Match 38.3%; Score 29.5; DB 10; Length 16;  
Best Local Similarity 61.5%; Pred. No. 3.6e+02;  
Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 2 DSL-SFQLGLYLS 13  
|||:|:|:

Db 4 DTLTSYVLGYLS 16

## RESULT 13

US-10-293-418-2145  
; Sequence 2145, Application US/10293418  
; Publication No. US2003022396A1

## ; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523p2

; CURRENT FILING DATE: 2002-11-27

; PRIOR FILING DATE: 2002-11-27

; PRIOR FILING DATE: 2001-11-16

; PRIOR FILING DATE: 2001-11-16

; PRIOR FILING DATE: 2001-12-19

; PRIOR FILING DATE: 2001-12-19

; PRIOR FILING DATE: 2001-06-15

; PRIOR FILING DATE: 2001-06-15

; PRIOR FILING DATE: 2001-05-25

; PRIOR FILING DATE: 2001-05-25

; PRIOR FILING DATE: 2001-03-21

; PRIOR FILING DATE: 2001-03-21

; PRIOR FILING DATE: 2001-03-16

; PRIOR FILING DATE: 2001-03-16

; PRIOR FILING DATE: 2000-10-17

; PRIOR FILING DATE: 2000-10-17

; PRIOR FILING DATE: 2000-06-16

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2145

; LENGTH: 16

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-293-418-2145

## Query Match

Best Local Similarity 38.3%; Score 29.5; DB 14; Length 16;

Matches 8; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 2 DSL-SFQGLGYLS 13

Db 4 DTLTSYVLGYLS 16

## RESULT 14

US-10-197-954-26

; Sequence 26, Application US/10197954

; Publication No. US20030119021A1

## ; GENERAL INFORMATION:

; APPLICANT: K"ster, Hubert

; APPLICANT: Siddiqi, Suhail

; TITLE OF INVENTION: Capture Compounds, Collections Thereof

; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex

; TITLE OF INVENTION: Compositions

; FILE REFERENCE: 24743-2305

; CURRENT FILING DATE: 2002-07-16

; PRIOR FILING DATE: 2002-07-16

; PRIOR FILING DATE: 2001-07-16

; PRIOR FILING DATE: 2001-07-16

; PRIOR FILING DATE: 2001-08-21

; PRIOR FILING DATE: 2002-03-11

; NUMBER OF SEQ ID NOS: 149

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 26

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo Sapien

; NAME/KEY: AMIDATION

; LOCATION: 11  
US-10-197-954-26

## Query Match

Best Local Similarity 37.7%; Score 29; DB 14; Length 11;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LBSLSFQLGL 10

Db 2 MDSLAFSGGL 11

## RESULT 15

US-09-974-879-297

; Sequence 297, Application US/09974879

; Publication No. US20030028003A1

## ; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 125 Human Secreted Proteins

; FILE REFERENCE: P2020P2

; CURRENT FILING DATE: 2001-10-12

; PRIOR FILING DATE: 2000-10-13

; PRIOR FILING DATE: 2001-03-28

; PRIOR FILING DATE: 1999-05-05

; PRIOR FILING DATE: 1998-11-04

; PRIOR FILING DATE: 1997-11-07

; PRIOR FILING DATE: 1997-11-07

; PRIOR FILING DATE: 1997-11-07

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; PRIOR FILING DATE: 1997-11-07

; PRIOR FILING DATE: 1997-11-07

Search completed: November 14, 2004, 12:27:00  
Job time : 35.4255 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 11.8085 Seconds  
(without alignments)  
84.242 Million cell updates/sec

Title: US-09-831-253F-9

Perfect score: 77  
Sequence: 1 LDSLSFQLGLYLSPH 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTGJS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/bagkfilesi.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	41.6	16	4	US-09-712-368-9
2	30	39.0	15	4	US-09-514-245-55
3	30	39.0	15	4	US-09-514-245-98
4	30	39.0	21	4	US-08-943-667-12
5	29	37.7	13	4	US-08-753-7508-64
6	29	37.7	17	3	US-08-523-373-18
7	28	36.4	15	4	US-09-514-245-99
8	28	36.4	17	3	US-09-025-769B-240
9	28	36.4	17	4	US-09-490-070A-240
10	28	36.4	17	4	US-09-490-153-240
11	28	36.4	20	1	US-07-990-893-9
12	27	35.1	7	4	US-09-463-239-29
13	27	35.1	9	4	US-09-239-043D-1855
14	27	35.1	10	3	US-08-159-339A-458
15	27	35.1	10	4	US-09-239-043D-620
16	27	35.1	10	4	US-09-239-043D-1944
17	27	35.1	11	4	US-09-239-043D-467
18	27	35.1	11	4	US-09-239-043D-580
19	27	35.1	11	4	US-09-239-043D-1867
20	27	35.1	15	1	US-08-102-738-20
21	27	35.1	15	4	US-09-009-953-264
22	27	35.1	15	4	US-09-239-043D-2188
23	27	35.1	20	1	US-09-618-592-7
24	27	35.1	20	2	US-08-797-842-7
25	27	35.1	23	4	US-09-423-097-7
26	26.5	34.4	12	3	US-09-298-924-19
27	26	33.8	8	3	US-08-913-842-28

28	26	33.8	9	4	US-09-311-784A-271
29	26	33.8	9	4	US-09-601-729-70
30	26	33.8	10	3	US-08-159-339A-472
31	26	33.8	10	3	US-08-159-339A-503
32	26	33.8	12	4	US-09-407-687-34
33	26	33.8	14	1	US-07-914-280-14
34	26	33.8	14	5	PCT-US93-06625-14
35	26	33.8	15	4	US-09-148-712-7
36	26	33.8	22	3	US-09-439-313-557
37	26	33.8	23	4	US-09-511-204B-10
38	25	32.5	8	3	US-08-444-818-557
39	25	32.5	9	1	US-08-336-618-2
40	25	32.5	12	4	US-09-389-956-52
41	25	32.5	15	1	US-08-049-783-11
42	25	32.5	15	1	US-08-158-232-22
43	25	32.5	15	1	US-08-304-626-22
44	25	32.5	15	1	US-08-316-301A-23
45	25	32.5	15	2	US-08-611-928-22

ALIGNMENTS

RESULT 1

US-09-712-368-9  
; Sequence 9, Application US/09712368  
; Patent No. 6593108  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Qingyun  
; APPLICANT: McDonald, Terrence P.  
; APPLICANT: Howard, Andrew D.  
; APPLICANT: Iwaasa, Hisashi  
; APPLICANT: Sano, Hideki  
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR  
; FILE REFERENCE: 20579Y  
; CURRENT APPLICATION NUMBER: US/09/712,368  
; CURRENT FILING DATE: 2000-11-14  
; PRIOR APPLICATION NUMBER: 60/165,871  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 60/188,977  
; PRIOR FILING DATE: 2000-03-13  
; PRIOR APPLICATION NUMBER: 60/198,029  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MCH-R2 Segment  
US-09-712-368-9

Query Match 41.6%; Score 32; DB 4; Length 16;  
Best Local Similarity 54.5%; Pred. No. 10;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 3 SLSFQLGLYLS 13

Db 5 TLAFYVGYLS 15

RESULT 2

US-09-514-245-55  
; Sequence 55, Application US/09514245  
; Patent No. 6703023  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre  
; APPLICANT: BLANCHARD, Philippe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire

```
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-09-514-245-55

Query Match          39.0%; Score 30; DB 4; Length 15;
Best Local Similarity 35.7%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSPQLGLYLSL 14
   : : : : : : : :
Db 2 VNELRNIGQLFPP 15

RESULT 3
US-09-514-245-98
; Sequence 98, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/09/514,245
; CURRENT FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-98

Query Match          39.0%; Score 30; DB 4; Length 15;
Best Local Similarity 35.7%; Pred. No. 23;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDSLSPQLGLYLSL 14
   : : : : : : : :
Db 2 VNELRNIGQLFPP 15

RESULT 4
US-08-943-667-12
; Sequence 12, Application US/08943667
; Patent No. 6734001
; GENERAL INFORMATION:
; APPLICANT: Alessi, Dario R
; TITLE OF INVENTION: ENZYME
; NUMBER OF SEQUENCES: 35
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaesckle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,667
; FILING DATE: 03-OCT-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9705462.1
; FILING DATE: 17-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9712826.8
; FILING DATE: 19-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9717253.0
; FILING DATE: 15-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Braman, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87792.97R421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-943-667-12

Query Match          39.0%; Score 30; DB 4; Length 21;
Best Local Similarity 70.0%; Pred. No. 36;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LDSLSPQLGL 10
   ||| ||| :|
Db 12 LDSNSFELD 21

RESULT 5
US-08-753-750B-64
; Sequence 64, Application US/08753750B
; Patent No. 6610506
; GENERAL INFORMATION:
; APPLICANT: Lo, Reggie Y.C.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Potter, Andrew A.
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
```

; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-08-753-750B-64

Query Match 37.7%; Score 29; DB 4; Length 13;  
Best Local Similarity 66.7%; Pred. No. 31;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SLSFQLGLY 11  
| : : : :  
Db 4 SESWELGY 12

RESULT 6  
US-08-523-373-18  
; Sequence 18, Application US/08523373  
; Patent No. 6037145  
; GENERAL INFORMATION:  
; APPLICANT: Yabuta, Masayuki  
; APPLICANT: Ohsuye, Kazuhiro  
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314-3187  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/523,373  
; FILING DATE: 05-SEP-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-238595  
; FILING DATE: 07-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-296028  
; FILING DATE: 07-NOV-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 001560-251  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: C-terminal  
US-08-523-373-18

Query Match 37.7%; Score 29; DB 3; Length 17;  
Best Local Similarity 33.3%; Pred. No. 43;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 LDSLSFQLGLYSPH 15  
: : : : :  
Db 2 IEDHPELRYRRHH 16

RESULT 7  
US-09-514-245-99

; Sequence 99, Application US/09514245  
; Patent No. 6703023  
; GENERAL INFORMATION:  
; APPLICANT: JESTIN, Andre  
; APPLICANT: ALBINA, Emanuel  
; APPLICANT: Le CANN, Pierre  
; APPLICANT: BLANCHARD, Phillipe  
; APPLICANT: HUTET, Evelyne  
; APPLICANT: ARNAULD, Claire  
; APPLICANT: TRUONG, Catherine  
; APPLICANT: MAHE, Dominique  
; APPLICANT: CARIOLET, Roland  
; APPLICANT: MADEC, Francois  
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEAS  
; FILE REFERENCE: 065691/0176  
; CURRENT APPLICATION NUMBER: US/09/514,245  
; CURRENT FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: FR 97/15396  
; PRIOR FILING DATE: 1997-12-05  
; NUMBER OF SEQ ID NOS: 170  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 99  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Type A PWD circovirus  
US-09-514-245-99

Query Match 36.4%; Score 28; DB 4; Length 15;  
Best Local Similarity 45.5%; Pred. No. 58;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LSFQLGLYLP 14  
| : : : :  
Db 1 LRFNIGQLP 11

RESULT 8  
US-09-025-769B-240  
; Sequence 240, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 240:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-025-769B-240

Query Match 36.4%; Score 28; DB 3; Length 17;  
Best Local Similarity 55.6%; Pred. No. 67;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QLGLYLSPH 15  
:| |||  
DB 3 RLQAYLKPH 11

RESULT 9  
US-09-490-070A-240  
; Sequence 240, Application US/09490070A  
; Patent No. 6696248  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman  
White & McAuliffe  
STREET: 1666 K Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,070A  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Colin G. Sandercock, Esq.  
REGISTRATION NUMBER: 31,298  
REFERENCE/DOCKET NUMBER: 37629-0005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 912-2020  
TELEFAX: (202) 912-2020  
INFORMATION FOR SEQ ID NO: 240:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 240:  
US-09-490-070A-240

Query Match 36.4%; Score 28; DB 4; Length 17;  
Best Local Similarity 55.6%; Pred. No. 67;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QLGLYLSPH 15  
:| |||  
DB 3 RLQAYLKPH 11

RESULT 10  
US-09-490-153-240  
; Sequence 240, Application US/09490153  
; Patent No. 6706484  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,153  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769B  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)596-9000  
TELEFAX: (212)596-9090  
INFORMATION FOR SEQ ID NO: 240:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 240:  
US-09-490-153-240

Query Match 36.4%; Score 28; DB 4; Length 17;  
Best Local Similarity 55.6%; Pred. No. 67;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QLGLYLSPH 15  
:| |||  
DB 3 RLQAYLKPH 11

RESULT 11  
US-07-990-893-9  
; Sequence 9, Application US/07990893  
; Patent No. 5547841  
; GENERAL INFORMATION:  
; APPLICANT: Marotta, Charles A.  
; APPLICANT: Zain, Sayeeda



;; TITLE OF INVENTION: Genetic Sequences Coding For Alzheimer  
;; TITLE OF INVENTION: Amyloid From Brain  
;; NUMBER OF SEQUENCES: 18  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Sterne, Kesler, Goldstein & Fox  
;; STREET: 1225 Connecticut Avenue  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: U.S.A.  
;; ZIP: 20036  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/07/990,893  
;; FILING DATE: 19921215  
;; CLASSIFICATION: 536  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Esmond, Robert W.  
;; REGISTRATION NUMBER: 32,893  
;; REFERENCE/DOCKET NUMBER: 0932.0250003  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 466-0800  
;; TELEFAX: (202) 833-8716  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 20 amino acids  
;; TYPE: AMINO ACID  
;; TOPOLOGY: both  
;; US-07-990-893-9

Query Match 36.4%; Score 28; DB 1; Length 20;  
Best Local Similarity 41.7%; Pred. No. 83;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LDSLSFQLGGLYL 12  
| : |||:::  
Db 5 LNREEFQLGIPV 16

RESULT 12  
US-09-463-239-29  
; Sequence 29, Application US/09463239  
; Patent No. 6700039  
; GENERAL INFORMATION:  
; APPLICANT: Jepson, Ian  
; APPLICANT: Ebner, Marcus  
; APPLICANT: Sonnewald, Uwe  
; TITLE OF INVENTION: Genetic Method for Controlling Sprouting  
; FILE REFERENCE: 109846.178  
; CURRENT APPLICATION NUMBER: US/09/463,239  
; CURRENT FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: PCT/GB98/02023  
; PRIOR FILING DATE: 1998-07-10  
; PRIOR APPLICATION NUMBER: EP 97113118.0  
; PRIOR FILING DATE: 1997-07-30  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 29  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amino acid sequence encoding MOT isolated from potato.  
US-09-463-239-29

Query Match 35.1%; Score 27; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3.8e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FQLGLYL 12

Db 1 FQLGLNL 7

RESULT 13  
US-09-239-043D-1855  
; Sequence 1855, Application US/09239043D  
; Patent No. 6689363  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Vitello, Maria A.  
; APPLICANT: Livingston, Brian D.  
; APPLICANT: Celis, Esteban  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus  
; FILE REFERENCE: 2060.0060007  
; CURRENT APPLICATION NUMBER: US/09/239,043D  
; CURRENT FILING DATE: 1999-01-27  
; PRIOR APPLICATION NUMBER: US 09/189,702  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 08/978,291  
; PRIOR FILING DATE: 1997-11-25  
; PRIOR APPLICATION NUMBER: US 08/820,360  
; PRIOR FILING DATE: 1997-03-12  
; PRIOR APPLICATION NUMBER: US 60/013,363  
; PRIOR FILING DATE: 1996-03-13  
; PRIOR APPLICATION NUMBER: US 08/461,603  
; PRIOR FILING DATE: 1995-06-05  
; PRIOR APPLICATION NUMBER: US 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; PRIOR APPLICATION NUMBER: US 08/344,824  
; PRIOR FILING DATE: 1994-11-23  
; PRIOR APPLICATION NUMBER: US 08/278,634  
; PRIOR FILING DATE: 1994-07-21  
; PRIOR APPLICATION NUMBER: US 08/205,713  
; PRIOR FILING DATE: 1994-03-04  
; PRIOR APPLICATION NUMBER: US 08/197,484  
; PRIOR FILING DATE: 1994-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2579  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1855  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Orthohepadnaviridae hepatitis B virus  
US-09-239-043D-1855

Query Match 35.1%; Score 27; DB 4; Length 9;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LGLYLSPH 15  
| : |||:::  
Db 1 LGIHLNPN 8

RESULT 14  
US-08-159-339A-458  
; Sequence 458, Application US/08159339A  
; Patent No. 6037135  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding peptides and Their  
; TITLE OF INVENTION: Uses

NUMBER OF SEQUENCES: 1254  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/159,339A  
FILING DATE: 29-NOV-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/926,666  
FILING DATE: 07-AUG-1992  
APPLICATION NUMBER: US 08/027,746  
FILING DATE: 05-MAR-1993  
APPLICATION NUMBER: US 08/103,396  
FILING DATE: 06-AUG-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Ellen Lauver  
REGISTRATION NUMBER: 32,762  
REFERENCE/DOCKET NUMBER: 018623-005030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
TELEX:  
INFORMATION FOR SEQ ID NO: 458:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-159-339A-458

Query Match 35.1%; Score 27; DB 3; Length 10;  
Best Local Similarity 50.0%; Pred. No. 55;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 8 LGLYLSPH 15  
||:|:|:  
Db 2 LGIHLNPN 9

## RESULT 15

US-09-239-043D-620  
Sequence 620, Application US/09239043D  
Patent No. 6689363  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Vitello, Maria A.  
APPLICANT: Livingston, Brian D.  
APPLICANT: Celis, Esteban  
APPLICANT: Kubo, Ralph T.  
APPLICANT: Grey, Howard M.  
APPLICANT: Chesnut, Robert  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus  
FILE OF INVENTION: Using Peptide and Nucleic Acid Compositions  
FILE REFERENCE: 2060.006007  
CURRENT APPLICATION NUMBER: US/09/239,043D  
CURRENT FILING DATE: 1999-01-27  
PRIOR APPLICATION NUMBER: US 09/189,702  
PRIOR FILING DATE: 1998-11-10  
PRIOR APPLICATION NUMBER: US 08/978,291

PRIOR FILING DATE: 1997-11-25  
PRIOR APPLICATION NUMBER: US 08/820,360  
PRIOR FILING DATE: 1997-03-12  
PRIOR APPLICATION NUMBER: US 60/013,363  
PRIOR FILING DATE: 1996-03-13  
PRIOR APPLICATION NUMBER: US 08/461,603  
PRIOR FILING DATE: 1995-06-05  
PRIOR APPLICATION NUMBER: US 08/347,610  
PRIOR FILING DATE: 1994-12-01  
PRIOR APPLICATION NUMBER: US 08/344,824  
PRIOR FILING DATE: 1994-11-23  
PRIOR APPLICATION NUMBER: US 08/278,634  
PRIOR FILING DATE: 1994-07-21  
PRIOR APPLICATION NUMBER: US 08/205,713  
PRIOR FILING DATE: 1994-03-04  
PRIOR APPLICATION NUMBER: US 08/197,484  
PRIOR FILING DATE: 1994-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2579  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 620  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Orthohepadnaviridae hepatitis B virus  
US-09-239-043D-620  
Query Match 35.1%; Score 27; DB 4; Length 10;  
Best Local Similarity 50.0%; Pred. No. 55;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
QY 8 LGLYLSPH 15  
||:|:|:  
Db 2 LGIHLNPN 9  
Search completed: November 14, 2004, 12:08:51  
Job time : 12.8085 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:45:35 ; Search time 37 Seconds  
(without alignments)  
31.205 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	38.1	11	2 PQ0731	unidentified 5.7/3
2	22	34.9	7	2 PH1602	Ig H chain V-D-J r
3	20	31.7	10	2 S69159	cystathionine gamm
4	19	30.2	7	2 PT0586	T-cell receptor be
5	18	28.6	10	2 D61440	polygalacturonase
6	18	28.6	12	2 S69123	proton-translocati
7	17	27.0	6	2 I49808	D-SP2.5 region - m
8	17	27.0	6	2 PT0519	T-cell receptor be
9	17	27.0	6	2 PT0650	T-cell receptor be
10	17	27.0	9	2 SI3889	phosphoenolpyruvat
11	17	27.0	12	2 A29169	phospholipase A2 (
12	16	25.4	4	2 PT0661	T-cell receptor be
13	16	25.4	7	2 S09652	hypothetical prote
14	16	25.4	7	2 PX0008	glucuronosyltransf
15	16	25.4	7	4 I55382	hypothetical pepti
16	16	25.4	9	2 A43848	cell surface adhes
17	16	25.4	9	2 G85802	hypothetical prote
18	16	25.4	10	2 C39191	hypothetical prote
19	16	25.4	10	2 PQ0753	beta-fructofuranos
20	16	25.4	10	2 PT0310	Ig heavy chain CRD
21	16	25.4	11	2 S05002	corazonin - Americ
22	16	25.4	12	2 PN0581	tyrosine 3-monooxy
23	16	25.4	12	2 PN0580	tyrosine 3-monooxy
24	16	25.4	12	2 PN0579	tyrosine 3-monooxy
25	16	25.4	12	2 PN0577	tyrosine 3-monooxy
26	16	25.4	12	2 PN0576	tyrosine 3-monooxy
27	16	25.4	12	2 PT0274	Ig heavy chain CRD
28	16	25.4	12	2	
29	16	25.4	12	2 I77529	estrogen receptor

30	16	25.4	12	2 PQ0776	NADH2 dehydrogenas
31	15	23.8	5	2 PT0624	T-cell receptor be
32	15	23.8	6	2 S66195	alcohol dehydrogen
33	15	23.8	6	2 PT0587	T-cell receptor be
34	15	23.8	7	2 S09066	globulin IV alpha
35	15	23.8	8	2 PT0588	neuromodulatory pe
36	15	23.8	10	2 C41946	T-cell receptor ga
37	15	23.8	11	1 LFTWWE	probable trypEG lea
38	15	23.8	11	2 S66196	alcohol dehydrogen
39	15	23.8	11	2 CS3652	znhr protein - pse
40	15	23.8	11	2 D41946	T-cell receptor ga
41	15	23.8	12	2 I64829	gene HEXA protein
42	15	23.8	12	2 S16204	6-phosphofructokin
43	15	23.8	12	2 A28955	polyalialoglycoprot
44	15	23.8	12	2	
45	15	23.8	12	2 A61503	sterol carrier pro

ALIGNMENTS

RESULT 1  
PQ0731  
unidentified 5.7/35K protein [imported] - rice (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: PQ0731  
R;Komatsu, S.; Kajiwara, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993  
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensio

A;Reference number: PQ0696  
A;Accession: PQ0731  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-11 <KOM>  
A;Cross-references: UNIPROT:Q7M1U2

Query Match 38.1%; Score 24; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATMIW 9  
DB 1 ATVW 5

RESULT 2  
PH1602  
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1602  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1602  
A;Molecule type: DNA  
A;Residues: 1-7 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 34.9%; Score 22; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIWT 10  
DB 2 ASSLWT 7

RESULT 3  
S69159

cystathionine gamma-synthase - spinach (fragment)  
C:Species: Spinacia oleracea (spinach)  
C:Date: 12-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 09-Jul-2004  
C:Accession: S69159  
R:Ravanel, S.; Droux, M.; Douce, R.  
Arch. Biochem. Biophys. 316, 572-584, 1995  
A:Title: Methionine biosynthesis in higher plants. I. Purification and characterization  
A:Reference number: S69159, MUID:95142682; PMID:7840669  
A:Accession: S69159  
A:Molecule type: protein  
A:Residues: 1-10 <RAV>  
A:Cross-references: UNIPROT:Q7MLJ3  
C:Keywords: chloroplast

Query Match 31.7%; Score 20; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 6.9e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLDATMI 8  
Db 2 TAVDAAA 9

## RESULT 4

PT0586  
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0586; PT0592  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0586  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-7 <FEE>  
A:Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)  
C:Keywords: T-cell receptor

Query Match 30.2%; Score 19; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIW 9  
Db 1 ASSIW 5

## RESULT 5

D61440  
polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)  
C:Species: Aspergillus sp.  
C:Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: D61440  
R:Stratilova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jornvall, H.  
J. Protein Chem. 12, 15-22, 1993  
A:Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and structure  
A:Reference number: A61440; MUID:93151962; PMID:8427629  
A:Accession: D61440  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-10 <STR>  
A:Cross-references: UNIPROT:Q7M501  
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 28.6%; Score 18; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDA 5  
Db 6 TSADA 10

## RESULT 6

S69123  
proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)  
C:Species: Rhodospirillum rubrum  
C:Date: 10-Mar-1998 #sequence\_revision 24-Apr-1998 #text\_change 24-Apr-1998  
C:Accession: S69123  
R:Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.  
Eur. J. Biochem. 228, 719-726, 1995  
A:Title: Properties of the soluble polypeptide of the proton-translocating transhydrogenase.  
A:Reference number: S69123; MUID:95255277; PMID:7737169  
A:Accession: S69123  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <DIG>

Query Match 28.6%; Score 18; DB 2; Length 12;  
Best Local Similarity 40.0%; Pred. No. 2.1e+03;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIW 9  
Db 2 ADVVV 6

## RESULT 7

I49808  
D-SP2.5 region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I49808  
R:Kurosawa, Y.; Tonegawa, S.  
J. Exp. Med. 155, 201-218, 1982  
A:Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity I  
A:Reference number: I49808; MUID:82099938; PMID:6798155  
A:Accession: I49808  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: GB:J00432; NID:g194370; PIDN:AAA37904.1; PID:9450452  
C:Genetics:  
A:Gene: Igh

Query Match 27.0%; Score 17; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIWT 10  
Db 1 STMVT 6

## RESULT 8

PT0519  
T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0519  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0519  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FEE>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 27.0%; Score 17; DB 2; Length 6;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIW 9  
| : : |  
Db 1 ASSLM 5

## RESULT 9

PT0650  
T-cell receptor beta chain V-D-J region (121-3BF) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0650  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0650  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <FEE>  
A;Experimental source: day 4 postnatal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 27.0%; Score 17; DB 2; Length 6;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLDAT 6  
| : : |  
Db 2 SSDAT 6

## RESULT 10

S13989  
Phosphoenolpyruvate carboxylase (EC 4.1.1.31) - maize  
C;Species: Zea mays (maize)  
C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C;Accession: S13989  
R;Jiao, J.; Chollet, R.

Arch. Biochem. Biophys. 283, 300-305, 1990  
A;Title: Regulatory phosphorylation of serine-15 in maize phosphoenolpyruvate carboxylase  
A;Reference number: S13889; MUID:91112741; PMID:2148863  
A;Accession: S13889  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-9 <LIA>  
A;Cross-references: UNIPROT:Q43267; UNIPROT:Q41197  
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 27.0%; Score 17; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLDATM 7  
| : : |  
Db 3 SIDAQL 8

## RESULT 11

A29169  
Phospholipase A2 (EC 3.1.1.4) precursor - sheep (fragment)  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 02-Jun-1988 #sequence\_revision 02-Jun-1988 #text\_change 16-Aug-2004  
C;Accession: A29169  
R;Dutilh, C.E.; Van Doren, P.J.; Verheul, F.E.A.M.; De Haas, G.H.  
Eur. J. Biochem. 53, 91-97, 1975  
A;Title: Isolation and properties of phospholipase A2 from ox and sheep pancreas.  
A;Reference number: A94661  
A;Accession: A29169  
A;Molecule type: protein  
A;Residues: 1-12 <DUT>  
A;Cross-references: UNIPROT:Q7M3E5  
C;Superfamily: Phospholipase A2

C;Keywords: carboxylic ester hydrolase; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
Query Match 27.0%; Score 17; DB 2; Length 12;  
Best Local Similarity 28.6%; Pred. No. 3.2e+03;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDATMIW 9  
| : : |  
Db 4 LNSRALW 10

## RESULT 12

PT0661  
T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
C;Accession: PT0661  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0661  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-4 <FEE>  
A;Cross-references: UNIPROT:Q8BZQ7; UNIPROT:Q8CCN5  
A;Experimental source: day 4 postnatal thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 25.4%; Score 16; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 WT 10  
| : : |  
Db 3 WT 4

## RESULT 13

S09652  
Hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)  
C;Species: Enterobacter cloacae  
C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 08-Oct-1999  
C;Accession: S09652  
R;Vliegventhart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.  
Antimicrob. Agents Chemother. 33, 1153-1159, 1989  
A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant in  
A;Reference number: S09651; MUID:90024972; PMID:2552900  
A;Accession: S09652  
A;Molecule type: DNA  
A;Residues: 1-7 <VLI>  
A;Cross-references: EMBL:X51534; NID:g40878; PIDN:CAA35914.1; PID:g581034

Query Match 25.4%; Score 16; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIW 9  
| : : |  
Db 2 IIW 4

## RESULT 14

PX0008  
glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)  
N;Alternate names: UDP-glucuronyltransferase  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 07-Feb-1997  
C;Accession: PX0008  
R;Yokota, H.; Yuasa, A.; Sato, R.  
J. Biochem. 104, 531-536, 1988  
A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver

A;Reference number: PX0008; MUID:89197852; PMID:3149280

A;Accession: PX0008

A;Molecule type: protein

A;Residues: 1-7 <YOK>

C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 25.4%; Score 16; DB 2; Length 7;

Best Local Similarity 33.3%; Pred. No. 2.8e+05;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MW 9

Db :|

4 LVW 6

#### RESULT 15

I55382

hypothetical peptide PA11 promoter region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 20-Apr-2000

C;Accession: I55382

R;Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.

J. Biol. Chem. 268, 10739-10745, 1993

A;Title: The two allele sequences of a common polymorphism in the promoter of the plasmi

A;Reference number: I55382; MUID:93266509; PMID:8388372

A;Accession: I55382

A;Status: translation not shown; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-7 <DAW>

A;Cross-references: GB:M91557; NID:g190020; PIDN:AAA60110.1; PID:g190021

C;Comment: This is the hypothetical translation of a sequence from the PA11 gene promote

C;Genetics:

A;Gene: GDB:PA11

A;Cross-references: GDB:120297; OMIM:173360

A;Map position: 7q21.3-7q22

Query Match 25.4%; Score 16; DB 4; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 WT 10

Db :|

1 WT 2

Search completed: November 14, 2004, 12:55:21

Job time : 38 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:16:33 ; Search time 79.6667 Seconds  
(without alignments)  
66.619 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLILQGPVYVSWL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 238011

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US05\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US04\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US03\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US02\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US00\_PUBCOMB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	33	41.2	14	14	US-10-083-768-39
2	33	41.2	14	14	US-10-083-768-216
3	33	41.2	14	15	US-10-609-217-67
4	33	41.2	14	15	US-10-632-388-67
5	33	41.2	14	15	US-10-651-723-67
6	33	41.2	14	15	US-10-645-761-67
7	33	41.2	14	15	US-10-666-696-67
8	33	41.2	14	15	US-10-653-048-67
9	32	40.0	14	14	US-10-083-768-37
10	31	38.8	6	15	US-10-243-613-25
11	31	38.8	9	15	US-10-428-335-69
12	31	38.8	12	10	US-09-990-832C-71
13	31	38.8	15	9	US-09-760-397-6

14	31	38.8	15	14	US-10-324-182-6	Sequence 6, Appli
15	30	37.5	9	10	US-09-077-439A-13	Sequence 13, Appli
16	30	37.5	9	13	US-10-205-150-9	Sequence 9, Appli
17	30	37.5	9	14	US-10-079-167-66	Sequence 66, Appli
18	30	37.5	9	14	US-10-360-836-66	Sequence 66, Appli
19	30	37.5	9	15	US-10-057-475B-10639	Sequence 10639, A
20	30	37.5	9	15	US-10-057-475B-10660	Sequence 10660, A
21	30	37.5	9	15	US-10-057-475B-10715	Sequence 10715, A
22	30	37.5	9	15	US-10-154-884B-10639	Sequence 10639, A
23	30	37.5	9	15	US-10-154-884B-10660	Sequence 10660, A
24	30	37.5	9	15	US-10-154-884B-10715	Sequence 10715, A
25	30	37.5	9	15	US-10-367-580-146	Sequence 146, App
26	30	37.5	9	15	US-10-367-593-146	Sequence 146, App
27	30	37.5	9	15	US-10-367-594-146	Sequence 146, App
28	30	37.5	9	15	US-10-367-654-146	Sequence 146, App
29	30	37.5	9	15	US-10-367-658-146	Sequence 146, App
30	30	37.5	9	15	US-10-367-668-146	Sequence 146, App
31	30	37.5	9	16	US-10-367-674-146	Sequence 146, App
32	30	37.5	9	16	US-10-653-624-66	Sequence 66, Appl
33	30	37.5	9	16	US-10-833-439-66	Sequence 66, Appl
34	30	37.5	9	17	US-10-833-745-66	Sequence 66, Appl
35	30	37.5	9	17	US-10-833-744-66	Sequence 66, Appl
36	30	37.5	9	17	US-10-686-943-66	Sequence 66, Appl
37	30	37.5	12	16	US-10-654-623-3	Sequence 3, Appli
38	29	36.2	9	9	US-09-915-543-8	Sequence 8, Appli
39	29	36.2	9	14	US-10-322-579-8	Sequence 8, Appli
40	29	36.2	9	15	US-10-664-859-8	Sequence 8, Appli
41	29	36.2	9	15	US-10-398-104-140	Sequence 140, App
42	29	36.2	11	15	US-10-449-829A-35	Sequence 35, Appl
43	29	36.2	11	15	US-10-398-104-280	Sequence 280, App
44	29	36.2	11	16	US-10-652-334-12	Sequence 12, Appl
45	29	36.2	12	15	US-10-328-916-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1  
US-10-083-768-39  
; Sequence 39, Application US/10083768  
; Publication No. US20030158116A1  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; Cwirla, Steven B.  
; Duffin, David J.  
; Gates, Christian  
; Haselden, Sherril S.  
; Mattheakis, Larry C.  
; Schatz, Peter J.  
; Wagstrom, Christopher R.  
; Wrighton, Nicholas C.  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; THROMBOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/083,768  
; FILING DATE: 27-Feb-2002  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-10-083-768-39

Query Match 41.2%; Score 33; DB 14; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPPVSWL 15  
| | | : | | |  
DB 3 LVGPSSMSWL 12

RESULT 2  
US-10-083-768-216  
; Sequence 216, Application US/10083768  
; Publication No. US20030158116A1  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; Wiria, Steven E.  
; Duffin, David J.  
; Gates, Christian  
; Haselden, Sherril S.  
; Matheakis, Larry C.  
; Schatz, Peter J.  
; Wagstrom, Christopher R.  
; Wrighton, Nicholas C.  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; THROMBOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/083,768  
; FILING DATE: 27-Feb-2002  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3065USW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 216:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 216:  
US-10-083-768-216

Query Match 41.2%; Score 33; DB 14; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPPVSWL 15  
| | | : | | |  
DB 3 LVGPSSMSWL 12

RESULT 3  
US-10-609-217-67  
; Sequence 67, Application US/10609217  
; Publication No. US20040044188A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/609,217  
; CURRENT FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-609-217-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPPVSWL 15  
| | | : | | |  
DB 3 LVGPSSMSWL 12

RESULT 4  
US-10-632-388-67  
; Sequence 67, Application US/10632388  
; Publication No. US20040053845A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/632,388  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-632-388-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;



QY 6 LOGPPYVSWL 15  
| | | : | | |  
Db 3 LVGPSLSMSWL 12

RESULT 5

US-10-651-723-67  
; Sequence 67, Application US/10651723  
; Publication No. US20040057953A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/651,723  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-651-723-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15  
| | | : | | |  
Db 3 LVGPSLSMSWL 12

RESULT 6

US-10-645-761-67  
; Sequence 67, Application US/10645761  
; Publication No. US20040071712A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/645,761  
; CURRENT FILING DATE: 2003-08-18  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-645-761-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15  
| | | : | | |  
Db 3 LVGPSLSMSWL 12

RESULT 7

US-10-666-696-67  
; Sequence 67, Application US/10666696  
; Publication No. US20040077022A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; APPLICANT: GUDAS, JEAN MARIE  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527A  
; CURRENT APPLICATION NUMBER: US/10/666,696  
; CURRENT FILING DATE: 2003-09-19  
; PRIOR APPLICATION NUMBER: US/09/563,286C  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/428,082  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1157  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-mimetic peptide  
US-10-666-696-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15  
| | | : | | |  
Db 3 LVGPSLSMSWL 12

RESULT 8

US-10-653-048-67  
; Sequence 67, Application US/10653048  
; Publication No. US20040087778A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/653,048  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-653-048-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVSWL 15  
| | | | : | | |  
Db 3 LVGPSLMSWL 12

## RESULT 9

US-10-083-768-37  
; Sequence 37, Application US/10083768  
; Publication No. US20030158116A1

## GENERAL INFORMATION:

APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; Cwikla, Steven E.  
; Duffin, David J.  
; Gates, Christian  
; Haselden, Sherril S.  
; Matheakis, Larry C.  
; Schatz, Peter J.  
; Wagstrom, Christopher R.  
; Wrighton, Nicholas C.  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; THROMBOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/083,768  
; FILING DATE: 27-Feb-2002  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3065USW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000

## INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-10-083-768-37

Query Match 40.0%; Score 32; DB 14; Length 14;  
Best Local Similarity 55.6%; Pred. No. Se+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 OGPPVSWL 15  
| | | | : | | |  
Db 3 OGPTLTAWL 11

## RESULT 10

US-10-243-613-25  
; Sequence 25, Application US/10243613  
; Publication No. US20040053823A1

## GENERAL INFORMATION:

APPLICANT: Smith, Jeffrey W.  
; APPLICANT: Chen, Emily I.  
; APPLICANT: Kridel, Steven J.

; TITLE OF INVENTION: Selective Substrates for Matrix  
; TITLE OF INVENTION: Metalloproteinases

; FILE REFERENCE: P-LJ 5432  
; CURRENT APPLICATION NUMBER: US/10/243,613  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: US 09/953,592

; PRIOR FILING DATE: 2001-09-14

; NUMBER OF SEQ ID NOS: 129

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic construct

US-10-243-613-25

Query Match 38.8%; Score 31; DB 15; Length 6;  
Best Local Similarity 83.3%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 PYVSWL 15  
| | | | |  
Db 1 PYVIWL 6

## RESULT 11

US-10-428-335-69  
; Sequence 69, Application US/10428335  
; Publication No. US20040009186A1

## GENERAL INFORMATION:

APPLICANT: BAE Joo-eun  
; APPLICANT: KLINGEMANN, Hans G.  
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES  
; FILE REFERENCE: 047940-0128  
; CURRENT APPLICATION NUMBER: US/10/428,335  
; CURRENT FILING DATE: 2003-05-02  
; PRIOR APPLICATION NUMBER: US 10/138,469  
; PRIOR FILING DATE: 2002-05-03  
; NUMBER OF SEQ ID NOS: 179  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 69

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-428-335-69

Query Match 38.8%; Score 31; DB 15; Length 9;  
Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPVSWL 15  
| | | | |  
Db 3 PPIFSWL 9

## RESULT 12

US-09-990-832C-71  
; Sequence 71, Application US/0990832C  
; Publication No. US20030149235A1

## GENERAL INFORMATION:

APPLICANT: University Court of the University of Glasgow  
; TITLE OF INVENTION: Targeting peptides  
; FILE REFERENCE: PC/MC/JM/P11910US  
; CURRENT APPLICATION NUMBER: US/09/990,832C  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 71  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

OTHER INFORMATION: Targeting peptide sequence  
US-09-990-832C-71

Query Match 38.8%; Score 31; DB 10; Length 12;  
Best Local Similarity 44.4%; Pred. No. 6.2e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 LILQGPYPV 12  
|::|||:  
Db 4 LLIEYPPYI 12

RESULT 13  
US-09-760-397-6  
; Sequence 6, Application US/09760397  
; Patent No. US20020009781A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D. D.  
; APPLICANT: Gavit, Patrick D.  
; TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production  
; FILE REFERENCE: 1103/11041US01  
; CURRENT APPLICATION NUMBER: US/09760,397  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/271,970  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human  
US-09-760-397-6

Query Match 38.8%; Score 31; DB 9; Length 15;  
Best Local Similarity 71.4%; Pred. No. 7.6e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPVVSWM 15  
|||  
Db 2 PPKVGWL 8

RESULT 14  
US-10-324-182-6  
; Sequence 6, Application US/10324182  
; Publication No. US20030194782A1  
; GENERAL INFORMATION:  
; APPLICANT: Better, Marc D. D.  
; APPLICANT: Gavit, Patrick D.  
; TITLE OF INVENTION: Improved Methods for Recombinant Peptide Production  
; FILE REFERENCE: 1103/11041US01  
; CURRENT APPLICATION NUMBER: US/10/324,182  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US/09/271,970  
; PRIOR FILING DATE: 1999-03-18  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Human  
US-10-324-182-6

Query Match 38.8%; Score 31; DB 14; Length 15;  
Best Local Similarity 71.4%; Pred. No. 7.6e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPVVSWM 15  
|||  
Db 2 PPKVGWL 8

RESULT 15

US-09-077-439A-13  
; Sequence 13, Application US/09077439A  
; Publication No. US20030202989A1  
; GENERAL INFORMATION:  
; APPLICANT: Collier, R. John  
; APPLICANT: Blanke, Steven R.  
; APPLICANT: Milne, Jill C.  
; APPLICANT: Benson, Ericka L.  
; APPLICANT: Ballard, Jimmy D.  
; APPLICANT: Starnbach, Michael N.  
; TITLE OF INVENTION: Use of Toxin Peptides and/or Affinity  
; TITLE OF INVENTION: Handles for Delivering Compounds into Cells  
; FILE REFERENCE: 00246/187002  
; CURRENT APPLICATION NUMBER: US/09/077,439A  
; CURRENT FILING DATE: 1999-04-08  
; PRIOR APPLICATION NUMBER: PCT/US96/20463  
; PRIOR FILING DATE: 1996-12-13  
; PRIOR APPLICATION NUMBER: US 60/019,275  
; PRIOR FILING DATE: 1996-06-07  
; PRIOR APPLICATION NUMBER: US 60/008,518  
; PRIOR FILING DATE: 1995-12-13  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-077-439A-13

Query Match 37.5%; Score 30; DB 10; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 PYVSWL 15  
|||  
Db 2 PYLWGL 7

Search completed: November 14, 2004, 13:36:59  
Job time : 80.6667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:55:26 ; Search time 93.3333 Seconds  
(without alignments)  
57.653 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLILQGPVYVSWL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 605831

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	15	3 AAY92952	Aay92952 Transform
2	80	100.0	15	3 AAY93104	Aay93104 Transform
3	33	41.2	14	2 AAW09483	Aaw09483 Thrombopo
4	33	41.2	14	2 AAW36634	Aaw36634 Thrombopo
5	33	41.2	14	2 AAW36767	Aaw36767 Thrombopo
6	33	41.2	14	3 AAB17011	Aab17011 TPO-mimet
7	33	41.2	14	4 AAU25853	Aau25853 Human thr
8	33	41.2	14	5 ABB72897	Abb72897 TPO mimet
9	33	41.2	14	7 ADJ73048	Adj73048 TPO mimet
10	33	41.2	14	8 ADJ52683	Adj52683 CHI delet
11	33	41.2	14	8 ADJ51644	Adj51644 CHI delet
12	33	41.2	15	5 ABB05646	Abb05646 Human thy
13	32	40.0	9	8 ADK03181	Adk03181 Hepatitis
14	32	40.0	10	8 ADK03184	Adk03184 Hepatitis
15	32	40.0	11	2 AAW83368	Aaw83368 PpGI met
16	32	40.0	14	2 AAW09481	Aaw09481 Thrombopo
17	32	40.0	14	2 AAW36632	Aaw36632 Thrombopo
18	32	40.0	14	4 AAU25851	Aau25851 Human thr
19	32	40.0	15	5 AAU97014	Aau97014 Human coa
20	31.5	39.4	14	4 AAM96969	Aam96969 Human pep
21	31	38.8	6	6 ABR55023	Abr55023 MMP-2 sel
22	31	38.8	6	6 ADK14204	Adk14204 Matrix me
23	31	38.8	9	2 AAW37010	Aaw37010 TRP-2 der
24	31	38.8	9	8 ADN28269	Adn28269 Human CD3
25	30	37.5	8	2 AAW25563	Aaw25563 Synthetic

ALIGNMENTS

RESULT 1

AAV92952

ID AAY92952 standard; peptide; 15 AA.

XX AC AAY92952;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide #8.

XX KW Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1; competitive inhibition; collagen synthesis stimulation inhibitor; liver; extracellular matrix degradation inhibitor; mimetops; cirrhosis.

XX OS Homo sapiens.

XX FN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

Ezquerro Saenz JJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

Borras Cuesta F;

WPI; 2000-411935/35.

Peptides that antagonize binding of transforming growth factor betal, useful for treatment of liver disease, especially cirrhosis, are partial sequences of the factor or its receptors.

Claim 9; Page 82; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding of transforming growth (TGF) factor betal (TGF-b1) to its receptor in vivo which have partial amino acid sequences identical, or similar, with those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent examples of the peptides of the invention. The peptides act by competitive inhibition of the binding of TGF-b1 to its receptors, e.g. they are inhibitors of stimulation of collagen synthesis in liver cells and inhibitors of synthesis of proteolytic enzymes able to degrade the extracellular matrix. The peptides, their mimetops and/or DNA (or expression systems) encoding the peptides are used for treatment of liver disease, specifically cirrhosis

```

XX SQ Sequence 15 AA;
Query Match 100.0%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. NO. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAVLILQGPYPVSWL 15
Db 1 EAVLILQGPYPVSWL 15

RESULT 2
AAW93104
ID AAY93104 standard; peptide; 15 AA.
XX AC AAY93104;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide PI50.
XX KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.
XX OS Homo sapiens.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX PI Borras Cuesta F;
XX WPI; 2000-411935/35.
XX PT Peptides that antagonize binding of transforming growth factor betal.
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.
XX PS Disclosure; Page 33; 86pp; Spanish.
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis
XX SQ Sequence 15 AA;
Query Match 100.0%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. NO. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAVLILQGPYPVSWL 15
Db 1 EAVLILQGPYPVSWL 15

RESULT 3
AAW09483
ID AAW09483 standard; protein; 14 AA.
XX AC AAW09483;
XX DT 10-SEP-1997 (first entry)
XX DE Thrombopoietin receptor binding peptide.
XX KW Haematology; thrombocytopenia; TPO; TR; proliferation;
XX KW bone marrow transfusion; chemotherapy; radiation therapy.
XX OS Synthetic.
XX PN WO9640189-A1.
XX PD 19-DEC-1996.
XX PF 05-JUN-1996; 96WO-US008998.
XX PR 07-JUN-1995; 95US-00472371.
XX PR 07-JUN-1995; 95US-00473604.
XX PR 07-JUN-1995; 95US-00476168.
XX PR 07-JUN-1995; 95US-00478128.
XX PR 07-JUN-1995; 95US-00484090.
XX PR 07-JUN-1995; 95US-00485301.
XX PA (GLAX ) GLAXO GROUP LTD.
XX PI Dower WJ, Barrett RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;
XX PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX WPI; 1997-051883/05.
XX PT Thrombopoietin receptor-binding/activating peptide(s) and peptide
XX PT mimetic(s) - useful in treatment of haematological disorders, esp.
XX PT thrombocytopenia resulting from chemotherapy, etc.
XX PS Disclosure; Page 26; 106pp; English.
XX CC The present sequence is a peptide which binds to thrombopoietin (TPO)
XX CC receptor (TR). The compound can be used for treating patients suffering
XX CC from haematological disorders and thrombocytopenia resulting from
XX CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide
XX CC may also be used to maintain the proliferation and growth of TPO-
XX CC dependent cell lines and for use in biological research, for detecting
XX CC TPO receptors on living cells
XX SQ Sequence 14 AA;
Query Match 41.2%; Score 33; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. NO. 2.4e-02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15
Db 3 LVGPSLMSWL 12

RESULT 4
AAW36634
ID AAW36634 standard; peptide; 14 AA.
XX AC AAW36634;
XX DT 11-MAR-1998 (first entry)
XX DE Thrombopoietin receptor binding peptide.
XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;
XX KW haematological disorder; thrombocytopenia; chemotherapy;
XX KW radiation therapy; bone marrow transfusion; diagnosis;
XX KW signal transduction; receptor activation; cell culture.

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XX OS Synthetic.  
 XX PN WO9640750-A1.  
 XX PD 19-DEC-1996.  
 XX PF 07-JUN-1996; 96WO-US009623.  
 XX PR 07-JUN-1995; 95US-00478128.  
 XX PR 07-JUN-1995; 95US-00485301.  
 XX PA (GLAX ) GLAXO GROUP LTD.  
 XX PI Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;  
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;  
 XX WPI; 1997-052226/05.  
 XX PT Peptides and peptide mimetics which bind to and activate the  
 PT thrombopoietin receptor - useful in treatment of haematological  
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.  
 XX PS Disclosure; Page 26; 106pp; English.  
 XX CC The present peptide, which binds the thrombopoietin receptor (TR), can be  
 CC used to treat disorders which are susceptible to treatment with a  
 CC thrombopoietin agonist, preferably haematological disorders and  
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone  
 CC marrow transfusions. It can also be used diagnostically, e.g. to  
 CC investigate the mechanism of thrombopoietin signal transduction and  
 CC receptor activation, or to maintain the proliferation and growth of  
 CC thrombopoietin dependent cell lines  
 XX SQ Sequence 14 AA;  
 Query Match 41.2%; Score 33; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 LQGPYPVSWL 15  
 | | | : | | |  
 DB 3 LVGPSLMSWL 12  
 RESULT 5  
 AAW36767 AAW36767 standard; peptide; 14 AA.  
 XX ID AAW36767  
 XX AC AAW36767;  
 XX DT 11-MAR-1998 (first entry)  
 XX DE Thrombopoietin receptor binding peptide.  
 XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;  
 KW haematological disorder; thrombocytopenia; chemotherapy;  
 KW radiation therapy; bone marrow transfusion; diagnosis;  
 KW signal transduction; receptor activation; cell culture.  
 XX OS Synthetic.  
 XX PH Key Location/Qualifiers  
 FT Disulfide-bond 1. 14  
 FT Modified-site 14  
 FT /note= "NH2-Cys"  
 XX PN WO9640750-A1.  
 XX PD 19-DEC-1996.  
 XX PR 07-JUN-1996; 96WO-US009623.  
 XX PF Novel composition of matter comprising an Fc domain and pharmacologically  
 PT active peptides, useful for treating cancer and autoimmune diseases.

PR 07-JUN-1995; 95US-00478128.  
 PR 07-JUN-1995; 95US-00485301.  
 XX (GLAX ) GLAXO GROUP LTD.  
 XX PA Dower WJ, Barret RW, Cwirla SE, Duffin DJ, Gates CM, Johnson SS;  
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;  
 XX WPI; 1997-052226/05.  
 XX PT Peptides and peptide mimetics which bind to and activate the  
 PT thrombopoietin receptor - useful in treatment of haematological  
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.  
 XX PS Example 9; Page 75; 106pp; English.  
 XX CC The present peptide, which binds the thrombopoietin receptor (TR), can be  
 CC used to treat disorders which are susceptible to treatment with a  
 CC thrombopoietin agonist, preferably haematological disorders and  
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone  
 CC marrow transfusions. It can also be used diagnostically, e.g. to  
 CC investigate the mechanism of thrombopoietin signal transduction and  
 CC receptor activation, or to maintain the proliferation and growth of  
 CC thrombopoietin dependent cell lines  
 XX SQ Sequence 14 AA;  
 Query Match 41.2%; Score 33; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 LQGPYPVSWL 15  
 | | | : | | |  
 DB 3 LVGPSLMSWL 12  
 RESULT 6  
 AAB17011 AAB17011 standard; peptide; 14 AA.  
 XX ID AAB17011  
 XX AC AAB17011;  
 XX DT 31-OCT-2000 (first entry)  
 XX DE TPO-mimetic peptide sequence SEQ ID NO:67.  
 XX KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
 KW autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
 KW immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;  
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;  
 KW thrombosis; pharmaceutical.  
 XX OS Synthetic.  
 XX PN WO200024782-A2.  
 XX PD 04-MAY-2000.  
 XX PF 25-OCT-1999; 99WO-US025044.  
 XX PR 23-OCT-1998; 98US-0105371P.  
 XX PR 22-OCT-1999; 99US-00428082.  
 XX PA (AMGE-) AMGEN INC.  
 XX PI Feige U, Liu C, Cheetham J, Boone TC;  
 XX WPI; 2000-350702/30.  
 XX Novel composition of matter comprising an Fc domain and pharmacologically  
 PT active peptides, useful for treating cancer and autoimmune diseases.

XX PS Claim 19; Page 217; 608pp; English.

XX CC The present invention describes composition of matter (I) comprising an

XX CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:

XX CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each

XX CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-

XX CC (L2)d-P2-(L3)e-P3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,

XX CC P3, and P4 = are each independently sequences of pharmacologically active

XX CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,

XX CC c, d, e, and f = are each independently 0 or 1, provided that at least 1

XX CC of a and b is 1. The composition can have cytostatic, antiasthmatic,

XX CC thrombolytic and immunosuppressive activities. DNAs, vectors and host

XX CC cells from the present invention can be used for producing pharmaceutical

XX CC compositions. The compositions are useful for treating cancer, asthma,

XX CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than

XX CC a Fab domain) can provide a longer half-life or incorporate functions

XX CC such as Fc receptor binding, protein A binding, complement fixation, and

XX CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to

XX CC AAB18003 represent nucleotide and amino acid sequences used in the

XX CC exemplification of the present invention

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 3; Length 14;

Best Local Similarity 60.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPPYVSWL 15

Db 3 LVGPSLMSWL 12

RESULT 7

AAU25853

ID AAU25853 standard; peptide; 14 AA.

AC AAU25853;

DT 17-DEC-2001 (first entry)

XX Human thrombopoietin receptor (TPO-R) activator peptide #39.

XX Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;

XX haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;

XX bone marrow transplantation; haematological disorder; platelet disorder;

XX enzyme-linked immunosorbent assay; in situ staining; biological fluid;

XX tissue homogenate; fluorescence-activated cell sorting; Western blotting;

XX in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.

XX OS Homo sapiens.

XX US6251864-B1.

XX 26-JUN-2001.

XX 01-MAR-2000; 2000US-00516704.

XX 07-JUN-1995; 95US-00478128.

XX 07-JUN-1995; 95US-00485301.

XX 07-JUN-1996; 96WO-US009623.

XX 15-AUG-1996; 96US-00699027.

XX (GLAXO) GLAXO GROUP LTD.

XX Dower WJ, Barrett RW, Cwirila SE, Gates CM, Schatz PJ;

XX Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;

XX Yin Q;

XX WPI; 2001-564142/63.

XX Activating thrombopoietin receptors in cells, used to treat

XX thrombocytopenia and hematological disorders, comprises contacting cells

PT with peptides and peptide mimetics attached to hydrophilic polymers.

PS Disclosure; Col 20; 128pp; English.

XX Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that

XX bind to and activate the human thrombopoietin receptor (TPO-R). Methods

XX of activating thrombopoietin receptors in cells comprise contacting the

XX cells with effective amounts of peptides and peptide mimetics attached to

XX hydrophilic polymers. The methods are used to treat thrombocytopenia such

XX as that due to chemotherapy, radiation therapy or bone-marrow

XX transplantation and to prevent thrombocytopenia in patients at risk. The

XX sequences are used to treat and prevent haematological disorders

XX including thrombocytopenia and platelet disorders. They are used in vitro

XX as unique tools for understanding the biological role of thrombopoietin

XX (TPO) and to develop other compounds that bind to and activate the TPO

XX receptor. The peptides can be used to detect TPO receptors on living

XX cells and fixed cells, in biological fluids, in tissue homogenates, and

XX in purified or natural biological materials. They may also be used for in

XX situ staining, fluorescence-activated cell sorting, Western blotting and

XX enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can

XX be used for in vitro expansion of megakaryocytes and their committed

XX progenitors alone or in conjunction with additional cytokines

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 4; Length 14;

Best Local Similarity 60.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPPYVSWL 15

Db 3 LVGPSLMSWL 12

RESULT 8

ABB72897

ID ABB72897 standard; peptide; 14 AA.

XX ABB72897;

XX 05-APR-2002 (first entry)

XX TPO mimetic peptide SEQ ID NO:67.

XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IGG; EPO;

XX erythropoietin; TPO; tumour necrosis factor alpha inhibitor;

XX TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMP;

XX TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;

XX MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;

XX cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;

XX antianaemic; anorectic; antiinfertility; haemostatic; dermatological;

XX neuroprotective; inflammatory disease; autoimmune disease; tumour growth;

XX cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;

XX sleep disorder; neurological degenerative disease; anaemia;

XX thrombocytopenia; metastatic tumour; systemic lupus erythematosus;

XX Fanconi's syndrome.

XX OS Homo sapiens.

XX Synthetic.

XX WO200183525-A2.

XX 08-NOV-2001.

XX 02-MAY-2001; 2001WO-US014310.

XX 03-MAY-2000; 2000US-00563286.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham JC, Boone TC, Gudas JM;

XX WPI; 2002-130313/17.



XX Novel vehicle-peptide molecule or its multimers useful for treating  
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 PT diabetic retinopathy, obesity, sleep disorders and infertility.  
 XX  
 XX Claim 39; Page 44; 176pp; English.  
 XX  
 CC The present invention describes a vehicle-peptide molecule (I) or its  
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,  
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and  
 CC neuroprotective activities. (I) can be used as a therapeutic or  
 CC prophylactic agent as well as for screening purposes. (I) is useful for  
 CC diagnosing diseases characterised by dysfunction of their associated  
 CC protein of interest, for identifying normal or abnormal proteins of  
 CC interest, as a part of diagnostic kit to detect the presence of their  
 CC proteins of interest in a biological sample. Additionally, (I) is useful  
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-  
 CC mimetic compounds are useful for treating disorders characterised by low  
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising  
 CC compounds are useful for treating conditions that involve an existing  
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 5; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 LQGPYPVSWL 15  
 ||| :|||  
 Db 3 LVGPSLMSWL 12

RESULT 9  
 ADJ73048  
 ID ADJ73048 standard; peptide; 14 AA.

XX AC ADJ73048;

XX DT 06-MAY-2004 (first entry)

XX DE TPO mimetic peptide sequence SeqID 502.

XX KW mimetic; CDR mimetibody; gene therapy; transgenic; immune;  
 KW cardiovascular; infectious; malignant; neurologic disease; anaemia;  
 KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;  
 KW TPO.

XX OS Synthetic.

XX PN WO2003084477-A2.

XX PD 16-OCT-2003.

XX PF 24-MAR-2003; 2003WO-US009139.

XX PR 29-MAR-2002; 2002US-0368791P.

XX PA (CENZ ) CENTOCOR INC.

XX PI Heavner GA, Knight DM, Scallion BJ, Ghayeb J;

XX DR WPI; 2003-804237/75.

XX PT New CDR mimetibody comprising a portion of a heavy or light chain

PT variable region comprising human framework or ligand binding region,  
 PT useful for preparing a composition for treating e.g., immune,  
 PT cardiovascular or neurologic disease.  
 XX  
 XX Disclosure; SEQ ID NO 502; 97pp; English.

CC This invention relates to novel mammalian CDR mimetibodies, specific  
 CC portions or variants thereof. Specifically, it refers to an antibody  
 CC fragment where a protein has been inserted into, or replaces a portion  
 CC of, one or more CDR regions, such that each CDR mimetibody comprises at  
 CC least one portion of a heavy chain or light chain variable region, which  
 CC itself comprises at least one human framework region and at least one  
 CC ligand binding region (LBR). The present invention describes human  
 CC mimetibodies, including modified immunoglobulins and cleavage products  
 CC that can be useful in gene therapy and the generation of transgenic  
 CC plants and animals. Furthermore, the CDR mimetibody is useful for  
 CC preparing compositions for modulating, treating or reducing the symptoms  
 CC of immune, cardiovascular, infectious, malignant and/or neurologic  
 CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,  
 CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This  
 CC peptide sequence is a TPO mimetic peptide sequence used to make a  
 CC mimetibody of the invention.

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 7; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 LQGPYPVSWL 15  
 ||| :|||  
 Db 3 LVGPSLMSWL 12

RESULT 10  
 ADJ52683  
 ID ADJ52683 standard; peptide; 14 AA.

XX AC ADJ52683;

XX DT 06-MAY-2004 (first entry)

XX DE CH1 deleted mimetibody-related peptide SeqID502.

XX KW CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;  
 KW hypotensive; neuroprotective; nootropic; antibacterial; virucide;  
 KW fungicide; gene therapy; immune disorder; cardiovascular disease;  
 KW arrhythmia; hypertension; heart failure; neurodegenerative;  
 KW multiple sclerosis; dementia; Alzheimer's disease; anaemia;  
 KW cancerous condition; infectious disease; bacterial infection;  
 KW viral infection; fungal infection.

XX OS Unidentified.

XX OS Synthetic.

XX PN WO2004002417-A2.

XX PD 08-JAN-2004.

XX PF 27-JUN-2003; 2003WO-US020347.

XX PR 28-JUN-2002; 2002US-0392431P.

XX PA (CENZ ) CENTOCOR INC.

XX PI Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;  
 PI Kutoloski KA;

XX DR WPI; 2004-082870/08.

XX PT New CH1-deleted mimetibody polypeptides and nucleic acids, useful for  
 PT modulating, treating, alleviating, preventing an immune, cardiovascular,  
 PT or neurodegenerative disease or disorder, anaemia, cancer, or infectious

PT diseases.  
XX  
PS Claim 2; SEQ ID NO 502; 129pp; English.  
XX  
CC This invention relates to CHI deleted mimetibodies (and the DNA sequences  
CC which encode them), compositions, methods and uses. The invention may be  
CC useful for the development of compounds with an immunosuppressive,  
CC cardiovascular, cardiac, hypotensive, neuroprotective, nootropic,  
CC antibacterial, virucide or fungicide activity. In addition, the disclosed  
CC sequences may prove useful for gene therapy. The CHI-deleted mimetibody  
CC is useful for diagnosing or treating a disease condition in a cell,  
CC tissue, organ or animal, specifically for modulating, treating,  
CC alleviating, preventing the incidence for or reducing the symptoms of an  
CC immune, cardiovascular (for example arrhythmia, hypertension or heart  
CC failure), or neurodegenerative (for example multiple sclerosis, dementia  
CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous  
CC conditions, or infectious diseases (for example bacterial, viral or  
CC fungal infection). The present sequence is that of a peptide which may be  
CC used during the creation of a mimetibody of the invention.  
XX  
SQ Sequence 14 AA;  
  
Query Match 41.2%; Score 33; DB 8; Length 14;  
Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 6 LOGPPYVSWL 15  
| | | | |  
Db 3 LVGPGLMSWL 12  
  
RESULT 11  
ADJ51644  
ID ADJ51644 standard; peptide; 14 AA.  
XX  
AC ADJ51644;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE CHI deleted mimetibody-related peptide SeqID502.  
XX  
KW CHI deleted mimetibody; osteopathic; cardiovascular-Gen;  
KW dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;  
KW gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;  
KW antiallergic; muscular-Gen; cytostatic; antiinflammatory; neuroleptic;  
KW ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;  
KW TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;  
KW dental disorder; oral disorder; dermatological disorder; ear disorder;  
KW nose disorder; throat disorder; endocrine disorder; metabolic disorder;  
KW gastrointestinal disorder; gynaecological disorder; hepatic disorder;  
KW obstetric disorder; haematologic disorder; immunological disorder;  
KW allergic disorder; infectious disorder; musculoskeletal disorder;  
KW oncological disorder; neurological disorder; nutritional disorder;  
KW ophthalmologic disorder; pediatric disorder; psychiatric disorder;  
KW renal disorder; pulmonary disorder.  
XX  
OS Unidentified.  
OS Synthetic.  
XX  
XX WO2004002424-A2.  
XX  
XX 08-JAN-2004.  
XX  
XX 30-JUN-2003; 2003WO-US020495.  
XX  
XX 28-JUN-2002; 2002US-0392431P.  
XX  
XX 19-SEP-2002; 2002US-0412144P.  
XX  
XX (CENZ ) CENTOCOR INC.  
XX  
XX Heavner GA, Knight DM, Grayeb J, Scallon BJ, Nespor TC;  
XX Kutoloski KA;  
XX

DR WPI; 2004-082872/08.  
XX  
PT New CHI deleted mimetibody polypeptide and nucleic acid, useful for  
PT diagnosing, preventing or treating cardiovascular, dermatologic,  
PT endocrine, gastrointestinal, gynecologic, infectious, neurologic and  
PT nutritional disorders.  
XX  
PS Claim 15; SEQ ID NO 502; 123pp; English.  
XX  
CC This invention relates to CHI deleted mimetibodies (and the DNA sequences  
CC which encode them), compositions, methods and uses. The invention may be  
CC useful for the development of compounds with an osteopathic,  
CC cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,  
CC gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,  
CC immunomodulator, antiallergic, muscular-Gen, cytostatic,  
CC antiinflammatory, neuroleptic, ophthalmological, nephrotropic or  
CC respiratory-Gen activity acting as a tumour necrosis factor (TNF)-  
CC modulator or cytokine-agonist. The methods and compositions of the  
CC present invention are useful for the diagnosis, prevention and/or  
CC treatment of diseases or conditions associated with aberrant expression  
CC or activity of the CHI deleted mimetibody, such as a bone or joint,  
CC cardiovascular, dental or oral, dermatological, ear, nose or throat,  
CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,  
CC obstructive, haematologic, immunological, allergic, infectious,  
CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,  
CC pediatric, psychiatric renal or pulmonary disorders. The present  
CC sequence is that of a peptide which may be used during the creation of a  
CC mimetibody of the invention.  
XX  
SQ Sequence 14 AA;  
  
Query Match 41.2%; Score 33; DB 8; Length 14;  
Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 6 LOGPPYVSWL 15  
| | | | |  
Db 3 LVGPGLMSWL 12  
  
RESULT 12  
ABB05646  
ID ABB05646 standard; peptide; 15 AA.  
XX  
AC ABB05646;  
XX  
DT 29-APR-2002 (first entry)  
XX  
DE Human thyroglobulin 38 protein N-terminal peptide SEQ ID NO:7.  
XX  
KW Human; thyroglobulin 38; cytostatic; antiinflammatory; simple goitre;  
KW thyroiditis; hyperthyroidism; hypothyroidism; thyroid tumour;  
KW nodular goitre.  
XX  
OS Homo sapiens.  
XX  
XX CN1321665-A.  
XX  
XX 14-NOV-2001.  
XX  
XX 29-APR-2000; 2000CN-00115532.  
XX  
XX 29-APR-2000; 2000CN-00115532.  
XX  
XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
XX  
XX Mao Y, Xie Y;  
XX  
XX WPI; 2002-140635/19.  
XX  
XX Novel human thyroglobulin 38 and polynucleotide for coding this  
XX polypeptide, useful for treating diseases such as simple goiter,  
XX thyroiditis, hyperthyroidism, hypothyroidism, thyroid tumor and nodular

PT goiter.  
 XX  
 PS Example 5; Page 18 (Disclosure); 33pp; Chinese.  
 XX  
 CC The present invention describes human thyroglobulin 38 protein (I). (I)  
 CC has cytostatic and antiinflammatory activities. (I) and the  
 CC polynucleotide (II) encoding it can be used in the treatment of diseases  
 CC such as simple goitre, thyroiditis, hyperthyroidism, hypothyroidism,  
 CC thyroid tumour and nodular goitre. The present sequence represents the N-  
 CC terminal peptide of human thyroglobulin 38, which is used in an example  
 CC from the present invention  
 XX  
 SQ Sequence 15 AA;

Query Match 41.2%; Score 33; DB 5; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 2.6e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 LILQPPYVSW 14  
 :||| |||  
 Db 5 MMLQDKPYPDW 15

RESULT 13  
 ADK03181  
 ID ADK03181 standard; peptide; 9 AA.  
 XX  
 AC ADK03181;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Hepatitis C virus CTL epitope peptide #1011.  
 XX  
 KW pathogenic virus; alternative reading frame; antigenic determinant;  
 KW virucide; vaccine; therapeutic agent; infection; epitope peptide;  
 KW HLA-allele; CTL.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO2004011650-A2.  
 XX  
 PD 05-FEB-2004.  
 XX  
 PF 24-JUL-2003; 2003WO-EP008112.  
 XX  
 PR 24-JUL-2002; 2002AT-00001124.  
 PR 11-JUL-2003; 2003EP-00450171.  
 XX  
 PA (INTE-) INTERCELL AG.  
 XX  
 PI Mattner F, Schmidt W, Habel A;  
 XX  
 DR WPI; 2004-169243/16.  
 XX  
 PT New polypeptide encoded by an alternative reading frame of a pathogenic  
 PT virus comprising an antigenic determinant, useful for treating or  
 PT preventing an infection with the pathogenic virus.  
 XX  
 PS Claim 14; Page 70; 220pp; English.

XX  
 CC This invention relates to a novel polypeptide encoded by an alternative  
 CC reading frame of a pathogenic virus, where the polypeptide starts with a  
 CC methionine amino acid residue, which comprises an antigenic determinant  
 CC and more than 7 amino acid residues. The invention may be useful for the  
 CC production of compounds with a virucide activity or the development of a  
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
 CC agent. It is also useful for the manufacture of a medicament for treating  
 CC or preventing an infection with the pathogenic virus. The present  
 CC sequence is that of a hepatitis C virus CTL epitope peptide of the  
 CC invention.  
 XX  
 SQ Sequence 9 AA;

XX  
 SQ

Query Match 40.0%; Score 32; DB 8; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 QQPPYVSWL 15  
 :||| |||  
 Db 1 QQPPLVWML 9

RESULT 14  
 ADK03184  
 ID ADK03184 standard; peptide; 10 AA.  
 XX  
 AC ADK03184;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Hepatitis C virus CTL epitope peptide #1014.  
 XX  
 KW pathogenic virus; alternative reading frame; antigenic determinant;  
 KW virucide; vaccine; therapeutic agent; infection; epitope peptide;  
 KW HLA-allele; CTL.  
 XX  
 OS Hepatitis C virus.  
 XX  
 PN WO2004011650-A2.  
 XX  
 PD 05-FEB-2004.  
 XX  
 PF 24-JUL-2003; 2003WO-EP008112.  
 XX  
 PR 24-JUL-2002; 2002AT-00001124.  
 PR 11-JUL-2003; 2003EP-00450171.  
 XX  
 PA (INTE-) INTERCELL AG.  
 XX  
 PI Mattner F, Schmidt W, Habel A;  
 XX  
 DR WPI; 2004-169243/16.  
 XX  
 PT New polypeptide encoded by an alternative reading frame of a pathogenic  
 PT virus comprising an antigenic determinant, useful for treating or  
 PT preventing an infection with the pathogenic virus.  
 XX  
 PS Claim 14; Page 70; 220pp; English.

XX  
 CC This invention relates to a novel polypeptide encoded by an alternative  
 CC reading frame of a pathogenic virus, where the polypeptide starts with a  
 CC methionine amino acid residue, which comprises an antigenic determinant  
 CC and more than 7 amino acid residues. The invention may be useful for the  
 CC production of compounds with a virucide activity or the development of a  
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
 CC agent. It is also useful for the manufacture of a medicament for treating  
 CC or preventing an infection with the pathogenic virus. The present  
 CC sequence is that of a hepatitis C virus CTL epitope peptide of the  
 CC invention.  
 XX  
 SQ Sequence 10 AA;

Query Match 40.0%; Score 32; DB 8; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 7 QQPPYVSWL 15  
 :||| |||  
 Db 2 QQPPLVWML 10

RESULT 15  
 AAW83368  
 ID AAW83368 standard; peptide; 11 AA.  
 XX  
 AC AAW83368;  
 XX

```

XX 11-FEB-1999 (first entry)
DT
XX
DE PspGI methylase motif IV peptide.
XX
KW PspGI; type II restriction endonuclease; Pyrococcus; methylase;
KW recombinant.
XX
OS Pyrococcus sp.
XX
PN WO9851783-A1.
XX
XX 19-NOV-1998.
XX
XX 31-MAR-1998; 98WO-US006332.
XX
XX 15-MAY-1997; 97US-00856663.
XX
XX (NEWE ) NEW ENGLAND BIOLABS INC.
XX
XX Morgan RD, Chang Z;
PI
XX
DR WPI; 1999-009770/01.
XX
XX New Type II restriction endonuclease from Pyrococcus species G-I-H - and
PT DNA coding for the endonuclease, optionally with its methylase for
PT recombinant production of the restriction enzyme.
XX
PS Example; Page 32; 47pp; English.
XX
XX The present invention describes a type II restriction endonuclease,
CC designated PspGI, from Pyrococcus species G-I-H. The endonuclease,
CC recognises and cleaves the following base sequence before the first C at
CC the 5' end, to give a five base overhang at the 5' end: 5'-CC(A/T)GG-3'.
CC Also described are: (1) isolated DNA (I) obtainable from Pyrococcus
CC species G-I-H and coding for the PspGI restriction endonuclease; (2)
CC isolated DNA (II) obtainable from ATCC No. 98435 and coding for the PspGI
CC restriction endonuclease and methylase; (3) a recombinant DNA vector into
CC which (I) is inserted; (4) a cloning vector comprising (II); and (5) a
CC host cell transformed with the vector as in (3) or (4). The endonuclease
CC can be isolated using conventional protein purification techniques from
CC Pyrococcus sp. G-I-H. Alternatively, the endonuclease, along with its
CC corresponding methylase can be obtained using recombinant DNA techniques.
CC Restriction endonuclease PspGI is useful in genetic engineering. The DNA,
CC vectors and host cells are all useful for recombinantly producing the
CC endonuclease in commercial quantities. The present sequence represents
CC motif IV from the PspGI methylase
XX
SQ Sequence 11 AA;

```

```

Query Match          40.0%; Score 32; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      4 LILQGPY 11
        ||| |||
Db      2 LILTSPY 9

```

```

Search completed: November 14, 2004, 13:11:17
Job time : 95.3333 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:56:07 ; Search time 100 Seconds  
(without alignments)  
86.306 Million cell updates/sec

Title: US-09-831-253F-8  
Perfect score: 80  
Sequence: 1 EAVLILQGPVVSWL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	38.8	13	2 Q95925	Q95925 porphyra pu
2	29	36.2	13	2 Q95808	Q95808 gracilariop
3	28	35.0	13	1 SOVO SEPOF	P83567 sepiia offic
4	27	33.8	8	1 ALL5 CALVO	P41841 calliphora
5	27	33.8	13	1 PROX_ORYSA	P83647 oryza sativ
6	25	31.2	14	2 Q26075	Q26075 psammechinu
7	24	30.0	15	1 SODM STRGR	P80733 streptomyc
8	23	28.7	12	2 Q7M1H0	Q7M1H0 leonurus ar
9	23	28.7	13	2 Q04220	Q04220 plasmid p30
10	23	28.7	14	1 CALI CALGI	P20728 calotropis
11	23	28.7	14	2 P81801	P81801 streptomyc
12	23	28.7	15	2 Q9S8Z0	Q9S8Z0 hordeum vul
13	22.5	28.1	13	2 Q9R3R3	Q9R3R3 borrelia bu
14	22.5	28.1	15	2 Q8GL28	Q8GL28 borrelia bu
15	22	27.5	8	1 ACI THUAL	P18691 thunnus alb
16	22	27.5	8	1 LCK7 LEUMA	P19989 leucophaea
17	22	27.5	8	2 Q8GTG5	Q8GTG5 lycopersico
18	22	27.5	9	2 Q9H326	Q9H326 homo sapien
19	22	27.5	9	2 Q7M2M9	Q7M2M9 bos taurus
20	22	27.5	10	2 Q76MK9	Q76MK9 eurypharynx
21	22	27.5	10	2 Q76MW5	Q76MW5 eurypharynx
22	22	27.5	10	2 BAB7I40	BAB7I40 euryphary
23	22	27.5	10	2 BAB87148	BAB87148 euryphary
24	22	27.5	10	2 BAB87156	BAB87156 euryphary
25	22	27.5	10	2 BAB87164	BAB87164 euryphary
26	22	27.5	11	2 Q8GL19	Q8GL19 borrelia bu
27	22	27.5	11	2 Q8GL24	Q8GL24 borrelia bu
28	22	27.5	13	2 O61340	O61340 panulirus i
29	22	27.5	14	1 LPW_ECOLI	P03053 escherichia
30	22	27.5	15	2 Q9R3E1	Q9R3E1 legionella
31	22	27.5	15	2 Q9RQ22	Q9RQ22 salmonella

32	21	26.2	8	1 CCKN_MACEU	P30369 macropus eu
33	21	26.2	8	1 LCK1_LEUMA	P21140 leucophaea
34	21	26.2	8	1 LCK2_LEUMA	P21141 leucophaea
35	21	26.2	8	1 LCK8_LEUMA	P19990 leucophaea
36	21	26.2	8	1 PK1_PERAM	P82685 periplaneta
37	21	26.2	8	1 PK3_PERAM	P82687 periplaneta
38	21	26.2	8	1 PK5_PERAM	P82689 periplaneta
39	21	26.2	9	2 Q99193	Q99193 pseudomonas
40	21	26.2	10	2 Q7PHS9	Q7PHS9 anopheles g
41	21	26.2	10	2 Q7M2N0	Q7M2N0 bos taurus
42	21	26.2	10	2 O6EX62	O6EX62 hyptis suav
43	21	26.2	10	2 Q7LZC5	Q7LZC5 kassina mac
44	21	26.2	12	2 Q7LZ10	Q7LZ10 vipera lebe
45	21	26.2	15	1 UE15_HORVU	P34938 hordeum vul

ALIGNMENTS

RESULT 1  
Q95925 PRELIMINARY; PRT; 13 AA.  
AC Q95925;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome oxidase subunit 3 (Fragment).  
GN Names=cox3;  
OS Porphyra purpurea.  
OG Mitochondrion.  
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.  
OX NCBI\_TaxID=2787;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lang B.Franz., Goff L.J., Gray M.W.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U59763; AAB17951.1; -;  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1 1  
SQ SEQUENCE 13 AA; 1522 MW; 0831666D0E8C65B0 CRC64;

Query Match 38.8%; Score 31; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 3.9e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPVSW 14  
| | | |  
DB 3 PDYISW 8

RESULT 2  
Q95808 PRELIMINARY; PRT; 13 AA.  
ID Q95808;  
AC Q95808;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome oxidase subunit 3 (Fragment).  
GN Names=cox3;  
OS Gracilariopsis lemaneiformis.  
OG Mitochondrion.  
OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariiales; Gracilariaceae;  
OX Gracilariopsis.  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lang B.Franz., Goff L.J., Gray M.W.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U59764; AAB17950.1; -;  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1 1

```
SQ SEQUENCE 13 AA; 1565 MW; 305BD4028745B043 CRC64;
Query Match 36.2%; Score 29; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 8.5e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPVSWL 15
DB 1 FNYITWI 7

RESULT 3
SOVO SEPOF
ID SOVO SEPOF STANDARD; PRT; 13 AA.
AC P83567;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE SepOvototropin.
OS Sepia officinalis (Common cuttlefish)
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.
OX NCBI_TaxID=6610;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
RP AMIDATION.
RC TISSUE-Ovarian follicle;
RX MEDLINE=20483622; PubMed=11027583; DOI=10.1006/bbro.2000.3595;
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;
RT "The SepOvototropin: a new ovarian peptide regulating oocyte transport
RT in Sepia officinalis.";
RL Biochem. Biophys. Res. Commun. 276:1013-1018(2000).
CC -!- FUNCTION: Has myotropic activity targeting the genital tract.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg.
CC -!- MASS SPECTROMETRY: MW=1502.8; METHOD=MALDI; RANGE=1-13;
CC NOTE=Ref.1.
KW Amidation; Direct protein sequencing.
FT MOD_RES 13 Tyrosine amide.
SQ SEQUENCE 13 AA; 1503 MW; 483D5C7E34C72727 CRC64;

Query Match 35.0%; Score 28; DB 1; Length 13;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAVLIQPPY 11
DB 3 DSMLLQVPVY 13

RESULT 4
ALL5 CALVO
ID ALL5 CALVO STANDARD; PRT; 8 AA.
AC P41841;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Callatostatin 5 (Met-callatostatin 1) ([Hyp3]Met-callatostatin).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RX MEDLINE=932111980; PubMed=8460157;
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,
RA Thorpe A.;
RT "Callatostatins: neuropeptides from the blowfly Calliphora vomitoria
RT with sequence homology to cockroach allatostatins.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION, AND HYDROXYLATION.
```

```
RC TISSUE=Head;
RX MEDLINE=94342269; PubMed=8063725;
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;
RT "[Hyp3]Met-callatostatin. Identification and biological properties of
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";
RL J. Biol. Chem. 269:21059-21066(1994).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator and play
CC a role in the integration of information within the brain. May be
CC involved in the control of visceral muscles due to its ability to
CC behave as potent inhibitors of peristaltic movements. May also
CC fulfill a neurohormonal role on muscles of the gut and heart.
CC -!- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.
CC -!- SIMILARITY: Belongs to the allatostatin family.
DR PIR, E47393; E47393.
KW Amidation; Direct protein sequencing; Hydroxylation; Neuropeptide.
FT MOD_RES 3 Hydroxyproline (partial).
FT MOD_RES 3 8 Methionine amide.
SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;

Query Match 33.8%; Score 27; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPPY 11
DB 1 GPPY 4

RESULT 5
PROX ORYZA
ID PROX ORYZA STANDARD; PRT; 13 AA.
AC P83647;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Probable profilin LP04 (Fragments).
OS Oryza sativa (Rice)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Indica / IR64; TISSUE=Panicle;
RA Hosseini Salekdeh S.G., Bennett J.;
RT "Proteome analysis of rice panicle.";
RL Submitted (JUL-2003) to Swiss-Prot.
CC -!- FUNCTION: Binds to actin and affects the structure of the
CC cytoskeleton. At high concentrations, profilin prevents the
CC polymerization of actin, whereas it enhances it at low
CC concentrations. By binding to Pip2, it inhibits the formation of
CC IP3 and DG (By similarity).
CC -!- SUBUNIT: Occurs in many kinds of cells as a complex with monomeric
CC actin in a 1:1 ratio.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.4, its MW is: 14.0 kDa.
CC -!- SIMILARITY: Belongs to the profilin family.
DR InterPro; IPR002097; Profilin.
DR PROSITE; PS00414; PROFILIN; PARTIAL.
KW Actin-binding; Cytoskeleton; Direct protein sequencing;
FT NON_TER 1 1
FT NON_TER 5 6
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1362 MW; 0A3022BE0E52C68B CRC64;

Query Match 33.8%; Score 27; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AVLIQPP 10
DB 5 AYVLIQSEP 13
```

```
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 AVLILQGPY 11
Db 1 ATYTLPEPPY 10

RESULT 8
Q7M1H0 PRELIMINARY; PRT; 12 AA.
AC Q7M1H0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cycloleonorinin.
OS Leonurus artemisia (Sagebrush motherwort).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Lamiaceae; Lamiaceae; Leonurus.
OX NCBI_TaxID=4138;
RN [1]
RP SEQUENCE
RX MEDLINE=91300597; PubMed=2070452;
RA Kinoshita K., Tanaka J., Kuroda K., Koyama K., Natori S.,
RA Kinoshita T.;
RT "Cycloleonorinin, a cyclic peptide from Leonuri fructus.";
RL Chem. Pharm. Bull. 39:712-715(1991).
DR PIR; J00356; J00356.
SQ SEQUENCE 12 AA; 1354 MW; 300727313BC1B768 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 7.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 QGPY 11
Db 8 QYPPY 12

RESULT 9
Q04220 PRELIMINARY; PRT; 13 AA.
AC Q04220;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TraA protein (fragment).
GN Name=traA;
OS Plasmid P307.
OC Plasmid.
OC Plasmid.
OX NCBI_TaxID=2472;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91261994; PubMed=2096398;
RA Graus-Goeldner A., Graus H., Schlacher T., Hoegenauer G.;
RT "The sequences of genes bordering oriT in the enterotoxin plasmid
RT P307: Comparison with the sequences of plasmids F and R1.";
RL Plasmid 24:119-131(1990).
DR EMBL; M62986; AAA2525.1; -.
DR PIR; E37390; E37390.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0000746; P:conjugation; IEA.
DR InterPro; IPR008873; TraA.
DR Pfam; PF05513; TraA; 1.
KW Plasmid.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1259 MW; 864BB8ECD35FC2D5 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 8.6e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
Q26075 PRELIMINARY; PRT; 14 AA.
AC Q26075;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Histone H2A (Fragment).
OS Peamechinus miliaris (Sand sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinozoa; Echinacea; Echinacea; Echinacea; Echinacea;
OC Peamechinus.
OX NCBI_TaxID=7660;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85140235; PubMed=2858095;
RA Nordstrom J.L., Hall S.L., Kessler M.M.;
RT "Polyadenylation of sea urchin histone RNA sequences in transfected
RT COS cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:1094-1098(1985).
DR EMBL; M12542; AAA30028.1; -.
FT NON_TER 1 9 histone H2A.
FT CHAIN 1 9
SQ SEQUENCE 14 AA; 1620 MW; 298A3F878A462268 CRC64;

Query Match 31.2%; Score 25; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 4.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 LQPPYV 12
Db 5 LSGPPNI 11

RESULT 7
SODM_STRGR STANDARD; PRT; 15 AA.
AC P80733;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).
GN Names=sod2;
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE.
RC STRAIN=KCTC 9006; PubMed=8900409;
RX MEDLINE=97056084; PubMed=8900409;
RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
RA Kang S.-O.;
RT "Unique isozymes of superoxide dismutase in Streptomyces griseus.";
RL Arch. Biochem. Biophys. 334:341-348(1996).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron or zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Tetramer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; Sod Fe N; 1.
DR PROSITE; PS00088; SOD MN; PARTIAL.
DR Direct protein sequencing; Iron; Metal-binding; Oxidoreductase; Zinc.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;

Query Match 30.0%; Score 24; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.8e+03;
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QY 1 EAVLILQ 8
Db 2 DAILSVQ 9

RESULT 10
CALI_CALGI STANDARD; PRT; 14 AA.
AC P20728;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calotropin DI (EC 3.4.22.-) (Fragment)
OS Calotropis gigantea (Madar) (Bowstring hemp).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Apocynaceae; Asclepiadoideae; Asclepiadeae;
OC Calotropis.
OX NCBI_TaxID=4066;
RN [1]
RP SEQUENCE.
RA Bhattacharya D., Sengupta A., Sinha N.K.;
RA "Chemical modification and amino terminal sequence of calotropin DI
RT from Calotropis gigantea.";
RL Phytochemistry 26:633-636(1987).
CC -!- SIMILARITY: Belongs to peptidase family C1.
DR PIR: P70026; PT0026.
DR MEROPS: C01.011; -.
DR InterPro: IPR000169; Pept_cys_acsite.
DR PROSITE; PS00640; THIOL_PROTEASE ASN; PARTIAL.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
KW Direct protein sequencing; Hydrolyase; Pyrrolidone carboxylic acid;
KW Thiol protease.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1715 MW; D993F0276CDA4662 CRC64;

Query Match 28.7%; Score 23; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.3e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 QGPPYVSW 14
Db 1 QRPEYPVW 8

RESULT 11
P81801
ID P81801 PRELIMINARY; PRT; 14 AA.
AC P81801;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Puromycin-hydrolyzing enzyme (EC 3.-.-.-) (Fragment).
OS Streptomyces morookaensis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1970;
RN [1]
RP SEQUENCE.
RC STRAIN-JCM4673 / KCC S-0673;
RX PubMed=9538199;
RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;
RT "Purification and characterization of a puromycin-hydrolyzing enzyme
RT from blastocidin S-producing Streptomyces morookaensis.";
RL J. Biochem. 123:247-252(1998).
RN [2]
RP CHARACTERIZATION, AND FUNCTION.
RA Nishimura M., Matsuo H., Sugiyama M.;
RT "Blastocidin S-producing Streptomyces morookaensis possesses an enzyme
RT activity with hydrolyzes puromycin.";
RL FEMS Microbiol. Lett. 132:95-100(1995).

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CC -!- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF
CC THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-
CC TYROSINE MOIETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL
CC TEMPERATURE IS 45 DEGREES CELSIUS.
CC -!- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.
CC -!- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC
CC ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND
CC N-ETHYLMALIMIDE. PARTIALLY INHIBITED BY COBALT ION.
CC -!- SUBUNIT: MONOMER.
CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.
DR GO; GO:0004177; F:aminopeptidase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
KW Aminopeptidase; Hydrolase.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 PYVSW 14
Db 5 PYGAW 9

RESULT 12
Q9S8Z0
ID Q9S8Z0 PRELIMINARY; PRT; 15 AA.
AC Q9S8Z0;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Light-harvesting antenna of photosystem I 730, LHCI 730.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE.
RX MEDLINE=92267013; PubMed=1587270;
RA Knoetzel J., Svendsen I., Simpson D.J.;
RT "Identification of the photosystem I antenna polypeptides in barley.
RT Isolation of three pigment-binding antenna complexes.";
RL Eur. J. Biochem. 206:209-215(1992).
SQ SEQUENCE 15 AA; 1588 MW; 3975624AFD65202D CRC64;

Query Match 28.7%; Score 23; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 LQGPYV 12
Db 9 LQSPAYL 15

RESULT 13
Q9R3R3
ID Q9R3R3 PRELIMINARY; PRT; 13 AA.
AC Q9R3R3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Borrelia burgdorferi plasmid cp32-7, possible partition proteins,
DE complete cds (Borrelia burgdorferi plasmid cp32-6, possible partition
DE proteins, complete cds) (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp32-7, and plasmid cp32-6.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=1139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31; PLASMID=cp32-7, and cp32-6;

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RX MEDLINE=98361033; PubMed=9695920;  
RA Stevenson B., Castjens S., Rosa P.;  
RT "Evidence of past recombination events among the genes encoding the  
RT Erp antigens of *Borrelia burgdorferi*.";  
RL Microbiology 144:1869-1879(1998).  
DR EMBL; AF022483; AAC35454.1; -;  
DR EMBL; AF022482; AAC35450.1; -;  
KW Plasmid.  
FT NON TER  
SQ SEQUENCE 13 AA; 1551 MW; 4E441D04BF054373 CRC64;  
  
Query Match 28.1%; Score 22.5; DB 2; Length 13;  
Best Local Similarity 44.4%; Pred. NO. 1e+04;  
Matches 4; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
  
QY 7 QGPPYVSWL 15  
||| : :  
Db 1 QG-PLIKWI 8  
  
RESULT 14  
Q8GL28 PRELIMINARY; PRT; 15 AA.  
AC Q8GL28;  
DT 01-MAR-2003 (TReMBLrel. 23, Created)  
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Pf-50 protein (Fragment).  
GN Name-Pf-50;  
OS *Borrelia burgdorferi* (Lyme disease spirochete).  
OG Plasmid group cp32-3.  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sh-2-82;  
RX MEDLINE=22990544; PubMed=14629041;  
RA Stevenson B., Miller J.C.;  
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete  
RT erp genes generates sequence identity amidst diversity.";  
RL J. Mol. Evol. 57:309-324(2003).  
DR EMBL; AY142090; AAN17861.1; -;  
KW Plasmid.  
FT NON TER  
SQ SEQUENCE 15 AA; 1777 MW; 4E441D04BF501763 CRC64;  
  
Query Match 28.1%; Score 22.5; DB 2; Length 15;  
Best Local Similarity 44.4%; Pred. NO. 1.2e+04;  
Matches 4; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
  
QY 7 QGPPYVSWL 15  
||| : :  
Db 3 QG-PLIKWI 10  
  
RESULT 15  
ACI THUAL STANDARD; PRT; 8 AA.  
AC FI8651;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Angiotensin-converting enzyme inhibitor.  
OS *Thunnus albacares* (Yellowfin tuna) (Neothunnus macropterus).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;  
OC Scombridae; *Thunnus*.  
OX NCBI\_TaxID=8236;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Muscle;  
RX MEDLINE=88326322; PubMed=3415688;

RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;  
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna  
RT muscle.";  
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).  
CC -I- FUNCTION: Inhibits angiotensin-converting enzyme.  
DR PIR; A31570; A31570.  
KW Direct protein sequencing; Metalloprotease inhibitor.  
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;  
  
Query Match 27.5%; Score 22; DB 1; Length 8;  
Best Local Similarity 33.3%; Pred. NO. 1.8e+06;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 9 PPYVSW 14  
||| : :  
Db 1 PTHIKW 6  
  
Search completed: November 14, 2004, 13:16:23  
Job time : 101 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:03:52 ; Search time 18.3333 Seconds  
(without alignments)  
78.723 Million cell updates/sec

Title: US-09-831-253F-8  
Perfect score: 80  
Sequence: 1 EAVLLQGPPYVSWL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	38.8	13	2 S47361	T-cell antigen rec
2	27	33.8	8	2 E47393	neuropeptide calla
3	25	31.2	15	2 JN0730	hypothetical 1.7K
4	23	28.7	12	2 PH1675	Ig heavy chain V r
5	23	28.7	12	2 JU0356	cycloleucorinin -
6	23	28.7	13	2 PH1676	Ig heavy chain V r
7	23	28.7	13	2 E37390	traA protein - Esc
8	23	28.7	14	2 PH1677	Ig heavy chain V r
9	23	28.7	14	2 PH1705	Ig heavy chain V r
10	23	28.7	14	2 PT0026	calotropin DI - mu
11	23	28.7	15	2 PA0027	protein QAI00006 -
12	23	28.7	15	2 PH1616	Ig H chain V-D-J r
13	23	28.7	15	2 PH1610	Ig H chain V-D-J r
14	22	27.5	8	2 JS0317	leucokinin VII - M
15	22	27.5	8	2 A31570	angiotensin-conver
16	22	27.5	9	2 S26508	collagen alpha 2(V
17	22	27.5	10	2 H28027	protein P11 - curl
18	22	27.5	14	1 LFEWCW	trp operon leader
19	22	27.5	14	2 E90858	trp operon leader
20	22	27.5	14	2 B85761	trp operon leader
21	22	27.5	15	2 PQ0192	stylar glycoprotei
22	22	27.5	15	2 PQ0193	stylar glycoprotei
23	22	27.5	15	2 B56046	urinary tract ston
24	22	27.5	15	2 PN0662	dystrophin-associa
25	21	26.9	15	2 B45115	peptidylprolyl iso
26	21	26.2	8	2 PQ0012	cholecystokinin -
27	21	26.2	8	2 A43001	cholecystokinin -
28	21	26.2	8	2 JS0318	leucokinin VIII -
29	21	26.2	10	2 A13687	caerulein-like pep

collagen alpha 1(V  
glutathione transf  
lebetin 1 isoform  
dystrophin-associa  
stylar glycoprotei  
stylar glycoprotei  
dystrophin-associa  
Ig heavy chain CRD  
tryptophyllin, bas  
T-cell receptor be  
phyllocaerulein -  
Ig H chain V-D-J r  
caerulein - frog (  
triacylglycerol 11  
Ig heavy chain DJ  
bradykinin-potent

## ALIGNMENTS

## RESULT 1

S47361  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)

C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S47361  
R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A:Reference number: S47355

A:Accession: S47361

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: EMBL:235685; NID:G527459; PIDN:CAA84754.1; PID:G527460

C:Keywords: T-cell receptor

Query Match 38.8%; Score 31; DB 2; Length 13;  
Best Local Similarity 71.4%; Pred. No. 63;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ILQGGPY 11

Db 3 VLQGGPY 9

## RESULT 2

E47393  
neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)

C:Species: Calliphora vomitoria

C>Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: E47393

R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.

Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993

A>Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with sequ

A:Reference number: A47393; MUID:93211980; PMID:8460157

A:Accession: E47393

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <DUV>

A:Cross-references: UNIPROT:P41841

A:Experimental source: whole flies

A>Note: sequence extracted from NCBI backbone (NCBI:128482)

Query Match 33.8%; Score 27; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPPY 11

Db 1 GPPY 4

```
RESULT 3
JN0730
Hypothetical 1.7K protein - phage SPP1
N:Alternate names: hypothetical protein 42.1
C:Species: phage SPP1
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C:Accession: JN0730
R:Chai, S.; Szepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.
Gene 129, 41-49, 1993
A:Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPP1
A:Reference number: JN0729; MUID:93328123; PMID:8335259
A:Accession: JN0730
A:Molecule type: DNA
A:Residues: 1-15 <CHA>
A:Cross-references: EMBL:X65941

Query Match      31.2%; Score 25; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 7.2e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LILQGPVVS 13
DB 1 MLNNGPPFRS 10

RESULT 4
PH1675
Ig heavy chain V region (clone NP-6-7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1675
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1675
A:Molecule type: mRNA
A:Residues: 1-12 <MCH>
A:Experimental source: B cell
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      28.7%; Score 23; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15
DB 1 YTSWV 5

RESULT 5
JU0356
Cycloleaurinin - sagebrush motherwort
C:Species: Leonurus artemisia (sagebrush motherwort)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JU0356
R:Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.
Chem. Pharm. Bull. 39, 712-715, 1991
A:Title: Cycloleaurinin, a cyclic peptide from Leonuri fructus.
A:Reference number: JU0356; MUID:91300597; PMID:2070452
A:Accession: JU0356
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KIN>
A:Cross-references: UNIPROT:Q7MLH0

Query Match      28.7%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 QGPPY 11
```

```
DB 8 QYPPY 12

RESULT 6
PH1676
Ig heavy chain V region (clone NP-6-5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1676
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1676
A:Molecule type: mRNA
A:Residues: 1-13 <MCH>
A:Experimental source: B cell
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      28.7%; Score 23; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15
DB 1 YTSWV 5

RESULT 7
E37390
traA protein - Escherichia coli plasmid P307 (fragment)
C:Species: Escherichia coli
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: E37390; PQ0480
R:Graus-Goeldner, A.; Graus, H.; Schlacher, T.; Hoegenauer, G.
Plasmid 24, 113-131, 1990
A:Title: The sequences of genes bordering orit in the enterotoxin plasmid P307: comparison
A:Reference number: A37390; MUID:91261994; PMID:2096398
A:Accession: E37390
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <GRA>
A:Cross-references: UNIPROT:Q04220; GB:M62986; NID:gl50463; PIDN:AAA25525.1; PID:gl50463
C:Genetics:
A:Gene: traA
A:Genome: plasmid
C:Superfamily: fimbrial protein

Query Match      28.7%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAVLILQG 8
DB 2 DAILSVQG 9

RESULT 8
PH1677
Ig heavy chain V region (clone NP-6-6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1677
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1677
A:Molecule type: mRNA
A:Residues: 1-14 <MCH>
A:Experimental source: B cell
```

C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15  
DB 1 YTSWV 5

## RESULT 9

PHI705  
Ig heavy chain V region (clone ASC-1) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 17-Mar-1999  
C;Accession: PH1705  
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.  
J. Exp. Med. 178, 295-307, 1993  
A;Title: Antigen-driven B cell differentiation in vivo.  
A;Reference number: PH1675; MUID:93301607; PMID:8315385  
A;Accession: PH1705  
A;Molecule type: mRNA  
A;Residues: 1-14 <MCH>  
A;Experimental source: B cell  
A;Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 1.4e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15  
DB 1 YTSWV 5

## RESULT 10

PT0026  
calotropin DI - mudar (fragment)  
C;Species: Calotropis gigantea (mudar, madar)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: PT0026  
R;Bhattacharya, D.; Sengupta, A.; Sinha, N.K.  
Phytochemistry 26, 633-636, 1987  
A;Title: Chemical modification and amino terminal sequence of calotropin DI from Calotropis gigantea.  
A;Reference number: PT0026  
A;Accession: PT0026  
A;Molecule type: protein  
A;Residues: 1-14 <BHA>  
A;Cross-references: UNIPROT:P20728  
C;Comment: This enzyme is classified as a plant cysteine protease.  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.7%; Score 23; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 QGPPYVSW 14  
DB 1 QRPEYVW 8

## RESULT 11

PA0027  
protein QAL00006 - Arabidopsis thaliana (fragment)  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 30-Jun-1992 #sequence\_revision 06-Jan-1995 #text\_change 06-Jun-1997  
C;Accession: PA0027  
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A;Description: Separation and characterization of Arabidopsis proteins by two-dimension  
A;Reference number: PA0001  
A;Accession: PA0027  
A;Molecule type: protein  
A;Residues: 1-15 <RAM>  
A;Experimental source: callus

Query Match 28.7%; Score 23; DB 2; Length 15;  
Best Local Similarity 45.5%; Pred. No. 1.5e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VLILQPPYVS 13  
DB 1 VLKVVGPXPAS 11

## RESULT 12

PHI616  
Ig H chain V-D-J region (clone B-less 30) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1616  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1616  
A;Molecule type: DNA  
A;Residues: 1-15 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 15;  
Best Local Similarity 75.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 YVSW 14  
DB 11 YLSW 14

## RESULT 13

PHI610  
Ig H chain V-D-J region (wild-type clone 337) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1610  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1610  
A;Molecule type: DNA  
A;Residues: 1-15 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.5e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LQPPY 11  
DB 4 LNSPY 9

## RESULT 14

JS0317  
leucokinin VII - Madeira cockroach  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: JS0317

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
Comp. Biochem. Physiol. C 88, 31-34, 1987  
A;Title: Isolation; primary structure and synthesis of leucokinins VII and VIII: the fin  
A;Reference number: JS0317

A;Accession: JS0317  
A;Molecule type: protein  
A;Residues: 1-8 <HOL>  
A;Cross-references: UNIPROT:P19989  
C;Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile act  
C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 27.5%; Score 22; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPVSW 14  
| : |  
Db 2 PAFSSW 7

## RESULT 15

A31570  
angiotensin-converting enzyme inhibitor - yellowfin tuna  
C;Species: Thunnus albacares (yellowfin tuna)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C;Accession: A31570  
R;Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.  
Biochem. Biophys. Res. Commun. 155, 332-337, 1988  
A;Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.  
A;Reference number: A31570; MUID:88326322; PMID:3415688  
A;Accession: A31570  
A;Molecule type: protein  
A;Residues: 1-8 <KOH>  
A;Cross-references: UNIPROT:P18691  
A;Note: the source is designated as Neothunnus macropterus  
C;Superfamily: unassigned animal peptides  
C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 27.5%; Score 22; DB 2; Length 8;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 PPVSW 14  
| : |  
Db 1 PTHKW 6

Search completed: November 14, 2004, 13:17:23  
Job time : 19.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 11.8085 Seconds  
(without alignments)  
84.242 Million cell updates/sec

Title: US-09-831-253F-8  
Perfect score: 80  
Sequence: 1 EAVLIQGPPYVSWL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	41.2	14	2	US-08-764-640-39
2	33	41.2	14	3	US-08-973-225-39
3	33	41.2	14	3	US-08-973-225-216
4	33	41.2	14	3	US-09-244-298A-39
5	33	41.2	14	3	US-09-516-704-39
6	33	41.2	14	4	US-09-549-090-39
7	33	41.2	14	4	US-09-549-090-216
8	33	41.2	14	4	US-09-832-230A-39
9	33	41.2	14	4	US-09-428-082B-67
10	32	40.0	11	2	US-08-856-663-12
11	32	40.0	14	2	US-08-764-640-37
12	32	40.0	14	3	US-08-973-225-37
13	32	40.0	14	3	US-09-244-298A-37
14	32	40.0	14	3	US-09-516-704-37
15	32	40.0	14	4	US-09-549-090-37
16	32	40.0	14	4	US-09-832-230A-37
17	32	40.0	18	3	US-08-990-888-40
18	32	40.0	23	2	US-08-985-090-10
19	32	40.0	23	2	US-08-985-090-16
20	32	40.0	23	3	US-09-165-543-10
21	32	40.0	23	3	US-09-165-543-17
22	32	40.0	23	3	US-09-165-543-36
23	31	38.8	9	2	US-08-725-736D-19
24	31	38.8	9	3	US-09-162-368B-19
25	31	38.8	9	3	US-09-161-877B-19
26	31	38.8	15	3	US-09-271-970-6
27	31	38.8	15	4	US-09-760-397-6

28	31	38.8	18	2	US-08-764-640-46	Sequence 46, Appl
29	31	38.8	18	3	US-08-973-225-46	Sequence 46, Appl
30	31	38.8	18	3	US-09-244-298A-46	Sequence 46, Appl
31	31	38.8	18	3	US-09-516-704-46	Sequence 46, Appl
32	31	38.8	18	4	US-09-549-090-46	Sequence 46, Appl
33	31	38.8	18	4	US-09-832-230A-46	Sequence 46, Appl
34	30	37.5	7	1	US-07-807-043B-6	Sequence 6, Appl
35	30	37.5	9	1	US-08-299-849B-6	Sequence 6, Appl
36	30	37.5	9	1	US-08-464-318-6	Sequence 6, Appl
37	30	37.5	9	2	US-08-471-341-6	Sequence 6, Appl
38	30	37.5	9	2	US-08-461-566-6	Sequence 6, Appl
39	30	37.5	9	2	US-08-142-368A-6	Sequence 6, Appl
40	30	37.5	9	3	US-08-967-727-6	Sequence 6, Appl
41	30	37.5	9	3	US-09-064-964-2	Sequence 2, Appl
42	30	37.5	9	3	US-08-037-230D-6	Sequence 2, Appl
43	30	37.5	9	3	US-09-064-174-2	Sequence 2, Appl
44	30	37.5	9	4	US-09-583-850-6	Sequence 6, Appl
45	30	37.5	9	4	US-09-579-197-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1  
US-08-764-640-39  
; Sequence 39, Application US/08764640  
; Patent No. 5869451  
; Patent No. 5869451 5837683  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprence, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; APPLICANT: Yin, Qun  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 244  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/764,640  
; FILING DATE: 11-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-764-640-39

Query Match 41.2%; Score 33; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPYVSWL 15  
| | | | |  
DB 3 LVGPSLMSWL 12

## RESULT 2

US-08-973-225-39  
; Sequence 39, Application US/08973225A  
; Patent No. 6083913  
; GENERAL INFORMATION:

APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwiria, Steven E.  
Duffin, David J.  
Gates, Christian  
Haselden, Sherril S.  
Matheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC

COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,225A  
FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3065USW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-08-973-225-39

Query Match 41.2%; Score 33; DB 3; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPYVSWL 15  
| | | | |  
DB 3 LVGPSLMSWL 12

## RESULT 3

US-08-973-225-216  
; Sequence 216, Application US/08973225A  
; Patent No. 6083913  
; GENERAL INFORMATION:

APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwiria, Steven E.  
Duffin, David J.  
Gates, Christian  
Haselden, Sherril S.  
Matheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,225A  
FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3065USW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 216:

SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 216:

US-08-973-225-216

Query Match 41.2%; Score 33; DB 3; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPYVSWL 15  
| | | | |  
DB 3 LVGPSLMSWL 12

## RESULT 4

US-09-244-298A-39  
; Sequence 39, Application US/09244298A  
; Patent No. 612138  
; GENERAL INFORMATION:

APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwiria, Steven E.  
Gates, Christian  
Schatz, Peter J.  
Balasubramanian, Palaniappan  
Wagstrom, Christopher R.  
Hendren, Richard W.  
Deprence, Randolph B.  
Podduturi, Surekha  
Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
RECEPTOR  
NUMBER OF SEQUENCES: 244  
CORRESPONDENCE ADDRESS:



ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/244,298A  
FILING DATE: 11-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3281  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: linear  
MOLECULE TYPE: peptide  
US-09-244-298A-39

Query Match 41.2%; Score 33; DB 3; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVSWL 15  
Db 3 LVGPSLSWL 12

RESULT 5  
US-09-516-704-39  
Sequence 39, Application US/09516704  
Patent No. 6251864  
GENERAL INFORMATION:  
APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwirla, Steven E.  
Gates, Christian  
Schatz, Peter J.  
Balasubramanian, Palaniappan  
Wagstrom, Christopher R.  
Hendren, Richard W.  
Deprence, Randolph B.  
Podduturi, Surekha  
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR  
NUMBER OF SEQUENCES: 244  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/516,704  
FILING DATE: 01-Mar-2000  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3281  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-516-704-39

Query Match 41.2%; Score 33; DB 3; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPVSWL 15  
Db 3 LVGPSLSWL 12

RESULT 6  
US-09-549-090-39  
Sequence 39, Application US/09549090  
Patent No. 6465430  
GENERAL INFORMATION:  
APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwirla, Steven E.  
Duffin, David J.  
Gates, Christian  
Haselden, Sherril S.  
Mattheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.  
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR  
NUMBER OF SEQUENCES: 232  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/549,090  
FILING DATE: 13-Apr-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/973,225  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3065USW  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-549-090-39
Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPVVSWSL 15
DB 3 LVGPSLMSWL 12

RESULT 7
US-09-549-090-216
; Sequence 216, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; BARRETT, RONALD W.
; Cwiria, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Matheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,090
; FILING DATE: 13-Apr-2000
; PRIOR APPLICATION NUMBER: US 08/973,225
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-549-090-216
Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPVVSWSL 15
DB 3 LVGPSLMSWL 12

RESULT 8
US-09-832-230A-39
; Sequence 39, Application US/09832230A
; Patent No. 6506362
; GENERAL INFORMATION:
; APPLICANT: Dower, William J. et al
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,230A
; FILING DATE: 10-Apr-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-832-230A-39
Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPVVSWSL 15
DB 3 LVGPSLMSWL 12

RESULT 9
US-09-428-082B-67
; Sequence 67, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-09-428-082B-67

Query Match 41.2%; Score 33; DB 4; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPYVSWL 15  
| | | : | | |  
Db 3 LVGPSLMSWL 12

## RESULT 10

US-08-856-663-12  
Sequence 12, Application US/08856663  
Patent No. 5849558

## GENERAL INFORMATION:

APPLICANT: MORGAN, RICHARD  
APPLICANT: CHANG, ZHIYU  
TITLE OF INVENTION: DISCOVERY OF AND  
TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE  
TITLE OF INVENTION: PSPI RESTRICTION ENDONUCLEASE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: New England Biolabs, Inc.  
STREET: 32 Tozer Road  
CITY: Beverly  
STATE: MA  
COUNTRY: US  
ZIP: 01915

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/856,663  
FILING DATE: 15-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

## ATTORNEY/AGENT INFORMATION:

NAME: Williams, Gregory D  
REGISTRATION NUMBER: 30901  
REFERENCE/DOCKET NUMBER: NEB-127  
TELEPHONE: 978-927-5054  
TELEFAX: 978-927-1705  
TELEX:

## INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-08-856-663-12

Query Match 40.0%; Score 32; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 LILQPPY 11  
| | | : | | |  
Db 2 LILTSPY 9

## RESULT 11

US-08-764-640-37  
Sequence 37, Application US/08764640  
Patent No. 5869451  
Patent No. 5869451 5837683

## GENERAL INFORMATION:

APPLICANT: Dower, William J.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Gates, Christian  
APPLICANT: Schatz, Peter J.  
APPLICANT: Balasubramanian, Palaniappan  
APPLICANT: Wagstrom, Christopher R.  
APPLICANT: Hendren, Richard W.  
APPLICANT: Deprience, Randolph B.  
APPLICANT: Podduturi, Surekha  
APPLICANT: Yin, Qun  
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
TITLE OF INVENTION: RECEPTOR  
NUMBER OF SEQUENCES: 244  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,640  
FILING DATE: 11-DEC-1996  
CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3281  
TELEPHONE: 919-248-1000  
TELEFAX: 919-248-1000  
INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:

## TOPOLOGY:

MOLECULE TYPE: peptide

US-08-764-640-37

Query Match 40.0%; Score 32; DB 2; Length 14;  
Best Local Similarity 55.6%; Pred. No. 70;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QGPPYVSWL 15  
| | | : | | |  
Db 3 QGPTLTAWL 11

## RESULT 12

US-08-973-225-37  
Sequence 37, Application US/08973225A  
Patent No. 6083913

## GENERAL INFORMATION:

APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwirla, Steven E.  
Duffin, David J.  
Gates, Christian  
Haselden, Sherril S.  
Mattheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
THROMBOPOIETIN RECEPTOR  
NUMBER OF SEQUENCES: 232

1 ; CORRESPONDENCE ADDRESS:  
2 ADDRESSEE: Glaxo Wellcome  
3 STREET: Five Moore Drive, P.O. Box 13398  
4 CITY: Research Triangle Park  
5 STATE: NC  
6 COUNTRY: USA  
7 ZIP: 27709  
8  
9 COMPUTER READABLE FORM:  
10 MEDIUM TYPE: Floppy disk  
11 COMPUTER: IBM PC compatible  
12 OPERATING SYSTEM: PC-DOS/MS-DOS  
13 SOFTWARE: PatentIn Release #1.0, Version #1.30  
14  
15 CURRENT APPLICATION DATA:  
16 APPLICATION NUMBER: US/08/973,225A  
17 FILING DATE: 04-Dec-1997  
18 ATTORNEY/AGENT INFORMATION:  
19 NAME: Hrubiec, Robert T.  
20 REGISTRATION NUMBER: 36,392  
21 REFERENCE/DOCKET NUMBER: PK3065USW  
22 TELECOMMUNICATION INFORMATION:  
23 TELEPHONE: 919-248-1000  
24 INFORMATION FOR SEQ ID NO: 37:  
25 SEQUENCE CHARACTERISTICS:  
26 LENGTH: 14 amino acids  
27 TYPE: amino acid  
28 STRANDEDNESS: <Unknown>  
29 TOPOLOGY: linear  
30 MOLECULE TYPE: peptide  
31 SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
32  
33 US-08-973-225-37  
34  
35 Query Match 40.0%; Score 32; DB 3; Length 14;  
36 Best Local Similarity 55.6%; Pred. No. 70;  
37 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
38  
39 QY 7 QGPPYVSWL 15  
40 ||| :||  
41 Db 3 QGPTLTAWL 11  
42  
43 RESULT 13  
44 US-09-244-298A-37  
45 ; Sequence 37, Application US/09244298A  
46 ; Patent No. 6121238  
47 ; GENERAL INFORMATION:  
48 ; APPLICANT: Dower, William J.  
49 ; APPLICANT: Barrett, Ronald W.  
50 ; APPLICANT: Cwirla, Steven E.  
51 ; APPLICANT: Gates, Christian  
52 ; APPLICANT: Schatz, Peter J.  
53 ; APPLICANT: Balasubramanian, Palaniappan  
54 ; APPLICANT: Wagstrom, Christopher R.  
55 ; APPLICANT: Hendren, Richard W.  
56 ; APPLICANT: Deprence, Randolph B.  
57 ; APPLICANT: Podduturi, Surekha  
58 ; APPLICANT: Yin, Qun  
59 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
60 TITLE OF INVENTION: RECEPTOR  
61 NUMBER OF SEQUENCES: 244  
62 CORRESPONDENCE ADDRESS:  
63 ADDRESSEE: Glaxo Wellcome  
64 STREET: Five Moore Drive, P.O. Box 13398  
65 CITY: Research Triangle Park  
66 STATE: NC  
67 COUNTRY: USA  
68 ZIP: 27709  
69  
70 COMPUTER READABLE FORM:  
71 MEDIUM TYPE: Floppy disk  
72 COMPUTER: IBM PC compatible  
73 OPERATING SYSTEM: PC-DOS/MS-DOS  
74 SOFTWARE: PatentIn Release #1.0, Version #1.30  
75 CURRENT APPLICATION DATA:  
76 APPLICATION NUMBER: US/09/244,298A

1 ; FILING DATE: 11-DEC-1996  
2 CLASSIFICATION: 514  
3 ATTORNEY/AGENT INFORMATION:  
4 NAME: Hrubiec, Robert T.  
5 REGISTRATION NUMBER: 36,392  
6 REFERENCE/DOCKET NUMBER: PK3281  
7 TELECOMMUNICATION INFORMATION:  
8 TELEPHONE: 919-248-1000  
9 INFORMATION FOR SEQ ID NO: 37:  
10 SEQUENCE CHARACTERISTICS:  
11 LENGTH: 14 amino acids  
12 TYPE: amino acid  
13 STRANDEDNESS:  
14 TOPOLOGY: linear  
15 MOLECULE TYPE: peptide  
16 US-09-244-298A-37  
17  
18 Query Match 40.0%; Score 32; DB 3; Length 14;  
19 Best Local Similarity 55.6%; Pred. No. 70;  
20 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
21  
22 QY 7 QGPPYVSWL 15  
23 ||| :||  
24 Db 3 QGPTLTAWL 11  
25  
26 RESULT 14  
27 US-09-516-704-37  
28 ; Sequence 37, Application US/09516704  
29 ; Patent No. 6251864  
30 ; GENERAL INFORMATION:  
31 ; APPLICANT: Dower, William J.  
32 ; APPLICANT: Barrett, Ronald W.  
33 ; APPLICANT: Cwirla, Steven E.  
34 ; APPLICANT: Gates, Christian  
35 ; APPLICANT: Schatz, Peter J.  
36 ; APPLICANT: Balasubramanian, Palaniappan  
37 ; APPLICANT: Wagstrom, Christopher R.  
38 ; APPLICANT: Hendren, Richard W.  
39 ; APPLICANT: Deprence, Randolph B.  
40 ; APPLICANT: Podduturi, Surekha  
41 TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
42 TITLE OF INVENTION: RECEPTOR  
43 NUMBER OF SEQUENCES: 244  
44 CORRESPONDENCE ADDRESS:  
45 ADDRESSEE: Glaxo Wellcome  
46 STREET: Five Moore Drive, P.O. Box 13398  
47 CITY: Research Triangle Park  
48 STATE: NC  
49 COUNTRY: USA  
50 ZIP: 27709  
51  
52 COMPUTER READABLE FORM:  
53 MEDIUM TYPE: Floppy disk  
54 COMPUTER: IBM PC compatible  
55 OPERATING SYSTEM: PC-DOS/MS-DOS  
56 SOFTWARE: PatentIn Release #1.0, Version #1.30  
57 CURRENT APPLICATION DATA:  
58 APPLICATION NUMBER: US/09/516,704  
59 FILING DATE: 01-Mar-2000  
60 CLASSIFICATION: <Unknown>  
61 ATTORNEY/AGENT INFORMATION:  
62 NAME: Hrubiec, Robert T.  
63 REGISTRATION NUMBER: 36,392  
64 REFERENCE/DOCKET NUMBER: PK3281  
65 TELECOMMUNICATION INFORMATION:  
66 TELEPHONE: 919-248-1000  
67 INFORMATION FOR SEQ ID NO: 37:  
68 SEQUENCE CHARACTERISTICS:  
69 LENGTH: 14 amino acids  
70 TYPE: amino acid  
71 STRANDEDNESS: <Unknown>  
72 TOPOLOGY: linear  
73 MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-516-704-37

Query Match 40.0%; Score 32; DB 3; Length 14;  
Best Local Similarity 55.6%; Pred. No. 70;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15  
||| :||  
Db 3 QGPTLTAWL 11

RESULT 15

US-09-549-090-37  
; Sequence 37, Application US/09549090  
; Patent No. 6465430

GENERAL INFORMATION:

APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwirla, Steven E.  
Duffin, David J.  
Gates, Christian  
Haselden, Sherril S.  
Mattheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/549,090

FILING DATE: 13-Apr-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/973,225

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-549-090-37

Query Match 40.0%; Score 32; DB 4; Length 14;  
Best Local Similarity 55.6%; Pred. No. 70;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15  
||| :||  
Db 3 QGPTLTAWL 11

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 35.4255 Seconds  
(without alignments)  
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Title: US-09-831-253F-8

Perfect score: 80

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Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

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Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	33	41.2	14	14	US-10-083-768-216
4	33	41.2	14	15	US-10-609-217-67
5	33	41.2	14	15	US-10-632-388-67
6	33	41.2	14	15	US-10-651-723-67
7	33	41.2	14	15	US-10-645-761-67
8	33	41.2	14	15	US-10-666-696-67
9	33	41.2	14	15	US-10-653-048-67
10	33	41.2	18	14	US-10-006-593-33
11	33	41.2	18	14	US-10-307-724-33
12	32	40.0	14	14	US-10-083-768-37
13	32	40.0	21	15	US-10-424-599-256388

14	32	40.0	22	15	US-10-328-916-31	Sequence 31, Appl
15	32	40.0	23	9	US-09-350-206-10	Sequence 10, Appl
16	32	40.0	23	9	US-09-350-206-17	Sequence 17, Appl
17	32	40.0	23	9	US-09-350-206-36	Sequence 36, Appl
18	32	40.0	23	9	US-09-349-755-10	Sequence 10, Appl
19	32	40.0	23	9	US-09-349-755-17	Sequence 17, Appl
20	32	40.0	23	9	US-09-349-755-36	Sequence 36, Appl
21	32	40.0	23	9	US-09-166-334-10	Sequence 10, Appl
22	32	40.0	23	9	US-09-166-334-17	Sequence 17, Appl
23	32	40.0	23	9	US-09-166-334-36	Sequence 36, Appl
24	32	40.0	23	14	US-10-282-958-10	Sequence 10, Appl
25	32	40.0	23	14	US-10-282-958-17	Sequence 17, Appl
26	32	40.0	23	14	US-10-282-958-36	Sequence 36, Appl
27	32	40.0	23	14	US-10-422-262-2	Sequence 2, Appl
28	31.5	39.4	16	14	US-10-281-478-23	Sequence 23, Appl
29	31.5	39.4	16	14	US-10-281-478-95	Sequence 95, Appl
30	31.5	39.4	16	14	US-10-281-478-132	Sequence 132, Appl
31	31	38.8	6	15	US-10-243-613-25	Sequence 25, Appl
32	31	38.8	9	15	US-10-428-335-69	Sequence 69, Appl
33	31	38.8	12	10	US-09-990-832C-71	Sequence 71, Appl
34	31	38.8	15	9	US-09-760-397-6	Sequence 6, Appl
35	31	38.8	15	14	US-10-324-182-6	Sequence 35, Appl
36	31	38.8	18	14	US-10-006-593-35	Sequence 35, Appl
37	31	38.8	18	14	US-10-083-768-46	Sequence 46, Appl
38	31	38.8	18	14	US-10-307-724-35	Sequence 35, Appl
39	31	38.8	19	14	US-10-378-557-46	Sequence 46, Appl
40	31	38.8	23	14	US-10-106-698-8193	Sequence 8193, Ap
41	30	37.5	9	10	US-09-077-439A-13	Sequence 13, Appl
42	30	37.5	9	13	US-10-205-150-9	Sequence 9, Appl
43	30	37.5	9	14	US-10-079-167-66	Sequence 66, Appl
44	30	37.5	9	14	US-10-360-836-66	Sequence 66, Appl
45	30	37.5	9	15	US-10-057-475B-10639	Sequence 10639, A

ALIGNMENTS

RESULT 1

US-09-833-245-681  
; Sequence 681, Application US/09833245  
; Publication No. US20040010134A1  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229, 358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256, 931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199, 384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 681  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (13)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-833-245-681

Query Match 42.5%; Score 34; DB 11; Length 18;  
Best Local Similarity 66.7%; Pred. No. 31e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15

Db 4 QGCPHPSWL 12

RESULT 2  
US-10-083-768-39  
; Sequence 39, Application US/10083768  
; Publication No. US20030158116A1  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; Cwirla, Steven E.  
; Duffin, David J.  
; Gates, Christian  
; Haselden, Sherril S.  
; Mattheakis, Larry C.  
; Schatz, Peter J.  
; Wagstrom, Christopher R.  
; Wrighton, Nicholas C.  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; THROMBOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/083,768  
; FILING DATE: 27-Feb-2002  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3065USW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-10-083-768-39  
Query Match 41.2%; Score 33; DB 14; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 6 LOGPPYVSWL 15  
DB 3 LVGPSLMSWL 12  
RESULT 3  
US-10-083-768-216  
; Sequence 216, Application US/10083768  
; Publication No. US20030158116A1  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; Cwirla, Steven E.  
; Duffin, David J.  
; Gates, Christian  
; Haselden, Sherril S.  
; Mattheakis, Larry C.  
; Schatz, Peter J.  
; Wagstrom, Christopher R.

Wrighton, Nicholas C.  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; THROMBOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/083,768  
; FILING DATE: 27-Feb-2002  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3065USW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 216:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 216:  
US-10-083-768-216  
Query Match 41.2%; Score 33; DB 14; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 6 LOGPPYVSWL 15  
DB 3 LVGPSLMSWL 12  
RESULT 4  
US-10-609-217-67  
; Sequence 67, Application US/10609217  
; Publication No. US20040044188A1  
; GENERAL INFORMATION:  
; APPLICANT: PEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/609,217  
; CURRENT FILING DATE: 2003-08-27  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO: 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-609-217-67  
Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;



Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15  
| | | : | | |  
Db 3 LVGPSLSW 12

## RESULT 5

US-10-632-388-67  
; Sequence 67, Application US/10632388  
; Publication No. US20040053845A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/632,388  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-632-388-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15  
| | | : | | |  
Db 3 LVGPSLSW 12

## RESULT 6

US-10-651-723-67  
; Sequence 67, Application US/10651723  
; Publication No. US20040057953A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/651,723  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-651-723-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15  
| | | : | | |  
Db 3 LVGPSLSW 12

## RESULT 7

US-10-645-761-67  
; Sequence 67, Application US/10645761  
; Publication No. US20040071712A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/645,761  
; CURRENT FILING DATE: 2003-08-18  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-645-761-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15  
| | | : | | |  
Db 3 LVGPSLSW 12

## RESULT 8

US-10-666-696-67  
; Sequence 67, Application US/10666696  
; Publication No. US20040077022A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: BOONE, THOMAS CHARLES  
; APPLICANT: GUDAS, JEAN MARIE  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527A  
; CURRENT APPLICATION NUMBER: US/10/666,696  
; CURRENT FILING DATE: 2003-09-19  
; PRIOR APPLICATION NUMBER: US/09/563,286C  
; PRIOR FILING DATE: 2000-05-03  
; PRIOR APPLICATION NUMBER: 09/428,082  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1157  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-mimetic peptide  
US-10-666-696-67

Query Match 41.2%; Score 33; DB 15; Length 14;

Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15  
| | | : | | |  
DB 3 LVGPSLSMWL 12

RESULT 9  
US-10-653-048-67  
; Sequence 67, Application US/10653048  
; Publication No. US2004008778A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/653,048  
; CURRENT FILING DATE: 2003-08-29  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 67  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-10-653-048-67

Query Match 41.2%; Score 33; DB 15; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LOGPPYVSWL 15  
| | | : | | |  
DB 3 LVGPSLSMWL 12

RESULT 10  
US-10-006-593-33  
; Sequence 33, Application US/10006593  
; Publication No. US20030049683A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdiah, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
; FILE REFERENCE: 1087-2  
; CURRENT APPLICATION NUMBER: US/10/006,593  
; CURRENT FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: US 60/251,448  
; PRIOR FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/288,889  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/294,068  
; PRIOR FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 33  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: TPO mimetic with flanking amino acids  
US-10-006-593-33

Query Match 41.2%; Score 33; DB 14; Length 18;

Best Local Similarity 41.7%; Pred. No. 4.4e+02;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LILOGPPYVSWL 15  
: | : | | |  
DB 1 MIEGPTLRQWL 12

RESULT 11  
US-10-307-724-33  
; Sequence 33, Application US/10307724  
; Publication No. US20030232972A1  
; GENERAL INFORMATION:  
; APPLICANT: Bowdiah, Katherine S.  
; APPLICANT: Frederickson, Shana  
; APPLICANT: Renshaw, Mark  
; TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES  
; FILE REFERENCE: 1087-2c1p  
; CURRENT APPLICATION NUMBER: US/10/307,724  
; CURRENT FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: US 60/251,448  
; PRIOR FILING DATE: 2000-12-05  
; PRIOR APPLICATION NUMBER: US 60/288,889  
; PRIOR FILING DATE: 2001-05-04  
; PRIOR APPLICATION NUMBER: US 60/294,068  
; PRIOR FILING DATE: 2001-05-29  
; PRIOR APPLICATION NUMBER: US 10/006,593  
; PRIOR FILING DATE: 2001-12-05  
; NUMBER OF SEQ ID NOS: 134  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 33  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: TPO mimetic with flanking amino acids  
US-10-307-724-33

Query Match 41.2%; Score 33; DB 14; Length 18;  
Best Local Similarity 41.7%; Pred. No. 4.4e+02;  
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LILOGPPYVSWL 15  
: | : | | |  
DB 1 MIEGPTLRQWL 12

RESULT 12  
US-10-083-768-37  
; Sequence 37, Application US/10083768  
; Publication No. US20030158116A1  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; Barrett, Ronald W.  
; Cwirla, Steven E.  
; Duffin, David J.  
; Gates, Christian  
; Haselden, Sherril S.  
; Mattheakis, Larry C.  
; Schatz, Peter J.  
; Wagstrom, Christopher R.  
; Wrighton, Nicholas C.  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; THROMBOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:

;  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/083,768  
; FILING DATE: 27-Feb-2002  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3065USW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-10-083-768-37

Query Match 40.0%; Score 32; DB 14; Length 14;  
Best Local Similarity 55.6%; Pred. No. 5e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 QGPPVSVWL 15  
||| :||  
DB 3 QGFTLTAWL 11

## RESULT 13

US-10-424-599-256388  
; Sequence 256388, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 256388  
; LENGTH: 21  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_WRT3847\_73542C.1.pep  
US-10-424-599-256388

Query Match 40.0%; Score 32; DB 15; Length 21;  
Best Local Similarity 50.0%; Pred. No. 7.2e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 ILQGPPVSVW 14  
||: |||||  
DB 4 IIKNPPVVLW 13

## RESULT 14

US-10-328-916-31  
; Sequence 31, Application US/10328916  
; Publication No. US20040002114A1  
; GENERAL INFORMATION:  
; APPLICANT: Gregoire, Francine M.  
; APPLICANT: Johnson, Jeffrey D.  
; APPLICANT: Blume, John E.  
; APPLICANT: Metabolex, Inc.

;  
; TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor  
; TITLE OF INVENTION: Involved in Islet Cell Signaling  
; FILE REFERENCE: 016325-007210US  
; CURRENT APPLICATION NUMBER: US/10/328,916  
; CURRENT FILING DATE: 2003-01-06  
; PRIOR APPLICATION NUMBER: US 60/345,697  
; PRIOR FILING DATE: 2002-01-04  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 31  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:mouse IC-PCR  
; OTHER INFORMATION: Transmembrane IV domain  
US-10-328-916-31

Query Match 40.0%; Score 32; DB 15; Length 22;  
Best Local Similarity 46.2%; Pred. No. 7.6e+02;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 VLLIQPPVSVWL 15  
||: |||||  
DB 10 VTLLTGIPFVWL 22

## RESULT 15

US-09-350-206-10  
; Sequence 10, Application US/09350206  
; Patent No. US20020099199A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/350,206  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/042,780  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Elizabeth A. Hanley  
; REGISTRATION NUMBER: 33,505  
; REFERENCE/DOCKET NUMBER: MNI-032CP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)742-4214  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 23 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
US-09-350-206-10

Query Match 40.0%; Score 32; DB 9; Length 23;  
Best Local Similarity 50.0%; Pred. No. 7.9e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ILQGPVSW 14  
:|:|:  
Db 14 LLYGPALSW 23

Search completed: November 14, 2004, 12:27:00  
Job time : 36.4255 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 43.4043 Seconds  
(without alignments)  
123.973 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLILQPPYVSWL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A Geneseq\_23Sep04:\*
- 1: Geneseqp1980s:\*
  - 2: Geneseqp1990s:\*
  - 3: Geneseqp2000s:\*
  - 4: Geneseqp2001s:\*
  - 5: Geneseqp2002s:\*
  - 6: Geneseqp2003as:\*
  - 7: Geneseqp2003bs:\*
  - 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	15	3 AAY92952	Aay92952 Transform
2	80	100.0	15	3 AAY93104	Aay93104 Transform
3	36	45.0	23	3 AAY95812	Aay95812 Modified
4	34.5	43.1	19	7 ADF14790	Adf14790 Diabetes
5	34	42.5	18	4 ADE01738	Aae01738 Human gen
6	34	42.5	18	5 ABG63934	Abg63934 Human alb
7	34	42.5	18	2 ADL77199	Adl77199 Albumin f
8	33	41.2	14	2 AAW09483	Aaw09483 Thrombopo
9	33	41.2	14	2 AAW36634	Aaw36634 Thrombopo
10	33	41.2	14	2 AAW36767	Aaw36767 Thrombopo
11	33	41.2	14	3 AAB17011	Aab17011 TPO-mimet
12	33	41.2	14	4 AAU25853	Aau25853 Human thr
13	33	41.2	14	5 ABB72897	Abb72897 TPO mimet
14	33	41.2	14	7 ADJ73048	Adj73048 TPO mimet
15	33	41.2	14	8 ADJ52683	Adj52683 CHI delet
16	33	41.2	14	8 ADJ51644	Adj51644 CHI delet
17	33	41.2	15	5 ABB05646	Abb05646 Human thy
18	33	41.2	18	5 ABP51685	Abp51685 TPO mimet
19	33	41.2	18	8 ADQ16613	Adq16613 TPO mimet
20	33	41.2	19	2 AAR55260	Aar55260 N-termina
21	32	40.0	9	8 ADK03181	Adk03181 Hepatitis
22	32	40.0	10	8 ADK03184	Adk03184 Hepatitis
23	32	40.0	11	2 AAW83368	Aaw83368 PpGI met
24	32	40.0	14	2 AAW09481	Aaw09481 Thrombopo
25	32	40.0	14	2 AAW36632	Aaw36632 Thrombopo

26	32	40.0	14	4 AAU25851	Aau25851 Human thr
27	32	40.0	15	5 AAU97014	Aau97014 Human coa
28	32	40.0	17	8 ADM12614	Adm12614 Ii-key/hu
29	32	40.0	17	8 ADQ38847	Adq38847 Human Her
30	32	40.0	18	5 ABP48149	Abp48149 GHR bindi
31	32	40.0	23	2 AAW92981	Aaw92981 Human mAC
32	32	40.0	23	2 AAW92987	Aaw92987 Rat mACHR
33	32	40.0	23	2 AAG67842	Aag67842 Rat mACHR
34	32	40.0	23	2 AAG67835	Aag67835 Human mAC
35	32	40.0	23	2 AAG67849	Aag67849 Partial r
36	32	40.0	23	6 ABG76410	Abg76410 Human mus
37	32	40.0	23	6 ABG76424	Abg76424 Rat musca
38	32	40.0	23	6 ABG76417	Abg76417 Rat musca
39	32	40.0	23	8 ADJ55648	Adj55648 Short enz
40	31.5	39.4	14	4 AAM96969	Aam96969 Human pep
41	31.5	39.4	16	7 ADC99952	Adc99952 Murine AX
42	31.5	39.4	16	7 ADC99989	Adc99989 Murine AX
43	31.5	39.4	16	7 ADC99880	Adc99880 Murine AX
44	31	38.8	6	6 ABR55023	Abr55023 MMP-2 sel
45	31	38.8	6	8 ADK14204	Adk14204 Matrix me

ALIGNMENTS

RESULT 1

AA92952

ID AAY92952 standard; peptide; 15 AA.

AC AAY92952;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide #8.

XX Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;  
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

Borras Cuesta F;

WPI; 2000-411935/35.

PT Peptides that antagonize binding of transforming growth factor betal,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.

PS Claim 9; Page 82; 86pp; Spanish.

CC The invention relates to synthetic peptides that antagonise the binding  
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
CC vivo which have partial amino acid sequences identical, or similar, with  
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
CC examples of the peptides of the invention. The peptides act by  
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis

```

XX SQ Sequence 15 AA;
Query Match 100.0%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAVLILQGPYPVSWL 15
Db 1 EAVLILQGPYPVSWL 15

RESULT 2
AAY93104
ID AAY93104 standard; peptide; 15 AA.
XX AC AAY93104;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide P150.
XX KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX OS Homo sapiens.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX WPI; 2000-411935/35.
XX PT Peptides that antagonize binding of transforming growth factor betal,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX PS Disclosure; Page 33; 86pp; Spanish.
XX CC The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis
XX SQ Sequence 15 AA;
Query Match 100.0%; Score 80; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAVLILQGPYPVSWL 15
Db 1 EAVLILQGPYPVSWL 15

RESULT 3
AAY95812
ID AAY95812 standard; peptide; 23 AA.
XX AC AAY95812;
XX DT 07-NOV-2000 (first entry)
XX DE Modified human tissue plasminogen activator signal peptide.
XX LE Leptin; human; glycosylation; obesity; diabetes; hyperlipidemia;
KW antiobesity; antidiabetic; hyperlipemic; therapy; signal peptide;
KW tissue plasminogen activator; mutant; mutein.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200047741-A1.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000WO-US003652.
XX PR 12-FEB-1999; 99US-00249675.
XX PA (AMGE-) AMGEN INC.
XX PI Martin FH, Elliott SG;
XX WPI; 2000-524540/47.
XX CC Glycosylated leptin proteins having a Stokes' radius greater than that of
XX a naturally occurring glycosylated human leptin useful for treating
XX obesity, diabetes and the effects of high blood lipid content.
XX PS Example 14; Page 99; 156pp; English.
XX CC The present sequence is that of a human tissue plasminogen activator
XX signal peptide that is the same as the native signal peptide except that
XX the 3 C-terminal amino acid residues are Ser-Trp-Ser. The invention is
XX directed to glycosylated leptin proteins (see AAY95799-804) that have a
XX Stokes' radius greater than that of naturally occurring human leptin. A
XX claimed method for manufacturing a glycosylated leptin involves culturing
XX a host cell containing a DNA sequence encoding a signal peptide and a
XX glycosylated leptin protein. Preferred signal peptides have a peptidase
XX cleavage site optimized for glycosylation efficiency. When
XX lepinin-47+69+102 (see AAY95802) was expressed as a fusion with the
XX present signal peptide, the degree of glycosylation (on a scale of 1-5)
XX was 3.5 in COS host cells and 4 in CHO host cells. Glycosylated leptins,
XX or nucleic acids encoding them, are used in the treatment of obesity,
XX diabetes and the effects of high blood lipid content (claimed). They have
XX longer systemic circulation times in vivo than native leptins
XX SQ Sequence 23 AA;
Query Match 45.0%; Score 36; DB 3; Length 23;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 VLLILQGPYPVSW 14
Db 11 VLLILCGAVFVSW 22

RESULT 4
ADF14790
ID ADF14790 standard; peptide; 19 AA.
XX AC ADF14790;
XX DT 12-FEB-2004 (first entry)
XX DE Diabetes autoantigen-derived peptide - SEQ ID 285.

```

KW plant; deamidation; tissue transglutaminase; TG; celiac disease; CD;  
 KW gluten intolerance; autoimmune; rheumatoid arthritis; multiple sclerosis;  
 KW systemic lupus erythematosus; sjogren syndrome; diabetes;  
 KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;  
 KW dermatological; antiinflammatory.  
 XX Unidentified.  
 XX OS  
 XX PN EP1332760-A1.  
 XX PD 06-AUG-2003.  
 XX PP 04-FEB-2002; 2002EP-00075456.  
 XX PR 04-FEB-2002; 2002EP-00075456.  
 XX PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.  
 XX DR WPI; 2003-647889/62.  
 XX PT New gluten peptides or epitopes prone to deamidation by tissue  
 PT transglutaminase, useful for treating celiac disease or an autoimmune  
 PT disease, rheumatoid arthritis, multiple sclerosis, systemic lupus  
 PT erythematosus, or diabetes.  
 XX PS Claim 3; SEQ ID NO 285; 143pp; English.  
 XX CC The invention relates to a novel peptide or epitope which is prone to  
 CC deamidation by tissue transglutaminase (TG) and is a causative factor of  
 CC celiac disease (CD; gluten intolerance) or an autoimmune disease such as  
 CC rheumatoid arthritis, multiple sclerosis, systemic lupus erythematosus,  
 CC sjogren syndrome or diabetes. The peptide of the invention demonstrates  
 CC immunosuppressive, antirheumatic, antiarthritic, antidiabetic,  
 CC dermatological and antiinflammatory activities whilst pharmaceutical  
 CC compositions comprising the peptides or epitopes may be useful for the  
 CC treatment of a celiac disease or an autoimmune disease such as rheumatoid  
 CC arthritis, multiple sclerosis, systemic lupus erythematosus, sjogren  
 CC syndrome or diabetes. Gluten-derived peptides may be useful in the  
 CC preparation of therapeutic agents capable of eliminating a subset of  
 CC cells, particularly gluten-sensitive or auto-antigen sensitive T cells.  
 CC The current sequence is that of the diabetes autoantigen-derived peptide  
 CC of the invention.  
 XX SQ Sequence 19 AA;  
 Query Match 43.1%; Score 34.5; DB 7; Length 19;  
 Best Local Similarity 53.3%; Pred. No. 1.9e+02;  
 Matches 8; Conservative 5; Mismatches 1; Indels 1; Gaps 1;  
 QY 2 AVLI-LQGPYVSWL 15  
 :||: |||| :|:  
 Db 4 SVLVSLQGPLFLSVL 18  
 RESULT 5  
 AAE01738  
 ID AAE01738 standard; peptide; 18 AA.  
 XX AC AAE01738;  
 XX DT 18-JUL-2001 (first entry)  
 XX DE Human gene 19 encoded secreted protein HYASC80 fragment, SEQ ID NO:151.  
 XX KW Human; secreted protein; proliferative disorder; cancer; tumour;  
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;  
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
 KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
 KW gastrointestinal disorder; pregnancy-related disorder; gene therapy;  
 KW endocrine disorder; infection; wound healing; vulnery; cell culture;

KW chemotaxis; food additive; binding partner identification.  
 XX Homo sapiens.  
 XX PH Key Location/Qualifiers  
 FT Misc-difference 13 /label= Unknown  
 FT /note= "Encoded by MTM"  
 XX WO200134767-A2.  
 XX PD 17-MAY-2001.  
 XX PF 01-NOV-2000; 2000WO-US030036.  
 XX PR 05-NOV-1999; 99US-0163576P.  
 XX PR 27-JUL-2000; 2000US-0221366P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX Soppet DR, Komatsoulis G, Shi Y, Olsen HS, Ruben SM;  
 WPI; 2001-316492/33.  
 DR N-PSDB; AAD05559.  
 XX Isolated nucleic acid molecule encoding a human secreted protein is used  
 PT in preventing, treating or ameliorating a medical condition.  
 PT Claim 11; Page 514; 540pp; English.  
 XX CC AAD05492-AAD05564 represent cDNAs corresponding to 22 human secreted  
 CC protein genes, and AAE01672-AAE01743 represent the proteins they encode.  
 CC AAE01744-AAE01763 represent human secreted protein fragments or variants.  
 CC The secreted proteins and their genes are useful for preventing, treating  
 CC or ameliorating medical conditions, e.g., by protein or gene therapy.  
 CC Pathological conditions can be diagnosed by determining the amount of the  
 CC new protein in a sample or by determining the presence of mutations in  
 CC the new genes. Specific uses are described for each of the 22 genes,  
 CC based on the tissues in which they are most highly expressed, and include  
 CC developing products for the diagnosis or treatment of proliferative  
 CC disorders, cancer, tumours, foetal and developmental abnormalities,  
 CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune  
 CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,  
 CC neurological disorders (e.g., Alzheimer's disease, Parkinson's disease),  
 CC cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,  
 CC psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders,  
 CC angiogenic disorders, kidney disorders, gastrointestinal disorders,  
 CC pregnancy-related disorders, endocrine disorders, and infections. The  
 CC proteins can also be used to aid wound healing and epithelial cell  
 CC proliferation, to prevent skin aging due to sunburn, to maintain organs  
 CC before transplantation, for supporting cell culture of primary tissues,  
 CC to regenerate tissues, to identify their cognate ligands or binding  
 CC partners, and in chemotaxis, and can be used as a food additive or  
 CC preservative to modify storage properties. Antibodies specific for a  
 CC protein of the invention can be used in alleviating symptoms associated  
 CC with the disorders mentioned above, and in diagnostic immunoassays e.g.,  
 CC radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The  
 CC present sequence represents a human secreted protein fragment of the  
 CC invention  
 XX SQ Sequence 18 AA;  
 Query Match 42.5%; Score 34; DB 4; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 7 QGPPYVSWL 15  
 |||: |||:  
 Db 4 QGCPHPSWL 12  
 RESULT 6  
 ABG63934

ID ABG63934 standard; protein; 18 AA.  
 AC ABG63934;  
 XX  
 XX 27-AUG-2002 (first entry)  
 DT  
 XX Human albumin fusion protein #609.  
 DE  
 XX  
 XX Albumin fusion protein; therapeutic protein X; human albumin; HA;  
 KW human serum albumin; HSA; cancer; reproductive disorder;  
 KW digestive disorder; immune disorder; endocrine disorder;  
 KW haematopoietic disorder; neural disorder; connective disorder;  
 KW cytostatic; anti-infectivity; anti-inflammatory; anti-ulcer;  
 KW immunomodulator; anti-HIV; antidiabetic; haemostatic; neurotropic;  
 KW neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;  
 KW osteopathic; antiarthritic.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX WO200177137-A1.  
 PN  
 XX  
 XX 18-OCT-2001.  
 PD  
 XX  
 XX 12-APR-2001; 2001WO-US011988.  
 PF  
 XX  
 XX 12-APR-2000; 2000US-0229358P.  
 PR  
 XX 25-APR-2000; 2000US-0199384P.  
 PR  
 XX 21-DEC-2000; 2000US-0256931P.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX Rosen CA, Haseltine WA;  
 PI  
 XX WPI; 2002-010886/01.  
 DR  
 XX  
 XX New fusion protein for treating disease e.g. diabetes comprises an  
 PT albumin fused to a therapeutic protein.  
 PT  
 XX Claim 1; Page 912; 2102pp; English.  
 PS  
 XX The present invention relates to albumin fusion proteins comprising a  
 CC therapeutic protein X and human albumin (HA, also known as human serum  
 CC albumin, HSA). The proteins are useful for treating a disease or disorder  
 CC that may be modulated by therapeutic protein X. The albumin extends the  
 CC shelf-life of protein X, and may increase its biological in vitro/in vivo  
 CC activity. The protein is useful for treating and diagnosing disorders  
 CC such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's  
 CC disease, ulcerative colitis), immune disorders (e.g. acquired  
 CC immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),  
 CC haematopoietic disorders, neural disorders (e.g. Alzheimer's,  
 CC Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,  
 CC schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).  
 CC ABG63326-ABG65518 represent albumin fusion proteins of the invention  
 XX  
 SQ Sequence 18 AA;  
 Query Match 42.5%; Score 34; DB 5; Length 18;  
 Best Local Similarity 66.7%; Pred. NO. 2.1e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 Qy 7 QGPPYVSWL 15  
 Db 4 QGCPHPSWL 12  
 ||| : |||  
 ||| : |||  
 RESULT 7  
 ADL77199  
 ID ADL77199 standard; peptide; 18 AA.  
 XX  
 AC ADL77199;  
 XX  
 XX 20-MAY-2004 (first entry)  
 DT

XX  
 DE Albumin fusion protein related therapeutic protein X, SEQ ID NO 681.  
 XX  
 KW albumin fusion protein; cytostatic; antianaemic; antiarthritic;  
 KW antiasthmatic; anti-HIV; immunosuppressive; anti-inflammatory;  
 KW antipsoriatic; antibacterial; osteopathic; dermatological; antitumor;  
 KW immunomodulator; antiarrhythmic; cardiac; neurotropic; antilipemic;  
 KW nephrotropic; uropathic; neuroprotective; antiparkinsonian; tranquilizer;  
 KW antidiabetic; anabolic; hypertensive; vulnary; gene therapy; cancer;  
 KW reproductive system disorder; therapeutic protein.  
 OS Unidentified.  
 XX  
 PN US2004010134-A1.  
 XX  
 XX 15-JAN-2004.  
 PD  
 XX  
 XX 12-APR-2001; 2001US-00833245.  
 PF  
 XX  
 XX 12-APR-2000; 2000US-0229358P.  
 PR  
 XX 25-APR-2000; 2000US-0199384P.  
 PR  
 XX 21-DEC-2000; 2000US-0256931P.  
 XX  
 XX (ROSE/) ROSEN C A.  
 PA (HASE/) HASELTINE W A.  
 XX  
 XX Rosen CA, Haseltine WA;  
 PI  
 XX WPI; 2004-090519/09.  
 DR  
 XX  
 XX New albumin fusion proteins, useful for diagnosing, treating, preventing  
 PT or ameliorating diseases or disorders e.g. cancer, anemia, arthritis,  
 PT asthma, inflammatory bowel disease or Alzheimer's disease.  
 PT  
 XX  
 XX Disclosure; SEQ ID NO 681; 279pp; English.  
 PS  
 XX  
 XX The invention relates to a novel albumin fusion protein. The invention  
 CC further relates to: a composition comprising the albumin fusion protein  
 CC and a pharmaceutical carrier; a kit comprising the composition of the  
 CC albumin fusion protein formula; a method of treating a disease or  
 CC disorder in a patient comprising the step of administering the albumin  
 CC fusion protein; a method of treating a patient with a disease or disorder  
 CC that is modulated by Therapeutic protein: X, or its fragment or variant;  
 CC a method of extending the shelf life of Therapeutic protein: X, or its  
 CC fragment or variant; a nucleic acid molecule comprising a polynucleotide  
 CC sequence encoding the albumin fusion protein; a vector comprising the  
 CC nucleic acid molecule of the albumin fusion protein; and a host cell  
 CC comprising the nucleic acid molecule of the albumin fusion protein. The  
 CC albumin fusion protein and its compositions have the following  
 CC activities: cytostatic, antianaemic, antiarthritic, antiasthmatic, anti-  
 CC HIV, immunosuppressive, anti-inflammatory, antipsoriatic, antibacterial,  
 CC osteopathic, dermatological, antitumor, immunomodulator, antiarrhythmic,  
 CC cardiac, neurotropic, antilipemic, nephrotropic, uropathic,  
 CC neuroprotective, antiparkinsonian, tranquilizer, antidiabetic, anabolic,  
 CC hypertensive, and vulnary. The albumin fusion protein nucleic acid may  
 CC be used in gene therapy to treat disorders. The albumin fusion protein is  
 CC useful for diagnosing, treating, preventing or ameliorating diseases or  
 CC disorders comprising indication: Y. The diseases or disorders include:  
 CC cancer (e.g. leukaemia, colon, bone, breast, liver or lung cancer),  
 CC immune or haematopoietic diseases (e.g. anaemia, Hodgkin's disease, acute  
 CC lymphocytic anaemia, multiple myeloma, arthritis, asthma, AIDS,  
 CC autoimmune disease, inflammatory bowel disease, psoriasis or Lyme  
 CC disease), reproductive system disorders (e.g. prostatitis, inguinal  
 CC hernia, varicocele, penile carcinoma, ovarian adenocarcinoma or Sertoli-  
 CC Leydig tumours), musculoskeletal diseases (e.g. giant cell tumours,  
 CC Paget's disease, systemic lupus erythematosus, gout, muscular dystrophy  
 CC or cachexia), cardiovascular disease (e.g. rhabdomyomas, heart disease,  
 CC arrhythmia, cardiac arrest, heat valve disease, hypernatraemia or  
 CC hyponatraemia), mixed foetal diseases (e.g. foetal alcohol syndrome,  
 CC Down's syndrome, Patau syndrome, Turner's syndrome, Apter syndrome or Tay  
 CC -Sachs disease), excretory diseases (e.g. urinary incontinence, urinary  
 CC tract infections or renal disorders), neural or sensory disease (e.g.  
 CC Alzheimer's disease, Parkinson's disease, cerebral malaria, meningitis,



CC cerebellar ataxia, attention deficit disorder, autism or obsessive  
 CC compulsive disorder), respiratory disease (e.g. emphysema, lung cancer or  
 CC occupational lung disease), endocrine diseases (e.g. diabetes, Addison's  
 CC disease or glomerulonephritis), digestive diseases (e.g. portal  
 CC hypertension, irritable bowel disease, gastric atrophy or pancreatitis)  
 CC or connective tissue or epithelial diseases (e.g. Crohn's disease,  
 CC scleroderma, wound healing or epidermolysis bullosa). This sequence  
 CC represents a therapeutic protein X relating to the albumin fusion protein  
 CC of the invention. The sequence listing data for this specification was  
 CC downloaded from the USPTO website.

XX SQ Sequence 18 AA;

Query Match 42.5%; Score 34; DB 8; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 QGPPYVSWL 15  
 DB 4 QGCPHPSWL 12  
 |||:|

RESULT 8  
 AAW09483  
 ID AAW09483 standard; protein; 14 AA.

XX AC AAW09483;

XX DT 10-SEP-1997 (first entry)

XX DE Thrombopoietin receptor binding peptide.

XX KW Haematology; thrombocytopenia; TPO; TR; proliferation;  
 KW bone marrow transfusion; chemotherapy; radiation therapy.

XX OS Synthetic.

XX PN WO9640189-A1.

XX PD 19-DEC-1996.

XX PF 05-JUN-1996; 96WO-US008998.

XX PR 07-JUN-1995; 95US-00472371.

XX PR 07-JUN-1995; 95US-00473604.

XX PR 07-JUN-1995; 95US-00476168.

XX PR 07-JUN-1995; 95US-00478128.

XX PR 07-JUN-1995; 95US-00484090.

XX PR 07-JUN-1995; 95US-00485301.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Dower WJ, Barrett RW, Cwirila SE, Duffin DJ, Gates CM, Johnson SS;  
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX DR WPI; 1997-051883/05.

XX PT Thrombopoietin receptor-binding/activating peptide(s) and peptide  
 PT mimetic(s) - useful in treatment of haematological disorders, esp.  
 PT thrombocytopenia resulting from chemotherapy, etc.

XX PS Disclosure; Page 26; 106pp; English.

XX CC The present sequence is a peptide which binds to thrombopoietin (TPO)  
 CC receptor (TR). The compound can be used for treating patients suffering  
 CC from haematological disorders and thrombocytopenia resulting from  
 CC chemotherapy, radiation therapy or bone marrow transfusions. The peptide  
 CC may also be used to maintain the proliferation and growth of TPO-  
 CC dependent cell lines and for use in biological research, for detecting  
 CC TPO receptors on living cells

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPYVSWL 15  
 DB 3 LVGPSLMSWL 12  
 |||:|

RESULT 9

AAW36634

ID AAW36634 standard; peptide; 14 AA.

XX AC AAW36634;

XX DT 11-MAR-1998 (first entry)

XX DE Thrombopoietin receptor binding peptide.

XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;  
 KW haematological disorder; thrombocytopenia; chemotherapy;  
 KW radiation therapy; bone marrow transfusion; diagnosis;  
 KW signal transduction; receptor activation; cell culture.

XX OS Synthetic.

XX PN WO9640750-A1.

XX PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US009623.

XX PR 07-JUN-1995; 95US-00478128.

XX PR 07-JUN-1995; 95US-00485301.

XX PA (GLAX ) GLAXO GROUP LTD.

XX PI Dower WJ, Barrett RW, Cwirila SE, Duffin DJ, Gates CM, Johnson SS;  
 PI Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;

XX DR WPI; 1997-052226/05.

XX PT Peptides and peptide mimetics which bind to and activate the  
 PT thrombopoietin receptor - useful in treatment of haematological  
 PT disorders, esp. thrombocytopenia resulting from chemotherapy, etc.

XX PS Disclosure; Page 26; 106pp; English.

XX CC The present peptide, which binds the thrombopoietin receptor (TR), can be  
 CC used to treat disorders which are susceptible to treatment with a  
 CC thrombopoietin agonist, preferably haematological disorders and  
 CC thrombocytopenia resulting from chemotherapy, radiation therapy or bone  
 CC marrow transfusions. It can also be used diagnostically, e.g. to  
 CC investigate the mechanism of thrombopoietin signal transduction and  
 CC receptor activation, or to maintain the proliferation and growth of  
 CC thrombopoietin dependent cell lines

XX SQ Sequence 14 AA;

Query Match 41.2%; Score 33; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPYVSWL 15  
 DB 3 LVGPSLMSWL 12  
 |||:|

RESULT 10

AAW36767

ID AAW36767 standard; peptide; 14 AA.

XX AC AAW36767;

11-MAR-1998 (first entry)  
Thrombopoietin receptor binding peptide.  
Thrombopoietin receptor; binding peptide; treatment; agonist;  
haematological disorder; thrombocytopenia; chemotherapy;  
radiation therapy; bone marrow transfusion; diagnosis;  
signal transduction; receptor activation; cell culture.  
Synthetic.  
Key Location/Qualifiers  
Disulfide-bond 1.14  
Modified-site 14  
/note= "NH2-Cys"  
W09640750-A1.  
19-DEC-1996.  
07-JUN-1996; 96WO-US009623.  
07-JUN-1995; 95US-00478128.  
07-JUN-1995; 95US-00485301.  
(GLAX ) GLAXO GROUP LTD.  
Dower WJ, Barret RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;  
Mattheakis LC, Schatz PU, Wagstrom CR, Wrighton NC;  
WPI; 1997-052226/05.  
Peptides and peptide mimetics which bind to and activate the  
thrombopoietin receptor - useful in treatment of haematological  
disorders, esp. thrombocytopenia resulting from chemotherapy, etc.  
Example 9; Page 75; 106pp; English.  
The present peptide, which binds the thrombopoietin receptor (TR), can be  
used to treat disorders which are susceptible to treatment with a  
thrombopoietin agonist, preferably haematological disorders and  
thrombocytopenia resulting from chemotherapy, radiation therapy or bone  
marrow transfusions. It can also be used diagnostically, e.g. to  
investigate the mechanism of thrombopoietin signal transduction and  
receptor activation, or to maintain the proliferation and growth of  
thrombopoietin dependent cell lines  
Sequence 14 AA;  
Query Match 41.2%; Score 33; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 6 LQGPYPVSWL 15  
| | | | : | | |  
Db 3 LVGPPLMSWL 12  
RESULT 11  
AAB17011  
ID AAB17011 standard; peptide; 14 AA.  
AC AAB17011;  
DT 31-OCT-2000 (first entry)  
XX TPO-mimetic peptide sequence SEQ ID NO:67.  
XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
XX autoimmune disease; cytostatic; antiasthmatic; thrombolytic; VEGF;  
XX immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;  
XX inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
XX

OS Homo sapiens.  
 PN US6251864-B1.  
 XX  
 PD 26-JUN-2001.  
 XX  
 PF 01-MAR-2000; 2000US-00516704.  
 XX  
 PR 07-JUN-1995; 95US-00478128.  
 PR 07-JUN-1995; 95US-00485301.  
 PR 07-JUN-1996; 96MO-US009623.  
 PR 15-AUG-1996; 96US-00899027.  
 XX  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Dower WJ, Barrett RW, Cwirila SE, Gates CM, Schatz PU;  
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Deprince RB, Podduturi S;  
 PI Yin Q;  
 XX  
 DR WPI; 2001-564142/63.  
 XX  
 PT Activating thrombopoietin receptors in cells, used to treat  
 PT thrombocytopenia and hematological disorders, comprises contacting cells  
 PT with peptides and peptide mimetics attached to hydrophilic polymers.  
 XX  
 PS Disclosure; Col 20; 128pp; English.  
 XX  
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that  
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods  
 CC of activating thrombopoietin receptors in cells comprise contacting the  
 CC cells with effective amounts of peptides and peptide mimetics attached to  
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such  
 CC as that due to chemotherapy, radiation therapy or bone-marrow  
 CC transplantation and to prevent thrombocytopenia in patients at risk. The  
 CC sequences are used to treat and prevent hematological disorders  
 CC including thrombocytopenia and platelet disorders. They are used in vitro  
 CC as unique tools for understanding the biological role of thrombopoietin  
 CC (TPO) and to develop other compounds that bind to and activate the TPO  
 CC receptor. The peptides can be used to detect TPO receptors on living  
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and  
 CC in purified or natural biological materials. They may also be used for in  
 CC situ staining, fluorescence-activated cell sorting, Western blotting and  
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can  
 CC be used for in vitro expansion of megakaryocytes and their committed  
 CC progenitors alone or in conjunction with additional cytokines  
 XX  
 SQ Sequence 14 AA;  
 Query Match 41.2%; Score 33; DB 4; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 LQGPYPVSWL 15  
 | | | | : | | |  
 Db 3 LVGFSLSWSL 12  
 RESULT 13  
 ABB72897  
 ID ABB72897 standard; peptide; 14 AA.  
 XX  
 AC ABB72897;  
 XX  
 DT 05-APR-2002 (first entry)  
 XX  
 DE TPO mimetic peptide SEQ ID NO:67.  
 XX  
 KW Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;  
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TWP;  
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;  
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
 KW cytosstatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;

KW antianaemic; anorectic; antiinfertility; haemostatic; dermatological;  
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
 KW sleep disorder; neurological degenerative disease; anaemia;  
 KW thrombocytopenia; metastatic tumour; systemic lupus erythematosus;  
 KW Fanconi's syndrome.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200183525-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US014310.  
 XX  
 PR 03-MAY-2000; 2000US-00563286.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Feige U, Liu C, Cheestham JC, Boone TC, Gudas JM;  
 PI WPI; 2002-130313/17.  
 DR  
 XX Novel vehicle-peptide molecule or its multimers useful for treating  
 XX inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
 XX diabetic retinopathy, obesity, sleep disorders and infertility.  
 PT  
 PT  
 PT  
 PS Claim 39; Page 44; 176pp; English.  
 XX  
 CC The present invention describes a vehicle-peptide molecule (I) or its  
 CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,  
 CC cytosstatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,  
 CC antianaemic, anorectic, antiinfertility, haemostatic, dermatological and  
 CC neuroprotective activities. (I) can be used as a therapeutic or  
 CC prophylactic agent as well as for screening purposes. (I) is useful for  
 CC diagnosing diseases characterised by dysfunction of their associated  
 CC protein of interest, for identifying normal or abnormal proteins of  
 CC interest, as a part of diagnostic kit to detect the presence of their  
 CC proteins of interest in a biological sample. Additionally, (I) is useful  
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,  
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-  
 CC mimetic compounds are useful for treating disorders characterised by low  
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising  
 CC compounds are useful for treating conditions that involve an existing  
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet  
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic  
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,  
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777  
 CC represent amino acid and nucleic acid sequences used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 14 AA;  
 Query Match 41.2%; Score 33; DB 5; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 LQGPYPVSWL 15  
 | | | | : | | |  
 Db 3 LVGFSLSWSL 12  
 RESULT 14  
 ADJ73048  
 ID ADJ73048 standard; peptide; 14 AA.  
 XX  
 AC ADJ73048;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE TPO mimetic peptide sequence SeqID 502.

```

XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KW cardiovascular; infectious; malignant; neurologic disease; anaemia;
KW immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KW TPO.
XX OS Synthetic.
XX WO2003084477-A2.
XX PD 16-OCT-2003.
XX PF 24-MAR-2003; 2003WO-US009139.
XX PR 29-MAR-2002; 2002US-0368791P.
XX PA (CENZ ) CENTOCOR INC.
XX PI Heavner GA, Knight DM, Scallion BJ, Ghayeb J;
XX WPI; 2003-804237/75.
XX DR New CDR mimetibody comprising a portion of a heavy or light chain
XX PT variable region comprising human framework or ligand binding region,
XX PT useful for preparing a composition for treating e.g., immune,
XX PT cardiovascular or neurologic disease.
XX PS Disclosure; SEQ ID NO 502; 97pp; English.
XX CC This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms
CC of immune, cardiovascular, infectious, malignant and/or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This
CC peptide sequence is a TPO mimetic peptide sequence used to make a
CC mimetibody of the invention.
XX SQ Sequence 14 AA;
Query Match 41.2%; Score 33; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 LOGPPYVSWL 15
DB 3 LVGPSLMSWL 12
RESULT 15
ADJ52683
ID ADJ52683 standard; peptide; 14 AA.
XX AC ADJ52683;
XX DT 06-MAY-2004 (first entry)
XX DE CH1 deleted mimetibody-related peptide SeqID502.
XX KW CH1 deleted mimetibody; immunosuppressive; cardiovascular; cardiant;
KW hypotensive; neuroprotective; nontropic; antibacterial; virucide;
KW fungicide; gene therapy; immune disorder; cardiovascular disease;
KW arrhythmia; hypertension; heart failure; neurodegenerative;
KW multiple sclerosis; dementia; Alzheimer's disease; anaemia;
KW cancerous condition; infectious disease; bacterial infection;
KW viral infection; fungal infection.
KW Unidentified.
OS Synthetic.
XX WO2004002417-A2.
XX PD 08-JAN-2004.
XX PF 27-JUN-2003; 2003WO-US020347.
XX PR 28-JUN-2002; 2002US-0392431P.
XX PA (CENZ ) CENTOCOR INC.
XX PI Heavner GA, Knight DM, Ghayeb J, Scallion BJ, Nesspor TC;
XX PI Kutoloshki KA;
XX WPI; 2004-082870/08.
XX DR New CH1-deleted mimetibody polypeptides and nucleic acids, useful for
XX PT modulating, treating, alleviating, preventing an immune, cardiovascular,
XX PT or neurodegenerative disease or disorder, anemia, cancer, or infectious
XX PT diseases.
XX PS Claim 2; SEQ ID NO 502; 129pp; English.
XX CC This invention relates to CH1 deleted mimetibodies (and the DNA sequences
CC which encode them), compositions, methods and uses. The invention may be
CC useful for the development of compounds with an immunosuppressive,
CC cardiovascular, cardiant, hypotensive, neuroprotective, nontropic,
CC antibacterial, virucide or fungicide activity. In addition, the disclosed
CC sequences may prove useful for gene therapy. The CH1-deleted mimetibody
CC is useful for diagnosing or treating a disease condition in a cell,
CC tissue, organ or animal, specifically for modulating, treating,
CC alleviating, preventing the incidence or reducing the symptoms of an
CC immune, cardiovascular (for example arrhythmia, hypertension or heart
CC failure), or neurodegenerative (for example multiple sclerosis, dementia
CC or Alzheimer's disease) diseases or disorders, anaemia, cancerous
CC conditions, or infectious diseases (for example bacterial, viral or
CC fungal infection). The present sequence is that of a peptide which may be
CC used during the creation of a mimetibody of the invention.
XX SQ Sequence 14 AA;
Query Match 41.2%; Score 33; DB 8; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 LOGPPYVSWL 15
DB 3 LVGPSLMSWL 12
Search completed: November 14, 2004, 12:02:16
Job time : 45.4043 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 40.0532 Seconds  
(without alignments)  
215.479 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLIQGPYVSWL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	38.8	13	2 Q95925	Q95925 porphyra pu
2	31	38.8	23	2 Q700R6	Q700R6 sus scrofa
3	31	38.8	23	2 CAF32800	CAF32800 sus scrof
4	29	36.2	13	2 Q95808	Q95808 gracilariop
5	29	36.2	16	2 Q9QUW5	Q9QUW5 rattus sp.
6	29	36.2	22	1 MLP RANTE	P56924 rana tempor
7	28	35.0	13	1 SOVO SEPOF	P83567 sepiia offic
8	28	35.0	20	2 Q9UR76	Q9UR76 candida alb
9	27.5	34.4	18	1 D7A1 ACASC	P83402 acanthopagr
10	27	33.8	8	1 ALL5_CALVO	P41841 calliphora
11	27	33.8	13	1 PROX_ORYSA	P83647 oryza sativ
12	27	33.8	21	2 Q9PRQ1	Q9PRQ1 oncorhynch
13	26.5	33.1	17	2 Q9TR22	Q9TR22 bos taurus
14	26	32.5	16	2 Q9SPV1	Q9SPV1 nicotiana t
15	26	32.5	18	2 Q7MLG0	Q7MLG0 triticum ae
16	26	32.5	22	2 Q96JA7	Q96JA7 homo sapien
17	25	31.2	14	2 Q26075	Q26075 psammichin
18	25	31.2	16	2 Q6NT60	Q6NT60 homo sapien
19	25	31.2	16	2 AAH69320	AAH69320 homo sapi
20	25	31.2	18	2 Q9UCT9	Q9UCT9 homo sapien
21	25	31.2	20	2 Q8NED5	Q8NED5 homo sapien
22	25	31.2	22	2 Q85481	Q85481 rous sarcom
23	25	31.2	23	2 Q9TWJ9	Q9TWJ9 mytilus edu
24	24	30.0	15	1 SODM_STRGR	P80733 streptomyce
25	24	30.0	19	2 Q96TP8	Q96TP8 cryptococcu
26	24	30.0	19	2 Q9ZYW8	Q9ZYW8 ichneutes b
27	24	30.0	20	1 AROQ_ARYME	P46380 amycolatops
28	24	30.0	21	1 PIL3_ECOLI	P13948 escherichia
29	24	30.0	21	2 Q7S006	Q7S006 neurospora
30	24	30.0	22	2 Q52435	Q52435 burkholderi
31	24	30.0	23	2 Q96TH8	Q96TH8 cryptococcu

32 24 30.0 23 2 Q8XXZ2 Q8xxz2 ralstonia s  
33 23 28.7 12 2 Q7MIH0 Q7mih0 leonurus ar  
34 23 28.7 13 2 Q04220 Q04220 plasmid p30  
35 23 28.7 14 1 CAL1\_CALGI P20728 calotropis  
36 23 28.7 14 2 P81801 P81801 streptomyce  
37 23 28.7 15 2 Q9S8Z0 Q9s8z0 hordeum vul  
38 23 28.7 16 2 Q6LDB6 Q6ldb6 mus sp. mac  
39 23 28.7 16 2 AAG38018 Aag38018 mus muscu  
40 23 28.7 16 2 AAP13932 Aap13932 mus sp. m  
41 23 28.7 17 2 Q7SR67 Q7sr67 conger myri  
42 23 28.7 17 2 Q7SRF1 Q7srf1 conger myri  
43 23 28.7 17 2 Q7SRM2 Q7srm2 conger myri  
44 23 28.7 17 2 Q7SRK8 Q7srk8 conger myri  
45 23 28.7 17 2 Q75RT8 Q75rt8 conger myri

#### ALIGNMENTS

##### RESULT 1

Q95925 PRELIMINARY; PRT; 13 AA.  
AC Q95925;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome oxidase subunit 3 (Fragment).  
GN Name-cox3;  
OS Porphyra purpurea.  
OG Mitochondrion.  
OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.  
OX NCBI\_TaxID=2787;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lang B.Franz., Goff L.J., Gray M.W.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U59763; AAB17951.1; -.  
KW GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 1 1  
SQ SEQUENCE 13 AA; 1522 MW; 0831666D0E8C65B0 CRC64;

Query Match 38.8%; Score 31; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. NO. 3.9e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PPYVSW 14  
Db 3 PDYISW 8  
| | | |  
| | | |

##### RESULT 2

Q700R6 PRELIMINARY; PRT; 23 AA.  
AC Q700R6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Fas binding protein (fragment).  
GN Name=DAXX;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Barbosa A., Deneure O., Urien C., Milan D., Chardon P., Renard C.;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ629179; CAF32800.1; -.  
FT NON\_TER 1 1  
SQ SEQUENCE 23 AA; 2574 MW; 0B078824AA2E0517 CRC64;

```

Query Match          38.8%; Score 31; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 7e+02; 4; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 6 LQPPPVVSWL 15
DB 11 LQNPKPPI 20

RESULT 3
CAF32800 PRELIMINARY; PRT; 23 AA.
AC CAF32800;
DT 03-MAR-2004 (TrEMBLrel. 27, Created)
DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Fas binding protein (Fragment).
GN DAXX.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Barbosa A., Demeure O., Urien C., Milan D., Chardon P., Renard C.;
RT "A physical map of large segments of pig chromosome 7q1.1-ql.4:
RT comparative analysis with human chromosome 6p21.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ629179; CAF32800.1; -.
FT NON_TER 1 1
FT NON_TER 23 23
SQ SEQUENCE 23 AA; 2574 MW; 0B078824AA2E0517 CRC64;

Query Match          38.8%; Score 31; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 7e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 LQPPPVVSWL 15
DB 11 LQNPKPPI 20

RESULT 4
Q95808 PRELIMINARY; PRT; 13 AA.
AC Q95808;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit 3 (Fragment).
GN Namexco3;
OS Gracilariopsis lemaneiformis.
OG Mitochondrion.
OC Eukaryota; Rhodophyta; Florideophyceae; Gracilariaceae; Gracilariaceae;
OC Gracilariopsis.
OX NCBI_TaxID=2782;
RN [1]
RP SEQUENCE FROM N.A.
RA Lang B.Franz., Goff L.J., Gray M.W.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59764; AAB17950.1; -.
DR GO; GO:0005739; C.mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1565 MW; 305BD4028745B043 CRC64;

Query Match          36.2%; Score 29; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 8.5e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPVSWL 15
DB 1 PNYITWI 7

Query Match          38.8%; Score 31; DB 2; Length 23;
Best Local Similarity 50.0%; Pred. No. 7e+02; 4; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Gaps 0;

QY 6 LQPPPVVSWL 15
DB 11 LQNPKPPI 20

RESULT 5
Q9QUW5 PRELIMINARY; PRT; 16 AA.
AC Q9QUW5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Collagen-like heparin-binding glycoprotein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RA MEDLINE=96278823; PubMed=8662884;
RX Chernousov M.A., Stahl R.C., Carey D.J.;
RT "Schwann cells secrete a novel collagen-like adhesive protein that
RT binds N-syndecan.";
RL J. Biol. Chem. 271:13844-13853(1996).
SQ SEQUENCE 16 AA; 1329 MW; 0F03A38D20A9221C CRC64;

Query Match          36.2%; Score 29; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LQPP 10
DB 8 LQPP 12

RESULT 6
MLP_RANTE STANDARD; PRT; 22 AA.
AC P56324;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Melittin-like peptide (MLP).
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "temporins, antimicrobial peptides from the European red frog Rana
RT temporaria.";
RL Eur. J. Biochem. 242:788-792(1996).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Skin.
KW Amidation; Amphibian defense peptide; Direct protein sequencing.
FT MOD_RES 22 22 Glutamine amide.
SQ SEQUENCE 22 AA; 2313 MW; 0990320F9B0709B3 CRC64;

Query Match          36.2%; Score 29; DB 1; Length 22;
Best Local Similarity 43.8%; Pred. No. 1.5e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 2; Gaps 1;

QY 2 AVLILQG--PPVSWL 15
DB 5 ALKVLGLVPSIVSWV 20

RESULT 7
SOVO_SEPOF STANDARD; PRT; 13 AA.
ID SOVO_SEPOF
AC P83567;
DT 29-MAR-2004 (Rel. 43, Created)

```

DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE SepOvotropin.  
OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
OX NCBI\_TaxID=6610;  
RN [1]  
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND  
RP AMIDATION.  
RC TISSUE=Ovarian follicle;  
RX MEDLINE=20483622; PubMed=11027583; DOI=10.1006/bbrc.2000.3595;  
RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;  
RT "The SepOvotropin: a new ovarian peptide regulating oocyte transport  
RT in Sepia officinalis.";  
RL Biochem. Biophys. Res. Commun. 276:1013-1018(2000).  
CC -I- FUNCTION: Has myotropic activity targeting the genital tract.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg.  
CC -I- MASS SPECTROMETRY: MW=1502.8; METHOD=MALDI; RANGE=1-13;  
CC NOTE=Ref.1.  
KW Amidation; Direct protein sequencing.  
FT MOD RES 13 Tyrosine amide.  
SQ SEQUENCE 13 AA; 1503 MW; 483D5C7E34C72727 CRC64;  
Query Match 35.0%; Score 28; DB 1; Length 13;  
Best Local Similarity 45.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 EAVILQGPV 11  
DB ::::| | | |  
3 DSMLLQVPV 13  
RESULT 8  
QYUR76 PRELIMINARY; PRT; 20 AA.  
AC QYUR76;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
DE N-acetylglucosaminidase A (Fragment).  
OS Candida albicans (Yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=5476;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=94356217; PubMed=8075797;  
RA Molloy C., Cannon R.D., Sullivan P.A., Shepherd M.G.;  
RT "Purification and characterization of two forms of N-  
RT acetylglucosaminidase from Candida albicans showing widely different  
RT outer chain glycosylation.";  
RL Microbiology 140:1543-1553(1994).  
SQ SEQUENCE 20 AA; 2178 MW; DA602087EDDB4D47 CRC64;  
Query Match 35.0%; Score 28; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. No. 1.9e+03;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 3 VLILQGPVYVSW 14  
DB ::::| | | |  
3 VEILPAQSVTV 14  
RESULT 9  
ID D7A1 ACASC STANDARD; PRT; 18 AA.  
AC P83402;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1)

(Fragment).  
DE Acanthopagrus schlegelii (Black porgy).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;  
OC Sparidae; Acanthopagrus.  
OX NCBI\_TaxID=72011;  
RN [1]  
RP SEQUENCE, ACTIVITY, COFACTOR, AND SUBUNIT.  
RC TISSUE=Liver;  
RX MEDLINE=21956475; PubMed=11959129;  
RA Tang W.-K., Cheng C.H.K., Fong W.-P.;  
RT "First purification of the antiquitin protein and demonstration of its  
RT enzymatic activity.";  
RL FEBS Lett. 516:183-186(2002).  
CC -I- CATALYTIC ACTIVITY: An aldehyde + NAD(+) + H(2)O = an acid + NADH.  
CC -I- SUBUNIT: Homotetramer.  
CC -I- MISCELLANEOUS: Optimal pH is 9-10. The Km for acetaldehyde is 2.0  
CC mM and Vmax is 1.3 micromol/min x mg enzyme.  
CC -I- SIMILARITY: Belongs to the aldehyde dehydrogenase family.  
DR GO: GO:0004029; P:aldehyde dehydrogenase (NAD) activity; IDA.  
DR GO: GO:0006081; P:aldehyde metabolism; IDA.  
DR InterPro: IPR002086; Aldehyde dehydr.  
DR PROSITE: PS00070; ALDEHYDE\_DEHYDR\_CYS; PARTIAL.  
DR PROSITE: PS00687; ALDEHYDE\_DEHYDR\_GLU; PARTIAL.  
KW Direct protein sequencing; NAD; Oxidoreductase.  
FT NON TER 18  
SQ SEQUENCE 18 AA; 2059 MW; BFF8C3EF1A9B4047 CRC64;  
Query Match 34.4%; Score 27.5; DB 1; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.1e+03;  
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;  
QY 4 LILQGPVYVSW 15  
DB ::::| | | |  
3 LLINQPKY-SWL 13  
RESULT 10  
ALIS CALVO STANDARD; PRT; 8 AA.  
ID -ALIS CALVO  
AC P41841;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Callotostatin 5 (Met-callotostatin 1) ([Hyp3]Met-callotostatin).  
OS Calliphora vomitoria (Blue blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Calliphora.  
OX NCBI\_TaxID=27454;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93211980; PubMed=8460157;  
RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,  
RA Thorpe A.;  
RT "Callotostatins: neuropeptides from the blowfly Calliphora vomitoria  
RT with sequence homology to cockroach allatostatins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).  
RN [2]  
RP CHARACTERIZATION, AND HYDROXYLATION.  
RC TISSUE=Head;  
RX MEDLINE=94342269; PubMed=8063725;  
RA Duve H., Johnsen A.H., Scott A.G., East P., Thorpe A.;  
RT "[Hyp3]Met-callotostatin. Identification and biological properties of  
RT a novel neuropeptide from the blowfly Calliphora vomitoria.";  
RL J. Biol. Chem. 269:21059-21066(1994).  
CC -I- FUNCTION: May act as a neurotransmitter or neuromodulator and play  
CC a role in the integration of information within the brain. May be  
CC involved in the control of visceral muscles due to its ability to  
CC behave as potent inhibitors of peristaltic movements. May also  
CC fulfill a neurohormonal role on muscles of the gut and heart.  
CC -I- TISSUE SPECIFICITY: Neurons within brain and abdominal ganglion.

CC -1- SIMILARITY: Belongs to the allatostatin family.  
 DR PIR; E47393;  
 KW Amidation; Direct protein sequencing; Hydroxylation; Neuropeptide.  
 FT MOD\_RES 3 3 Hydroxyproline (partial).  
 FT MOD\_RES 8 8 Methionine amide.  
 SQ SEQUENCE 8 AA; 883 MW; 7D9879CABB477768 CRC64;  
 Query Match 33.8%; Score 27; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 GPPY 11  
 Db 1 GPPY 4  
 RESULT 11  
 PROX ORYSA STANDARD; PRT; 13 AA.  
 AC P8367; 13 AA.  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Probable profilin LP04 (Fragments).  
 OS Oryza sativa (Rice).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 CC Ehrhartoideae; Oryzoae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. Indica / IR64; TISSUE=Panicle;  
 RA Hosseini Salekdeh S.G., Bennett J.;  
 RT "Proteome analysis of rice panicle."  
 RL Submitted (JUL-2003) to Swiss-Prot.  
 CC -1- FUNCTION: Binds to actin and affects the structure of the  
 CC cytoskeleton. At high concentrations, profilin prevents the  
 CC polymerization of actin, whereas it enhances it at low  
 CC concentrations. By binding to FIP2, it inhibits the formation of  
 CC IP3 and DG (By similarity).  
 CC -1- SUBUNIT: Occurs in many kinds of cells as a complex with monomeric  
 CC actin in a 1:1 ratio.  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 4.4, its MW is: 14.0 kDa.  
 CC -1- SIMILARITY: Belongs to the profilin family.  
 DR InterPro; IPR002097; Profilin.  
 DR PROSITE; PS00414; PROFILIN; PARTIAL.  
 KW Actin-binding; Cytoskeleton; Direct protein sequencing;  
 KM Multigene family.  
 FT NON\_TER 1 1  
 FT NON\_CONS 5 6  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1362 MW; 0A3022EE0E52C68B CRC64;  
 Query Match 33.8%; Score 27; DB 1; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 AVLIQGGP 10  
 Db 5 AYNVIQGP 13  
 RESULT 12  
 Q9PRQ1 PRELIMINARY; PRT; 21 AA.  
 AC Q9PRQ1; 21 AA.  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 70 kDa cold acclimation-related protein (Fragment).  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 OX NCBI\_TaxID=8022;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=96184500; PubMed=8605981;  
 RA Yamashita M., Ojima N., Sakamoto T.;  
 RT "Induction of proteins in response to cold acclimation of rainbow  
 RT trout cells."  
 RL FEBS Lett. 382:261-264 (1996).  
 DR PIR; S62893; S62893.  
 DR HSP; 001853; 1E32.  
 SQ SEQUENCE 21 AA; 2129 MW; FF68D74564917510 CRC64;  
 Query Match 33.8%; Score 27; DB 2; Length 21;  
 Best Local Similarity 57.1%; Pred. No. 3e+03;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 LILQGGP 10  
 Db 2 LILYGGP 8  
 RESULT 13  
 Q9TR22 PRELIMINARY; PRT; 17 AA.  
 ID Q9TR22; 17 AA.  
 AC Q9TR22; 17 AA.  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)  
 DE NONAMELOGENIN glycoprotein (Fragment).  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=96126798; PubMed=8564801;  
 RA Funzi J.S., DenBesten P.K.;  
 RT "Purification of nonamelogenin proteins from bovine secretory  
 RT enamel."  
 RL Calif. Tissue Int. 57:379-384 (1995).  
 SQ SEQUENCE 17 AA; 2032 MW; 9D811CC8228B615D CRC64;  
 Query Match 33.1%; Score 26.5; DB 2; Length 17;  
 Best Local Similarity 45.5%; Pred. No. 2.9e+03;  
 Matches 5; Conservative 1; Mismatches 2; Indels 3; Gaps 1;  
 QY 8 GPP---YVSWL 15  
 Db 7 GPPPPYSEWM 17  
 RESULT 14  
 Q9SPV1 PRELIMINARY; PRT; 16 AA.  
 ID Q9SPV1; 16 AA.  
 AC Q9SPV1; 16 AA.  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 CC Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20023723; PubMed=10561067;  
 RA Foster E., Hattori J., Labbe H., Ouellet T., Fobert P.R., James L.E.,  
 RA Iyer V.N., Miki B.L.;  
 RT "A tobacco cryptic constitutive promoter, tCUP, revealed by T-DNA



RT tagging.";  
RL Plant Mol. Biol. 41:45-55(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Foster E., Hattori J., Labbe H., Bedard J., Johnson D., Ouellet T.,  
RA Miki B.;  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF133844; AAD56607.1; -  
KW Hypothetical protein.  
FT NON TER 16 16  
SQ SEQUENCE 16 AA; 1725 MW; 6A4C8A093666240D CRC64;  
  
Query Match 32.5%; Score 26; DB 2; Length 16;  
Best Local Similarity 45.5%; Pred. No. 3.3e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 EAVLILQPPY 11  
Db :||| |||  
4 QAVETLYSPFF 14  
  
RESULT 15  
Q7M1G0  
ID Q7M1G0 PRELIMINARY; PRT; 18 AA.  
AC Q7M1G0;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Gluten.  
OS Triticum aestivum (Wheat).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticaceae; Triticum.  
OX NCBI\_TaxID=4565;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92111773; PubMed=1309704;  
RA Fukudome S., Yoshikawa M.;  
RT "Opioid peptides derived from wheat gluten: their isolation and  
RT characterization.";  
RL FEBS Lett. 296:107-111(1992).  
DR PIR; S20322; S20322.  
SQ SEQUENCE 18 AA; 2120 MW; 09A80A087DE83926 CRC64;  
  
Query Match 32.5%; Score 26; DB 2; Length 18;  
Best Local Similarity 66.7%; Pred. No. 3.8e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 10 PYVSWL 15  
Db ||| |||  
9 PYGGWL 14

Search completed: November 14, 2004, 12:07:36  
Job time : 42.0532 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 9.25532 Seconds  
(without alignments)  
155.938 Million cell updates/sec

Title: US-09-831-253F-8  
Perfect score: 80  
Sequence: 1 EAVLILQGPPYVSWL 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	31	38.8	13	2 S47361	T-cell antigen rec
2	31	38.8	16	2 C49048	T-cell receptor be
3	31	38.8	20	2 S65884	translation initia
4	27	33.8	8	2 E47393	neuropeptide calla
5	27	33.8	17	2 S33609	extensin - maize (
6	27	33.8	21	2 S62893	cold-inducible pro
7	26	32.5	18	2 S20322	gluten - wheat
8	25	31.2	15	2 JN0730	hypothetical 1.7K
9	24	30.0	20	2 A47687	3-dehydroquinat d
10	24	30.0	23	2 PH1729	Ig heavy chain V r
11	24	30.0	23	2 I53401	monocyte chemotact
12	23	28.7	12	2 PH1675	Ig heavy chain V r
13	23	28.7	12	2 JU0356	cycloleucinin -
14	23	28.7	13	2 PH1676	Ig heavy chain V r
15	23	28.7	13	2 E37390	traA protein - Esc
16	23	28.7	14	2 PH1677	Ig heavy chain V r
17	23	28.7	14	2 PH1705	Ig heavy chain V r
18	23	28.7	14	2 PT0026	calotropin DI - mu
19	23	28.7	15	2 PA0027	protein QA100006 -
20	23	28.7	15	2 PH1616	Ig H chain V-D-J r
21	23	28.7	15	2 PH1610	Ig H chain V-D-J r
22	23	28.7	16	2 I57530	gene c-fms protein
23	23	28.7	17	2 I51203	myosin heavy chain
24	23	28.7	19	2 A48354	nonstructural prot
25	23	28.7	20	2 A05313	apolipoprotein A-I
26	23	28.7	20	2 PS0188	superoxide dismuta
27	23	28.7	21	2 PH1731	Ig heavy chain V r
28	23	28.7	21	2 PH1730	Ig heavy chain V r
29	23	28.7	21	2 PH1690	Ig heavy chain V r

Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
collagen alpha 1(I  
osmotin homolog -  
sormatin - sorghum  
glutamate-ammonia  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r  
Ig heavy chain V r

ALIGNMENTS

RESULT 1

S47361 T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

C;Accession: S47361

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T

A;Reference number: S47355

A;Accession: S47361

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>

A;Cross-references: EMBL:235685; NID:G527459; PIDN:CAA84754.1; PID:G527460

C;Keywords: T-cell receptor

Query Match 38.8%; Score 31; DB 2; Length 13;  
Best Local Similarity 71.4%; Pred. No. 63;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 ILQGPPY 11

Db 3 VLQGSFY 9

RESULT 2

C49048

T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)  
C;Species: Homo sapiens (man)

C;Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997

C;Accession: C49048

R;Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.

A;Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenil

A;Reference number: A49048; MUID:92387250; PMID:1387614

A;Accession: C49048

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-16 <SIO>

A;Experimental source: patient EV, IL-2R+ synovial T-cells

A;Note: sequence extracted from NCBI backbone (NCBIP:113265)

C;Keywords: T-cell receptor

Query Match 38.8%; Score 31; DB 2; Length 16;  
Best Local Similarity 83.3%; Pred. No. 78;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ILQGPP 10

Db 6 LLQGSFY 11

## RESULT 3

S65884

translation initiation factor eIF-1 - rabbit (fragments)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 07-May-1999

C:Accession: S65884

R:Kasperaitis, M.A.M.; Voorma, H.O.; Thomas, A.A.M.

FEBS Lett. 365, 47-50, 1995

A:Title: The amino acid sequence of eukaryotic translation initiation factor 1 and its

A:Reference number: S65884; MUID:95293122; PMID:7774713

A:Accession: S65884

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-9;10-16;17-20 &lt;KAS&gt;

## Query Match

Best Local Similarity 38.8%; Score 31; DB 2; Length 20;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAVLIQGPY 11

| | | | |

DB 9 EEVIQLQDPF 19

## RESULT 4

E47393

neuropeptide callatostatin 5 - bluebottle fly (Calliphora vomitoria)

C:Species: Calliphora vomitoria

C:Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: E47393

R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.

Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993

A:Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with sequen

A:Reference number: A47393; MUID:93211980; PMID:8460157

A:Accession: E47393

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 &lt;DUV&gt;

A:Cross-references: UNIPROT:P41841

A:Experimental source: whole flies

A&gt;Note: sequence extracted from NCBI backbone (NCBIP:128482)

## Query Match

Best Local Similarity 33.8%; Score 27; DB 2; Length 8;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPPY 11

| | | | |

DB 1 GPPY 4

## RESULT 5

S33609

extensin - maize (fragment)

C:Species: Zea mays (maize)

C:Date: 19-Mar-1997 #sequence\_revision 11-Jun-1999 #text\_change 11-Jun-1999

C:Accession: S33609

R:Murphy, J.M.; Hood, E.E.

Plant Mol. Biol. 21, 885-893, 1993

A:Title: Molecular basis for extensin size heterogeneity in two maize varieties.

A:Reference number: S33609; MUID:93222485; PMID:8467081

A:Accession: S33609

A:Molecule type: protein

A:Residues: 1-17 &lt;MUR&gt;

C:Keywords: glycoprotein; hydroxyproline

## Query Match

Best Local Similarity 33.8%; Score 27; DB 2; Length 17;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GPPY 11

| | | | |

DB 7 GPPY 10

## RESULT 6

S62893

cold-inducible protein, 70K - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1997 #text\_change 09-Jul-2004

C:Accession: S62893

R:Yamashita, M.; Ojima, N.; Sakamoto, T.

FEBS Lett. 382, 261-264, 1996

A:Title: Induction of proteins in response to cold acclimation of rainbow trout cells.

A:Reference number: S62893; MUID:96184500; PMID:8605981

A:Accession: S62893

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-21 &lt;YAM&gt;

A:Cross-references: UNIPROT:Q9PRQ1

## Query Match

Best Local Similarity 33.8%; Score 27; DB 2; Length 21;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 LILQGP 10

| | | | |

DB 2 LILYGP 8

## RESULT 7

S20322

Gluten - wheat

C:Species: Triticum aestivum (common wheat)

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C:Accession: S20322

R:Fukudome, S.; Yoshikawa, M.

FEBS Lett. 296, 107-111, 1992

A:Title: Opioid peptides derived from wheat gluten: their isolation and characterization

A:Reference number: S20322; MUID:92111773; PMID:1309704

A:Accession: S20322

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 &lt;FUK&gt;

A:Cross-references: UNIPROT:Q7MIG0

## Query Match

Best Local Similarity 32.5%; Score 26; DB 2; Length 18;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 PYVSWL 15

| | | | |

DB 9 PYGGWL 14

## RESULT 8

JN0730

hypothetical 1.7K protein - phage SP1

N:Alternate names: hypothetical protein 42.1

C:Species: phage SP1

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 17-Mar-1999

C:Accession: JN0730

R:Chai, S.; Szepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.

Gene 129, 41-49, 1993

A:Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SP1

A:Reference number: JN0729; MUID:93328123; PMID:8335259

A:Accession: JN0730

A:Molecule type: DNA

A:Residues: 1-15 &lt;CHA&gt;

A:Cross-references: EMBL:X65941

## Query Match

Best Local Similarity 31.2%; Score 25; DB 2; Length 15;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LILOPPYVS 13  
:: |||:  
Db 1 MLNNGPPFRS 10

## RESULT 9

A47687  
3-dehydroquininate dehydratase (EC 4.2.1.10) - Amycolatopsis methanolica (fragment)  
C;Species: Amycolatopsis methanolica  
C;Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A47687  
R;Euvierink, G.J.; Hessel, G.I.; Vrijbloed, J.W.; Coggins, J.R.; Dijkhuizen, L.  
J. Gen. Microbiol. 138, 2449-2457, 1992  
A;Title: Purification and characterization of a dual function 3-dehydroquininate dehydratase  
A;Reference number: A47687; MUID:93123995; PMID:1479361  
A;Accession: A47687  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-20 <EU>  
A;Cross-references: UNIPROT:P46380  
A;Experimental source: WV2  
A;Note: sequence extracted from NCBI backbone (NCBIP:122129)  
C;Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 30.0%; Score 24; DB 2; Length 20;  
Best Local Similarity 57.1%; Pred. No. 1.4e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VLILQGP 9  
|: |||:  
Db 3 VFVLNGP 9

## RESULT 10

PH1729  
Ig heavy chain V region (clone GCC-9) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 17-Mar-1999  
C;Accession: PH1729  
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.  
J. Exp. Med. 178, 295-307, 1993  
A;Title: Antigen-driven B cell differentiation in vivo.  
A;Reference number: PH1675; MUID:93301607; PMID:8315385  
A;Accession: PH1729  
A;Molecule type: mRNA  
A;Residues: 1-23 <MCH>  
A;Experimental source: B cell  
A;Note: the authors translated the codon ACA for residue 13 as Ala  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 30.0%; Score 24; DB 2; Length 23;  
Best Local Similarity 60.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15  
|: |||:  
Db 1 YTSWM 5

## RESULT 11

I53401  
monocyte chemotactic protein - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 21-Jul-2000  
C;Accession: I53401  
R;Steenbergen, E.J.; Verhagen, O.J.; van Leeuwen, E.F.; Behrendt, H.; Merle, P.A.; Weste  
Eur. J. Immunol. 24, 900-908, 1994  
A;Title: B precursor acute lymphoblastic leukemia third complementarity-determining region  
fetal life.  
A;Reference number: I53401; MUID:94200227; PMID:8149961  
A;Accession: I53401  
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA  
A;Residues: 1-23 <RES>  
A;Cross-references: GB:S69742; NID:9546303; PIDN:AAD14040.1; PID:94261740  
C;Genetics:  
A;Gene: IGH-VDJ

Query Match 30.0%; Score 24; DB 2; Length 23;  
Best Local Similarity 80.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PPVCS 13  
|||:  
Db 5 PPVCS 9

## RESULT 12

PH1675  
Ig heavy chain V region (clone NP-6-7) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 17-Mar-1999  
C;Accession: PH1675  
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.  
J. Exp. Med. 178, 295-307, 1993  
A;Title: Antigen-driven B cell differentiation in vivo.  
A;Reference number: PH1675; MUID:93301607; PMID:8315385  
A;Accession: PH1675  
A;Molecule type: mRNA  
A;Residues: 1-12 <MCH>  
A;Experimental source: B cell  
A;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 12;  
Best Local Similarity 60.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15  
|: |||:  
Db 1 YTSWV 5

## RESULT 13

JU0356  
cycloleucunin - sagebrush motherwort  
C;Species: Leonurus artemisia (sagebrush motherwort)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: JU0356  
R;Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.  
Chem. Pharm. Bull. 39, 712-715, 1991  
A;Title: Cycloleucunin, a cyclic peptide from Leonuri fructus.  
A;Reference number: JU0356; MUID:91300597; PMID:2070452  
A;Accession: JU0356  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <KIN>  
A;Cross-references: UNIPROT:Q7M1H0

Query Match 28.7%; Score 23; DB 2; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 QGPPY 11  
|: |||:  
Db 8 QYPPY 12

## RESULT 14

PH1676  
Ig heavy chain V region (clone NP-6-5) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 24-Feb-1994 #sequence\_revision 24-Feb-1994 #text\_change 17-Mar-1999  
C;Accession: PH1676  
R;McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.

J. Exp. Med. 178, 295-307, 1993  
A;Title: Antigen-driven B cell differentiation in vivo.  
A;Reference number: PH1675; MUID:93301607; PMID:8315385  
A;Accession: PH1676  
A;Molecule type: mRNA  
A;Residues: 1-13 <MCH>  
A;Experimental source: B cell  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 13;  
Best Local Similarity 60.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YVSWL 15  
| | |  
Db 1 YTSWV 5

## RESULT 15

E37390  
traA protein - Escherichia coli plasmid P307 (fragment)  
C;Species: Escherichia coli  
C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004  
C;Accession: E37390; PQ0480  
R;Graus-Goeldner, A.; Graus, H.; Schlacher, T.; Hoegenauer, G.  
Plasmid 24, 119-131, 1990  
A;Title: The sequences of genes bordering orit in the enterotoxin plasmid P307: comparison  
A;Reference number: A37390; MUID:91261994; PMID:2096398  
A;Accession: E37390  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-13 <GRA>  
A;Cross-references: UNIPROT:Q04220; GB:M62986; NID:G150463; PIDN:AAA25525.1; PID:G150468  
C;Genetics:  
A;Gene: traA  
A;Genome: plasmid  
C;Superfamily: fimbrial protein

Query Match 28.7%; Score 23; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAVLIQ 8  
:|:|:  
Db 2 DAILSVQ 9

Search completed: November 14, 2004, 12:03:14  
Job time : 10.2553 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 37.383 Seconds  
(without alignments)  
215.479 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72

Sequence: 1 SNPSYSAFQVDITD 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	40.3	18	2 Q9QV11	Q9qv11 rattus sp.
2	28	38.9	9	2 Q7RA82	Q7ra82 plasmodium
3	27	37.5	20	2 Q9QV82	Q9qv82 mus sp. s
4	26	36.1	13	2 Q79A22	Q79a22 borrelia bu
5	26	36.1	22	2 Q7M0L1	Q7m0l1 clostridium
6	25	34.7	10	2 Q76MM5	Q76mm5 eurypharynx
7	25	34.7	10	2 BAB87140	Bab87140 euryphary
8	25	34.7	11	2 Q7M154	Q7m154 bacillus th
9	25	34.7	12	2 Q7XB05	Q7xb05 zea mays (m
10	25	34.7	13	2 Q7X761	Q7x761 zea mays (m
11	25	34.7	14	2 F81801	F81801 streptomyc
12	25	34.7	14	2 Q9RS18	Q9rs18 vibrio algi
13	25	34.7	17	2 Q7XB06	Q7xb06 zea mays (m
14	25	34.7	18	2 Q7XB07	Q7xb07 zea mays (m
15	25	34.7	22	2 Q99LZ5	Q99lz5 mus musculu
16	24	33.3	8	2 Q91U19	Q91u19 influenza a
17	24	33.3	8	2 Q91U21	Q91u21 influenza a
18	24	33.3	12	2 Q9S550	Q9s550 streptococc
19	24	33.3	16	2 Q7RGW0	Q7rgw0 plasmodium
20	24	33.3	16	2 Q7RSP0	Q7rsp0 plasmodium
21	24	33.3	16	2 Q9TQV6	Q9tqv6 cryptocolagus
22	24	33.3	20	2 Q9ST52	Q9st52 vicia faba
23	24	33.3	21	2 Q7RK77	Q7rk77 plasmodium
24	24	33.3	21	2 Q8CJ69	Q8cj69 mus musculu
25	24	33.3	22	2 Q7R7E7	Q7r7e7 plasmodium
26	24	33.3	22	2 Q7RLB6	Q7rlb6 plasmodium
27	24	33.3	22	2 Q9QV59	Q9qv59 cavia (guin
28	23.5	32.6	19	2 Q8SEP2	Q8sep2 genista tyr
29	23.5	32.6	19	2 Q8SKW8	Q8skw8 genista val
30	23.5	32.6	19	2 Q8SKX1	Q8skx1 genista gae
31	23.5	32.6	19	2 Q8SKX3	Q8skx3 genista eph

32	23.5	32.6	19	2 Q8SKX5	Q8skx5 genista dor
33	23.5	32.6	19	2 Q8SKX7	Q8skx7 genista dem
34	23.5	32.6	19	2 Q8SKX9	Q8skx9 genista cil
35	23.5	32.6	21	2 Q7SHB6	Q7shb6 neurospora
36	23	31.9	10	2 Q76MK9	Q76mk9 eurypharynx
37	23	31.9	10	2 Q9FS93	Q9fs93 silene pent
38	23	31.9	10	2 BAB87148	Bab87148 euryphary
39	23	31.9	10	2 BAB87156	Bab87156 euryphary
40	23	31.9	10	2 BAB87164	Bab87164 euryphary
41	23	31.9	13	2 Q9FS94	Q9fs94 silene pent
42	23	31.9	13	2 Q9FSA8	Q9fsa8 silene bacc
43	23	31.9	14	2 Q9FS91	Q9fs91 silene sedo
44	23	31.9	14	2 Q9FS95	Q9fs95 silene pent
45	23	31.9	14	2 Q9FSB1	Q9fsb1 silene aega

ALIGNMENTS

RESULT 1  
Q9QV11 PRELIMINARY; PRT; 18 AA.  
AC Q9QV11  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Sucrase-alpha-dextrinase subunit beta, S-D subunit beta  
DE (fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=101118;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=92031479; PubMed=1931964;  
RA Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;  
RT "Structural and functional correlates of sucrase-alpha-dextrinase in  
RT intact brush border membranes.";  
RL Biochemistry 30:10399-10408(1991).  
FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 2122 MW; 68FF1ABAB7B24E49 CRC64;

Query Match 40.3%; Score 29; DB 2; Length 18;  
Best Local Similarity 45.5%; Pred. No. 3.6e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SNPSYSAFQVDI 11  
||| | : : :  
Db 5 SNPISLRLVEV 15

RESULT 2  
Q7RA82 PRELIMINARY; PRT; 9 AA.  
AC Q7RA82  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein (fragment).  
GN Names=PY06620;  
OS Plasmodium Yoelii Yoelii.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=73239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=17XNL;  
RX PubMed=12368865;  
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,  
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
RA Cho J.K., Quackenbush J., Sedegah M., Shoabibi A., Cummings L.M.,

RA Florens L., Yates P.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
 RA Carucci D.J.;  
 RT "Genome sequence and comparative analysis of the model rodent malaria  
 RT parasite *Plasmodium yoelii* yoelii";  
 RL Nature 419:512-519(2002).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABL01002263; EAA18865.1; -.  
 KW Hypothetical protein. 9  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 1001 MW; 4687ASAB476455B7 CRC64;  
 Query Match 38.9%; Score 28; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SNPYS 5  
 DB |||||  
 3 SNPYS 7  
 RESULT 3  
 Q9QVB2 PRELIMINARY; PRT; 20 AA.  
 ID Q9QVB2  
 AC Q9QVB2;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)  
 DE Serine protease (Fragment).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93020730; PubMed=1404084;  
 RA Damjanov A., Damjanov I.;  
 RT "Isolation of serine protease from granulated metrial gland cells of  
 RT mice and rats with lectin from *Dolichos biflorus*.";  
 RL J. Reprod. Fertil. 95:679-684(1992).  
 SQ SEQUENCE 20 AA; 2290 MW; 0A304F61A22C500D CRC64;  
 Query Match 37.5%; Score 27; DB 2; Length 20;  
 Best Local Similarity 71.4%; Pred. No. 9.6e+02;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SNPYSAP 7  
 DB |||||  
 11 SRPYMAF 17  
 RESULT 4  
 Q9A22 PRELIMINARY; PRT; 13 AA.  
 ID Q9A22  
 AC Q9A22;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Moxr protein (Fragment).  
 GN Name=moxr;  
 OS *Borrelia burgdorferi* (Lyme disease spirochete).  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=212;  
 RA Old I.G.;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X95668; CAA64970.1; -.

FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1484 MW; C7C2DF4CFD83A046 CRC64;  
 Query Match 36.1%; Score 26; DB 2; Length 13;  
 Best Local Similarity 40.0%; Pred. No. 9.2e+02;  
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 SAFQVDITID 14  
 DB |||||  
 3 SGFQIDSEVE 12  
 RESULT 5  
 Q7MOL1 PRELIMINARY; PRT; 22 AA.  
 ID Q7MOL1  
 AC Q7MOL1;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Exoenzyme C3 (Fragment).  
 OS *Clostridium botulinum*.  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium.  
 OX NCBI\_TaxID=1491;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=89338716; PubMed=2474453;  
 RA Toratani S., Yokosawa N., Yokosawa H., Ishii S.I., Oguma K.;  
 RT "Immuno-crossreactivity between botulinum neurotoxin type C1 or D and  
 RT exoenzyme C3";  
 RL FEBS Lett. 252:83-87(1989).  
 DR PIR; S05236; S05236.  
 FT NON\_TER 1  
 FT NON\_TER 22  
 SQ SEQUENCE 22 AA; 2449 MW; C3A42F8BE7FF41E3 CRC64;  
 Query Match 36.1%; Score 26; DB 2; Length 22;  
 Best Local Similarity 45.5%; Pred. No. 1.6e+03;  
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 SNPYSAFQVDI 11  
 DB |||||  
 3 SNTYQEFNTNI 13  
 RESULT 6  
 Q76MW5 PRELIMINARY; PRT; 10 AA.  
 ID Q76MW5  
 AC Q76MW5;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE NADH dehydrogenase subunit 2 (Fragment).  
 GN Name=ND2;  
 OS *Eurypharynx pelecyanoides* (pelican eel).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
 OC Eurypharyngidae; Eurypharynx.  
 OX NCBI\_TaxID=55117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22967687; PubMed=12949142;  
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-  
 RT scale gene rearrangements originated within the eels";  
 RL Mol. Biol. Evol. 20:1917-1924(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB046477; BAB87140.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.



KW Mitochondrion.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 34.7%; Score 25; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9  
| | | | |  
DB 2 NPYVMFLV 9

## RESULT 7

BAB871140  
ID BAB871140 PRELIMINARY; PRT; 10 AA.  
AC BAB871140;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, last annotation update)  
DE NADH dehydrogenase subunit 2 (Fragment).  
GN ND2.  
OS Eurypharynx pelecanoidea (pelican eel).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
OC Eurypharyngidae; Eurypharynx.  
OX NCBI\_TaxID=55117;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A;  
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Bels.";  
RL Mol. Biol. Evol. 20:1917-1924(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A;  
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB046477; BAB871140.1;  
KW Mitochondrion.  
FT NON TER 10  
SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 34.7%; Score 25; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9  
| | | | |  
DB 2 NPYVMFLV 9

## RESULT 8

Q7M154  
ID Q7M154 PRELIMINARY; PRT; 11 AA.  
AC Q7M154;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)  
DE Parasporal crystal protein, wax moth-specific (Fragment).  
OS Bacillus thuringiensis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1428;  
RN [1]  
RP SEQUENCE.  
RA Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,  
RA Stepanov V.M.;  
RT "Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity.";  
RN FEBS Lett. 232:249-251(1988).

DR PIR; S00616; S00616.  
FT NON TER 1  
SQ SEQUENCE 11 AA; 1237 MW; C6FF9BD64764444D CRC64;

Query Match 34.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5  
| | | | |  
DB 5 NNPYS 9

## RESULT 9

Q7XB05  
ID Q7XB05 PRELIMINARY; PRT; 12 AA.  
AC Q7XB05;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)  
DE Phytoene synthase 2 (Fragment).  
GN Name-psy2;  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Y-14;  
RX MEDLINE=22779048; PubMed=12897253;  
RA Palaisa K.A., Morgante M., Williams M., Rafaleki A.;  
RT "Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";  
RL Plant Cell 15:1795-1806(2003).  
DR EMBL; AY300568; AAP55307.1;  
FT NON TER 1  
SQ SEQUENCE 12 AA; 1335 MW; 9B1E0AA00869C325 CRC64;

Query Match 34.7%; Score 25; DB 2; Length 12;  
Best Local Similarity 54.5%; Pred. No. 1.3e+03;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11  
| | | | |  
DB 1 SDTVSKFPVDI 11

## RESULT 10

Q7X761  
ID Q7X761 PRELIMINARY; PRT; 13 AA.  
AC Q7X761;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)  
DE Phytoene synthase 2 (Fragment).  
GN Name-psy2;  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W-17, and W-50;  
RX MEDLINE=22779048; PubMed=12897253;  
RA Palaisa K.A., Morgante M., Williams M., Rafaleki A.;  
RT "Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";  
RL Plant Cell 15:1795-1806(2003).  
DR EMBL; AY300592; AAP55331.1;

DR EMBL; AY300599; AAP55338.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1449 MW; 981E0AA05615C325 CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 13;  
 Best Local Similarity 54.5%; Pred. No. 1.4e+03;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SNPYSAFQVDI 11  
 Db 2 SDTVSKFPVDI 12  
 RESULT 11  
 P81801 PRELIMINARY; PRT; 14 AA.  
 ID P81801;  
 AC P81801;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Puromycin-hydrolyzing enzyme (SC 3.-.-) (Fragment).  
 OS Streptomyces morookaensis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1970;  
 RN SEQUENCE.  
 RP STRAIN=JCM4673 / KCC S-0673;  
 RX PubMed=9538199;  
 RA Nishimura M., Matsumoto H., Nakamura A., Sugiyama M.;  
 RT "Purification and characterization of a puromycin-hydrolyzing enzyme from blastocidin S-producing Streptomyces morookaensis.";  
 RL J. Biochem. 123:247-252(1998).  
 RN CHARACTERIZATION, AND FUNCTION.  
 RP Nishimura M., Matsumoto H., Sugiyama M.;  
 RA "Blastocidin S-producing Streptomyces morookaensis possesses an enzyme activity with hydrolyzes puromycin.";  
 RT FEMS Microbiol. Lett. 132:95-100(1995).  
 CC -1- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF TYROSINE MOIETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL TEMPERATURE IS 45 DEGREES CELSIUS.  
 CC -1- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.  
 CC -1- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND N-ETHYLMALIMIDE. PARTIALLY INHIBITED BY COBALT ION.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.  
 DR GO; GO:0004177; F:aminopeptidase activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 KW Aminoamidase; Hydrolase.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 PYSAFQVDI 11  
 Db 5 PYGAWQSPI 13  
 RESULT 12  
 Q9R518 PRELIMINARY; PRT; 14 AA.  
 ID Q9R518;  
 AC Q9R518;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE L-2, 4-diaminobutyrate decarboxylase (Fragment).  
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;

OS Vibrio alginolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=663;  
 RN SEQUENCE.  
 RP MEDLINE=92381494; PubMed=1512577;  
 RX Yamamoto S., Tsuzaki Y., Tougou K., Shinoda S.;  
 RT "Purification and characterization of L-2,4-diaminobutyrate decarboxylase from Acinetobacter calcoaceticus.";  
 RL J. Gen. Microbiol. 138:1461-1465(1992).  
 RQ PIR; B44854; B44854.  
 SQ SEQUENCE 14 AA; 1643 MW; 9F1B13DD35168ABA CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 SAFQVDITI 13  
 Db 2 TAFEVDSNI 10  
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 Q7XB06 PRELIMINARY; PRT; 17 AA.  
 ID Q7XB06;  
 AC Q7XB06;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Phytoene synthase 2 (Fragment).  
 GN Name=psy2;  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=PI587132;  
 RX MEDLINE=22779048; PubMed=12897253;  
 RA Palaia K.A., Morgante M., Williams M., Rafalski A.;  
 RT "Contrasting effects of selection on sequence diversity and linkage disequilibrium at two phytoene synthase loci.";  
 RL Plant Cell 15:1795-1806(2003).  
 DR EMBL; AY300558; AAP55297.1; -.  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1869 MW; 8EB5FAA056459674 CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 17;  
 Best Local Similarity 54.5%; Pred. No. 1.9e+03;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SNPYSAFQVDI 11  
 Db 6 SDTVSKFPVDI 16  
 RESULT 14  
 Q7XB07 PRELIMINARY; PRT; 18 AA.  
 ID Q7XB07;  
 AC Q7XB07;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Phytoene synthase 2 (Fragment).  
 GN Name=psy2;  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;

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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=PI221785;
RX  MEDLINE=22779048; PubMed=12897253;
RA  Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT  "Contrasting effects of selection on sequence diversity and linkage
RL  disequilibrium at two phytoene synthase loci.";
RD  Plant Cell 15:1795-1806(2003).
DR  EMBL; AY300550; AAP55289.1; -.
FT  NON_TER 1
FT  NON_TER 18
FT  NON_TER 18
SQ  SEQUENCE 18 AA; 2000 MW; 8ECB4B9056459674 CRC64;

Query Match      34.7%; Score 25; DB 2; Length 18;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 SNPYSAFQVDI 11
DB  | : | | |
    7 SDTVSKFPVDI 17

RESULT 15
Q99LZ5 PRELIMINARY; PRT; 22 AA.
AC Q99LZ5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE AW125753 protein.
GN Name=Ptpn1; Synonyms=AW125753;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N;
RC TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002154; AA02154.1; -.
DR MGD; MGI:104574; Ptpn1.
SQ SEQUENCE 22 AA; 2559 MW; 34843A007475028A CRC64;

Query Match      34.7%; Score 25; DB 2; Length 22;
Best Local Similarity 44.4%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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QY 6 AFQVDITID 14  
| : | | : |  
DB 12 AYSVDASLD 20

Search completed: November 14, 2004, 12:07:34  
Job time : 37.383 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:04:13 ; Search time 23.3333 Seconds  
(without alignments)  
42.633 Million cell updates/sec

Title: US-09-831-253F-8

Perfect score: 80

Sequence: 1 EAVLILQPPYVSWL 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCRU COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	41.2	14	2	US-08-764-640-39
2	33	41.2	14	3	US-08-973-225-39
3	33	41.2	14	3	US-08-973-225-39
4	33	41.2	14	3	US-08-973-225-216
5	33	41.2	14	3	US-09-244-298A-39
6	33	41.2	14	3	US-09-516-704-39
7	33	41.2	14	4	US-09-549-090-39
8	33	41.2	14	4	US-09-549-090-216
9	33	41.2	14	4	US-09-832-230A-39
10	32	40.0	11	2	US-09-428-082B-67
11	32	40.0	11	2	US-08-856-663-12
12	32	40.0	14	3	US-08-764-640-37
13	32	40.0	14	3	US-08-973-225-37
14	32	40.0	14	3	US-09-244-298A-37
15	32	40.0	14	4	US-09-516-704-37
16	32	40.0	14	4	US-09-549-090-37
17	31	38.8	9	2	US-08-832-230A-37
18	31	38.8	9	3	US-08-725-726D-19
19	31	38.8	9	3	US-09-162-368B-19
20	31	38.8	15	3	US-09-271-970-6
21	31	38.8	15	4	US-09-760-397-6
22	30	37.5	7	1	US-07-807-043B-6
23	30	37.5	9	1	US-08-239-849B-6
24	30	37.5	9	1	US-08-464-318-6
25	30	37.5	9	2	US-08-471-341-6
26	30	37.5	9	2	US-08-461-566-6
27	30	37.5	9	2	US-08-142-368A-6

28	30	37.5	9	3	US-08-967-727-6	Sequence 6, Appli
29	30	37.5	9	3	US-09-064-964-2	Sequence 2, Appli
30	30	37.5	9	3	US-08-037-230D-6	Sequence 6, Appli
31	30	37.5	9	3	US-09-064-174-2	Sequence 2, Appli
32	30	37.5	9	4	US-09-583-850-6	Sequence 6, Appli
33	30	37.5	9	4	US-09-579-197-6	Sequence 6, Appli
34	30	37.5	9	4	US-09-404-026-6	Sequence 6, Appli
35	30	37.5	9	4	US-09-312-464-6	Sequence 6, Appli
36	30	37.5	9	4	US-09-454-204A-66	Sequence 66, Appli
37	30	37.5	9	4	US-09-168-832-2	Sequence 2, Appli
38	30	37.5	9	4	US-08-977-787-7	Sequence 7, Appli
39	30	37.5	13	4	US-08-977-787-8	Sequence 8, Appli
40	29	36.2	11	4	US-09-359-268A-12	Sequence 12, Appli
41	29	36.2	14	4	US-09-149-476-722	Sequence 722, App
42	29	36.2	15	2	US-08-764-640-213	Sequence 213, App
43	29	36.2	15	3	US-09-244-298A-213	Sequence 213, App
44	29	36.2	15	3	US-09-516-704-213	Sequence 213, App
45	29	36.2	15	4	US-09-268-480-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-08-764-640-39  
; Sequence 39, Application US/08764640  
; Patent No. 5869451  
; Patent No. 5869451 5837683  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprence, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; APPLICANT: Yin, Qun  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; TITLE OF INVENTION: RECEPTOR  
; NUMBER OF SEQUENCES: 244  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/764,640  
; FILING DATE: 11-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-764-640-39

Query Match 41.2%; Score 33; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15  
| | | : | | |  
DB 3 LVGPSLMSWL 12

## RESULT 2

US-08-973-225-39  
; Sequence 39, Application US/08973225A  
; Patent No. 6083913

## GENERAL INFORMATION:

APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwiria, Steven E.  
Duffin, David J.  
Gates, Christian  
Haselden, Sherril S.  
Matheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,225A

FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3065USW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 39:

SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:

US-08-973-225-39

Query Match 41.2%; Score 33; DB 3; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15  
| | | : | | |  
DB 3 LVGPSLMSWL 12

## RESULT 3

US-08-973-225-216

; Sequence 216, Application US/08973225A  
; Patent No. 6083913  
; GENERAL INFORMATION:

APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwiria, Steven E.  
Duffin, David J.  
Gates, Christian  
Haselden, Sherril S.  
Matheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,225A

FILING DATE: 04-Dec-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3065USW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 216:

SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 216:

US-08-973-225-216

Query Match 41.2%; Score 33; DB 3; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQGPYPVSWL 15  
| | | : | | |  
DB 3 LVGPSLMSWL 12

## RESULT 4

US-09-244-298A-39

; Sequence 39, Application US/09244298A  
; Patent No. 6121238

## GENERAL INFORMATION:

APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwiria, Steven E.  
Gates, Christian  
Schatz, Peter J.  
Balasubramanian, Palaniappan  
Wagstrom, Christopher R.  
Hendren, Richard W.  
Deprince, Randolph B.  
Poddaturi, Surekha  
Yin, Qun

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
RECEPTOR  
NUMBER OF SEQUENCES: 244  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/244,298A  
FILING DATE: 11-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3281  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-244-298A-39

Query Match 41.2%; Score 33; DB 3; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 LQPPPVSWL 15  
Db 3 LVGPMSWL 12

RESULT 5  
US-09-516-704-39  
Sequence 39, Application US/09516704  
Patent No. 6251864  
GENERAL INFORMATION:  
APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwirla, Steven E.  
Gates, Christian  
Schatz, Peter J.  
Balasubramanian, Palaniappan  
Wagstrom, Christopher R.  
Hendren, Richard W.  
Depincue, Randolph B.  
Poduturi, Surekha  
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A RECEPTOR  
NUMBER OF SEQUENCES: 244  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/516,704  
FILING DATE: 01-Mar-2000  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3281  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-516-704-39  
Query Match 41.2%; Score 33; DB 3; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 6 LQPPPVSWL 15  
Db 3 LVGPMSWL 12  
RESULT 6  
US-09-549-090-39  
Sequence 39, Application US/09549090  
Patent No. 6465430  
GENERAL INFORMATION:  
APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwirla, Steven E.  
Duffin, David J.  
Gates, Christian  
Haselden, Sherril S.  
Mattheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.  
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A THROMBOPOIETIN RECEPTOR  
NUMBER OF SEQUENCES: 232  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/549,090  
FILING DATE: 13-Apr-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/973,225  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3065USW  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear

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; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-549-090-39

Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPYVSWL 15
DB 3 LVGPSLMSWL 12

RESULT 7
US-09-549-090-216
; Sequence 216, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwirla, Steven E.
; Duffin, David J.
; Gates, Christian
; Haseligen, Sherril S.
; Matheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wrighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,090
; FILING DATE: 13-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/973,225
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 216:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-549-090-216

Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPYVSWL 15
DB 3 LVGPSLMSWL 12

; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-832-230A-39
; Sequence 39, Application US/09832230A
; Patent No. 6506362
; GENERAL INFORMATION:
; APPLICANT: Dower, William J. et al
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; RECEPTOR
; NUMBER OF SEQUENCES: 244
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/832,230A
; FILING DATE: 10-Apr-2001
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-832-230A-39

Query Match 41.2%; Score 33; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LQPPYVSWL 15
DB 3 LVGPSLMSWL 12

RESULT 9
US-09-428-082B-67
; Sequence 67, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: TPO-MIMETIC PEPTIDE  
US-09-428-082B-67

Query Match 41.2%; Score 33; DB 4; Length 14;  
Best Local Similarity 60.0%; Pred. No. 48;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 LQPPYVSWL 15  
| | | : | | |  
Db 3 LVGSLMSWL 12

## RESULT 10

US-08-856-663-12  
Sequence 12, Application US/08856663  
Patent No. 5849558

GENERAL INFORMATION:  
APPLICANT: MORGAN, RICHARD  
APPLICANT: CHANG, ZHIYU  
TITLE OF INVENTION: DISCOVERY OF AND  
TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE  
TITLE OF INVENTION: PSPI RESTRICTION ENDONUCLEASE  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: New England Biolabs, Inc.  
STREET: 32 Tozer Road  
CITY: Beverly  
STATE: MA  
COUNTRY: US  
ZIP: 01915

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/856,663  
FILING DATE: 15-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Williams, Gregory D  
REGISTRATION NUMBER: 30901  
REFERENCE/DOCKET NUMBER: NEB-127  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 978-927-5054  
TELEFAX: 978-927-1705  
TELEX:

INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-856-663-12

Query Match 40.0%; Score 32; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 54;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LILQPPY 11  
| | | | |  
Db 2 LILTSPPY 9

## RESULT 11

US-08-764-640-37  
Sequence 37, Application US/08764640  
Patent No. 5869451  
NUMBER OF SEQUENCES: 5837683

GENERAL INFORMATION:  
APPLICANT: Dower, William J.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Gates, Christian  
APPLICANT: Schatz, Peter J.  
APPLICANT: Balasubramanian, Palaniappan  
APPLICANT: Wagstrom, Christopher R.  
APPLICANT: Hendren, Richard W.  
APPLICANT: Deprince, Randolph B.  
APPLICANT: Poduturi, Surekha  
APPLICANT: Yin, Qun  
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
TITLE OF INVENTION: RECEPTOR  
NUMBER OF SEQUENCES: 244  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/764,640  
FILING DATE: 11-DEC-1996  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hrubiec, Robert T.  
REGISTRATION NUMBER: 36,392  
REFERENCE/DOCKET NUMBER: PK3281  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-248-1000  
INFORMATION FOR SEQ ID NO: 37:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-764-640-37

Query Match 40.0%; Score 32; DB 2; Length 14;  
Best Local Similarity 55.6%; Pred. No. 70;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15  
| | | | |  
Db 3 QGPTLTAWL 11

## RESULT 12

US-08-973-225-37  
Sequence 37, Application US/08973225A  
Patent No. 6083913

GENERAL INFORMATION:  
APPLICANT: Dower, William J.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Duffin, David J.  
APPLICANT: Gates, Christian  
APPLICANT: Haselden, Sherril S.  
APPLICANT: Mattheakis, Larry C.  
APPLICANT: Schatz, Peter J.  
APPLICANT: Wagstrom, Christopher R.  
APPLICANT: Wrighton, Nicholas C.  
TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR  
NUMBER OF SEQUENCES: 232

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Glaxo Wellcome
/ STREET: Five Moore Drive, P.O. Box 13398
/ CITY: Research Triangle Park
/ STATE: NC
/ COUNTRY: USA
/ ZIP: 27709
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/973,225A
/ FILING DATE: 04-Dec-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hrubiec, Robert T.
/ REGISTRATION NUMBER: 36,392
/ REFERENCE/DOCKET NUMBER: PK3065USW
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-248-1000
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 37:
/
/ US-08-973-225-37
/
/ Query Match 40.0%; Score 32; DB 3; Length 14;
/ Best Local Similarity 55.8%; Pred. No. 70;
/ Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
/
/ QY 7 QGPPYVSWL 15
/ DB 3 QGPTLTAWL 11
/
/ RESULT 13
/ US-09-244-298A-37
/ Sequence 37, Application US/09244298A
/ Patent No. 6121238
/ GENERAL INFORMATION:
/ APPLICANT: Dower, William J.
/ APPLICANT: Barrett, Ronald W.
/ APPLICANT: Cwirla, Steven E.
/ APPLICANT: Gates, Christian
/ APPLICANT: Schatz, Peter J.
/ APPLICANT: Balasubramanian, Palaniappan
/ APPLICANT: Wagstrom, Christopher R.
/ APPLICANT: Hendren, Richard W.
/ APPLICANT: Deprince, Randolph B.
/ APPLICANT: Podduturi, Surekha
/ APPLICANT: Yin, Qun
/ TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
/ TITLE OF INVENTION: RECEPTOR
/ NUMBER OF SEQUENCES: 244
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Glaxo Wellcome
/ STREET: Five Moore Drive, P.O. Box 13398
/ CITY: Research Triangle Park
/ STATE: NC
/ COUNTRY: USA
/ ZIP: 27709
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/244,298A
/ FILING DATE: 04-Dec-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hrubiec, Robert T.
/ REGISTRATION NUMBER: 36,392
/ REFERENCE/DOCKET NUMBER: PK3065USW
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-248-1000
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 37:
/
/ US-08-973-225-37
/
/ Query Match 40.0%; Score 32; DB 3; Length 14;
/ Best Local Similarity 55.8%; Pred. No. 70;
/ Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
/
/ QY 7 QGPPYVSWL 15
/ DB 3 QGPTLTAWL 11
/
/ RESULT 14
/ US-09-516-704-37
/ Sequence 37, Application US/09516704
/ Patent No. 6251864
/ GENERAL INFORMATION:
/ APPLICANT: Dower, William J.
/ APPLICANT: Barrett, Ronald W.
/ APPLICANT: Cwirla, Steven E.
/ APPLICANT: Gates, Christian
/ APPLICANT: Schatz, Peter J.
/ APPLICANT: Balasubramanian, Palaniappan
/ APPLICANT: Wagstrom, Christopher R.
/ APPLICANT: Hendren, Richard W.
/ APPLICANT: Deprince, Randolph B.
/ APPLICANT: Podduturi, Surekha
/ APPLICANT: Yin, Qun
/ TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
/ TITLE OF INVENTION: RECEPTOR
/ NUMBER OF SEQUENCES: 244
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Glaxo Wellcome
/ STREET: Five Moore Drive, P.O. Box 13398
/ CITY: Research Triangle Park
/ STATE: NC
/ COUNTRY: USA
/ ZIP: 27709
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/516,704
/ FILING DATE: 01-Mar-2000
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hrubiec, Robert T.
/ REGISTRATION NUMBER: 36,392
/ REFERENCE/DOCKET NUMBER: PK3281
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-248-1000
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
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/ FILING DATE: 11-DEC-1996
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hrubiec, Robert T.
/ REGISTRATION NUMBER: 36,392
/ REFERENCE/DOCKET NUMBER: PK3281
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-248-1000
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
/ US-09-244-298A-37
/
/ Query Match 40.0%; Score 32; DB 3; Length 14;
/ Best Local Similarity 55.6%; Pred. No. 70;
/ Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
/
/ QY 7 QGPPYVSWL 15
/ DB 3 QGPTLTAWL 11
/
/ RESULT 14
/ US-09-516-704-37
/ Sequence 37, Application US/09516704
/ Patent No. 6251864
/ GENERAL INFORMATION:
/ APPLICANT: Dower, William J.
/ APPLICANT: Barrett, Ronald W.
/ APPLICANT: Cwirla, Steven E.
/ APPLICANT: Gates, Christian
/ APPLICANT: Schatz, Peter J.
/ APPLICANT: Balasubramanian, Palaniappan
/ APPLICANT: Wagstrom, Christopher R.
/ APPLICANT: Hendren, Richard W.
/ APPLICANT: Deprince, Randolph B.
/ APPLICANT: Podduturi, Surekha
/ APPLICANT: Yin, Qun
/ TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
/ TITLE OF INVENTION: RECEPTOR
/ NUMBER OF SEQUENCES: 244
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Glaxo Wellcome
/ STREET: Five Moore Drive, P.O. Box 13398
/ CITY: Research Triangle Park
/ STATE: NC
/ COUNTRY: USA
/ ZIP: 27709
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/516,704
/ FILING DATE: 01-Mar-2000
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hrubiec, Robert T.
/ REGISTRATION NUMBER: 36,392
/ REFERENCE/DOCKET NUMBER: PK3281
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-248-1000
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
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SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
US-09-516-704-37

Query Match 40.0%; Score 32; DB 3; Length 14;  
Best Local Similarity 55.6%; Pred.No. 70;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15  
|||:|  
Db 3 QGPTLTAWL 11

RESULT 15

US-09-549-090-37  
; Sequence 37, Application US/09549090  
; Patent No. 6465430

GENERAL INFORMATION:

APPLICANT: Dower, William J.  
Barrett, Ronald W.  
Cwirla, Steven E.  
Duffin, David J.  
Gates, Christian  
Haselden, Sherril S.  
Mattheakis, Larry C.  
Schatz, Peter J.  
Wagstrom, Christopher R.  
Wrighton, Nicholas C.

TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
THROMBOPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 232

CORRESPONDENCE ADDRESS:

ADDRESSEE: Glaxo Wellcome  
STREET: Five Moore Drive, P.O. Box 13398  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/549,090

FILING DATE: 13-Apr-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/973,225

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hrubiec, Robert T.

REGISTRATION NUMBER: 36,392

REFERENCE/DOCKET NUMBER: PK3065USW

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-248-1000

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

US-09-549-090-37

Query Match 40.0%; Score 32; DB 4; Length 14;  
Best Local Similarity 55.6%; Pred.No. 70;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QGPPYVSWL 15  
|||:|  
Db 3 QGPTLTAWL 11

Search completed: November 14, 2004, 13:18:38  
Job time : 23.3333 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 13:32:33 ; Search time 22.5 Seconds  
(without alignments)  
59.868 Million cell updates/sec

Title: US-09-831-253F-7  
Perfect score: 72  
Sequence: 1 SNPSAFQVDITID 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2096

Minimum DB seq length: 0  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	34.7	11	2 S00616	parasporal crystal
2	25	34.7	14	2 B44854	L-2,4-diaminobutyr
3	23	31.9	13	2 A54326	glandular kallikre
4	22	30.6	12	2 A61360	vespakinin M - hor
5	22	30.6	14	2 PS0371	hypothetical prote
6	21	29.2	11	2 A40795	glycoprotein H-a -
7	21	29.2	12	2 S36899	ribosomal protein
8	21	29.2	13	2 PC2369	unidentified 85K p
9	20	27.8	9	2 S10784	enamelin i - bovin
10	20	27.8	11	2 PT0229	Ig heavy chain CRD
11	20	27.8	14	2 A59018	MUC1 enhancer bind
12	19	26.4	9	2 S36898	ribosomal protein
13	19	26.4	13	2 G22565	R-phycocerythrin ga
14	19	26.4	14	2 PT0077	proteochondroitin c
15	19	26.4	14	2 A28018	very late antigen-
16	18	25.0	8	2 D47393	neuropeptide calla
17	18	25.0	11	2 PT0250	Ig heavy chain CRD
18	18	25.0	12	2 S70344	amine oxidase (cop
19	18	25.0	13	2 D20907	Ig kappa-1 chain J
20	18	25.0	14	2 S23209	avenin alpha-2 - o
21	18	25.0	14	2 B56884	Pax-QNR, long form
22	17	23.6	8	2 I49404	prealbumin - weste
23	17	23.6	9	2 PQ0914	MHC class I histoc
24	17	23.6	10	2 PA0050	protein QA100052 -
25	17	23.6	10	2 C39111	Ig heavy chain C r
26	17	23.6	10	2 B33710	ornithine decarbox
27	17	23.6	11	2 PS0275	NADH2 dehydrogenas
28	17	23.6	11	2 A34243	H-hyosophorin - Ja
29	17	23.6	12	2 PH0771	T-cell receptor be

30 17 23.6 12 2 PH1462 T-cell receptor be  
31 17 23.6 12 2 PH1457 T-cell receptor be  
32 17 23.6 13 2 S47361 T-cell antigen rec  
33 17 23.6 13 2 S65612 tubulin alpha-chai  
34 17 23.6 14 2 PH1615 Ig H chain V-D-J r  
35 17 23.6 14 2 S07768 soluble hydrogenas  
36 17 23.6 14 2 A61362 bradykinin-like pe  
37 16 22.2 8 2 S71919 alcohol dehydrogen  
38 16 22.2 10 2 PH0916 T-cell receptor be  
39 16 22.2 11 2 A26930 ermG leader peptid  
40 16 22.2 11 2 A61365 phyllokinin - Rohd  
41 16 22.2 12 2 S26546 T-cell receptor be  
42 16 22.2 12 2 PT0257 Ig heavy chain CRD  
43 16 22.2 12 2 A61359 vespakinin x - hor  
44 16 22.2 13 2 A61288 spore proteinase g  
45 16 22.2 13 2 A33660 osteoclast functio

## ALIGNMENTS

## RESULT 1

S00616  
parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleriae)  
N:Alternate names: delta-endotoxin; parasporal crystal protein positive chain  
C:Species: Bacillus thuringiensis  
C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: S00616  
R:Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.  
FEBS Lett. 232, 249-251, 1988  
A:Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxi  
A:Reference number: S00615  
A:Accession: S00616  
A:Molecule type: protein  
A:Residues: 1-11 <CHE>  
A:Cross-references: UNIPROT:Q7M154  
C:Comment: This toxin is effective against the larvae of Galleria melonella (greater wax  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 34.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 2e+02; Mismatches 1; Indels 0; Gaps 0;  
Matches 4; Conservative 1;

QY 1 SNPYS 5  
DB 5 NNPYS 9

## RESULT 2

B44854  
L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.1-) - Vibrio alginolyticus (fragment)  
C:Species: Vibrio alginolyticus  
C:Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: B44854; B41817  
R:Yamamoto, S.; Tsuzaki, Y.; Tougou, K.; Shinoda, S.  
J. Gen. Microbiol. 139, 1461-1465, 1992  
A:Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from A  
A:Reference number: A44854; MUID:92381494; PMID:1512577  
A:Accession: B44854  
A:Molecule type: protein  
A:Residues: 1-14 <YAM>  
A:Cross-references: UNIPROT:Q09R5I8  
A:Note: sequence extracted from NCBI backbone (NCBIP:112332)  
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 34.7%; Score 25; DB 2; Length 14;  
Best Local Similarity 55.6%; Pred. No. 2.6e+02; Mismatches 5; Conservative 2; Indels 0; Gaps 0;  
Matches 5;

QY 5 SAFQVDITII 13  
DB 2 TAFEVDSNI 10

```

RESULT 3
A54326
glandular kallikrein-1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A54326
R:Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.
Mol. Cell. Endocrinol. 76, 181-190, 1991
A:Title: Identification and androgen-regulated expression of two major human glandular k
A:Reference number: A54326; MUID:92324494; PMID:1726490
A:Accession: A54326
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-13 <RIE>
A:Experimental source: prostate
A>Note: sequence extracted from NCBI backbone (NCBIP:108060)

Query Match      31.9%; Score 23; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5
Db 2 SHPYS 6

RESULT 4
A61360
vespakinin M - hornet (Vespa mandarinia)
C:Species: Vespa mandarinia
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: A61360
R:Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 24, 2896-2897, 1976
A:Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ven
A:Reference number: A61360; MUID:77114342; PMID:1017116
A:Accession: A61360
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KIS>
A:Cross-references: UNIPROT:Q7M3T3
C:Superfamily: unassigned animal peptides
C:Keywords: hydroxyproline; venom
F,4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match      30.6%; Score 22; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 7.7e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10
Db 6 FSPFRID 12

RESULT 5
PS0371
hypothetical protein (psaC region) - Synecchococcus sp. (fragment)
C:Species: Synecchococcus sp.
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: PS0371
R:Rhie, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A:Title: The psaC genes of Synecchococcus sp. PCC7002 and Cyanophora paradoxa: cloning an
A:Reference number: JS0694; MUID:92201692; PMID:1551590
A:Accession: PS0371
A:Molecule type: DNA
A:Residues: 1-14 <RHI>
A:Cross-references: GB:M86238; NID:g154574; PIDN:AAA27351.1; PID:g552030

Query Match      30.6%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;

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```

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 FOVDIT 12
Db 4 FKLDVT 9

RESULT 6
A40795
glycoprotein H-a - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 31-Dec-1993
C:Accession: A40795
R:Christie, D.L.; Batchelor, D.C.; Palmer, D.J.
J. Biol. Chem. 266, 15679-15683, 1991
A:Title: Identification of kex2-related proteases in chromaffin granules by partial amin
A:Reference number: A40795; MUID:91340701; PMID:1874725
A:Accession: A40795
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <CHR>
C:Keywords: glycoprotein

Query Match      29.2%; Score 21; DB 2; Length 11;
Best Local Similarity 30.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YSAFQVDITI 13
Db 2 YDINEIDINV 11

RESULT 7
S36899
ribosomal protein S6 - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36899
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36899
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <OHA>
C:Keywords: protein biosynthesis; ribosome

Query Match      29.2%; Score 21; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10
Db 3 PYEIMWVD 10

RESULT 8
PC2369
unidentified 85K protein [imported] - Bacillus cereus (strain ts-4) (fragment)
C:Species: Bacillus cereus
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: PC2369
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulation in
A:Reference number: PC2369; MUID:95218265; PMID:7766022
A:Accession: PC2369
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <MAS>
A:Cross-references: UNIPROT:Q7M0L4

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Query Match 29.2%; Score 21; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAF 7  
DB 8 NPWAKF 13

RESULT 9  
S10784  
enamelin i - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004  
C:Accession: S10784  
R:Strawich, E.; Glimcher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is also  
A:Reference number: S10780; PMID:90336641; PMID:2379503  
A:Accession: S10784  
A:Molecule type: protein  
A:Residues: 1-9 <STR>  
A:Cross-references: UNIPROT:O7M2M7  
C:Keywords: enamel; phosphoprotein

Query Match 27.8%; Score 20; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAF 7  
DB 2 PYDGF 6

RESULT 10  
PT0229  
Ig heavy chain CDR3 region (clone 1-115) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0229  
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; PMID:91108337; PMID:1899102  
A:Accession: PT0229  
A:Molecule type: DNA  
A:Residues: 1-11 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 27.8%; Score 20; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NPY 4  
DB 2 NPY 4

RESULT 11  
A59018  
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 08-May-1998  
C:Accession: A59018  
R:Abel, M.; Smith, C.J.; Larson, C.J.  
Submitted to the Protein Sequence Database, May 1998  
A:Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a bre  
A:Reference number: A59018  
A:Accession: A59018  
A:Molecule type: protein  
A:Residues: 1-14 <ABE>  
A:Experimental source: breast cancer cell line MCF-7

Query Match 27.2%; Score 21; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.3e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAF 7  
DB 8 NPWAKF 13

RESULT 9  
S10784  
enamelin i - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004  
C:Accession: S10784  
R:Strawich, E.; Glimcher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is also  
A:Reference number: S10780; PMID:90336641; PMID:2379503  
A:Accession: S10784  
A:Molecule type: protein  
A:Residues: 1-9 <STR>  
A:Cross-references: UNIPROT:O7M2M7  
C:Keywords: enamel; phosphoprotein

Query Match 27.8%; Score 20; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAF 7  
DB 2 PYDGF 6

RESULT 10  
PT0229  
Ig heavy chain CDR3 region (clone 1-115) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0229  
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; PMID:91108337; PMID:1899102  
A:Accession: PT0229  
A:Molecule type: DNA  
A:Residues: 1-11 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 27.8%; Score 20; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.6e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NPY 4  
DB 2 NPY 4

RESULT 11  
A59018  
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 08-May-1998  
C:Accession: A59018  
R:Abel, M.; Smith, C.J.; Larson, C.J.  
Submitted to the Protein Sequence Database, May 1998  
A:Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a bre  
A:Reference number: A59018  
A:Accession: A59018  
A:Molecule type: protein  
A:Residues: 1-14 <ABE>  
A:Experimental source: breast cancer cell line MCF-7

A:Note: 3-Val was also found  
C:Keywords: DNA binding; heterodimer

Query Match 27.8%; Score 20; DB 2; Length 14;  
Best Local Similarity 33.3%; Pred. No. 2.1e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQV 9  
DB 2 SQIYGSYQI 10

RESULT 12  
S36898  
ribosomal protein S8 - Mycobacterium bovis (fragment)  
C:Species: Mycobacterium bovis  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
C:Accession: S36898  
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
FEBS Lett. 331, 9-14, 1993  
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact  
A:Reference number: S36887; PMID:94009653; PMID:8405418  
A:Accession: S36898  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-9 <OHA>  
C:Keywords: protein biosynthesis; ribosome

Query Match 26.4%; Score 19; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAF 7  
DB 3 TDPIAAF 9

RESULT 13  
G22565  
R-phycoerythrin gamma-B chain - red alga (Gastrocloonium coulteri) (fragment)  
C:Species: Gastrocloonium coulteri  
C:Date: 07-Mar-1998 #sequence\_revision 07-Mar-1998 #text\_change 09-Jul-2004  
C:Accession: G22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; PMID:85182601; PMID:3886644  
A:Accession: G22565  
A:Molecule type: protein  
A:Residues: 1-13 <KLO>  
A:Cross-references: UNIPROT:Q7M268

Query Match 26.4%; Score 19; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 3e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PYSAFQ 8  
DB 7 PQAAFE 12

RESULT 14  
PT0077  
proteochondroitin core protein - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 04-Sep-1998  
C:Accession: PT0077  
R:Marcum, J.A.; Thompson, M.A.  
Biochem. Biophys. Res. Commun. 175, 706-712, 1991  
A:Title: The amino-terminal region of a proteochondroitin core protein, secreted by aorti  
om human bone.  
A:Reference number: PT0077; PMID:91207372; PMID:2018513  
A:Accession: PT0077

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-14 <MAR>  
C;Superfamily: decorin; leucine-rich alpha-2-glycoprotein repeat homology; proteoglycan

Query Match 26.4%; Score 19; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 DITID 14  
| | |  
Db 10 DFTLD 14

RESULT 15  
A28018  
very late antigen-1 alpha chain - human (fragment)  
N;Alternate names: VIA-1 alpha chain  
C;Species: Homo sapiens (man)  
C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 12-May-1994  
C;Accession: A28018  
R;Takada, Y.; Strominger, J.L.; Hemler, M.E.  
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987  
A;Title: The very late antigen family of heterodimers is part of a superfamily of molecu  
A;Reference number: A94151; MUID:87204112; PMID:3033641  
A;Accession: A28018  
A;Molecule type: protein  
A;Residues: 1-14 <TRK>  
C;Keywords: duplication; heterodimer; membrane protein

Query Match 26.4%; Score 19; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 3.2e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 FQVDI 11  
| | |  
Db 1 FNVDV 5

Search completed: November 14, 2004, 13:45:47  
Job time : 22.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:18:48 ; Search time 110.5 Seconds  
(without alignments)  
45.450 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72

Sequence: 1 SNPSAFQVDITID 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 359729299 residues

Total number of hits satisfying chosen parameters: 543373

Minimum DB seq length: 0  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	14	3	AA92951 Transform
2	72	100.0	14	3	AA93099 Transform
3	28	38.9	10	5	ABP47086 Human Bly
4	28	38.9	10	7	ADG97913 scFV VHCD
5	28	38.9	13	3	AA010012 H. pylori
6	28	38.9	13	4	AA086092
7	28	38.9	13	4	AA086060
8	27	37.5	11	7	ADH48572 ATP-depen
9	27	37.5	11	5	ABP46828 Human Bly
10	27	37.5	11	7	ADG97655 scFV VHCD
11	27	37.5	12	7	ADC44449 Endotheli
12	27	37.5	14	2	AA067117 Anti-infl
13	27	37.5	14	3	AA99306 HLA class
14	27	37.5	14	3	AA999201 HLA class
15	27	37.5	14	3	AA999305 HLA class
16	26.5	36.8	10	6	ABP60532 APRIL bin
17	26	36.1	7	2	AA083019 Calcium-i
18	26	36.1	7	2	AA083019 Calcium-i
19	26	36.1	7	2	AA013164 Ca-indepe
20	26	36.1	7	2	AA017850 Cytosolic
21	26	36.1	7	2	AA081826 Phospholi
22	26	36.1	7	5	AB082216 Calcium i
23	26	36.1	7	8	AD080708 Cotton wi
24	26	36.1	9	2	AA55426 HLA bindi
25	26	36.1	9	2	AA55528 HLA bindi

ALIGNMENTS

RESULT 1

AA92951  
ID AA92951 standard; peptide; 14 AA.

XX AC AA92951;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide #7.

XX KW Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;  
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Homo sapiens.

XX PN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
XX Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betaf,  
XX useful for treatment of liver disease, especially cirrhosis, are partial  
XX sequences of the factor or its receptors.

XX Claim 8; Page 82; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
XX of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in  
XX vivo which have partial amino acid sequences identical, or similar, with  
XX those of TGF-b1 and/or its receptors. Peptides AA92945-93133 represent  
XX examples of the peptides of the invention. The peptides act by  
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
XX they are inhibitors of stimulation of collagen synthesis in liver cells  
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the  
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or  
XX expression systems) encoding the peptides are used for treatment of liver  
XX disease, specifically cirrhosis

AA088035 CD66, pept  
AA021773 MHC bindi  
AA999258 HLA class  
AA999308 HLA class  
AA068251 Human G-p  
AA035820 Hepatitis  
AA035821 Hepatitis  
AA049445 Human leu  
AA086080 H. pylori  
AA086048 H. pylori  
AA018651 Human can  
AA017659 Human can  
AA007147 Human can  
AA007334 Human can  
AA018452 Human can  
AA0494198 Mouse HUI  
AA096234 Human com  
AA017761 Human can  
AA018701 Human can  
AA017498 Human can

```
XX SQ Sequence 14 AA;
    Query Match      100.0%; Score 72; DB 3; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1.2e-06;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPSAFQVDITID 14
Db 1 SNPSAFQVDITID 14

RESULT 2
AAY93099
ID AAY93099 standard; peptide; 14 AA.
XX AAY93099;
AC
XX
XX 08-NOV-2000 (first entry)
XX Transforming growth factor inhibitory peptide P145.
DE
XX
XX Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Homo sapiens.
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borras Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor beta1,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Disclosure; Page 31; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
XX vivo which have partial amino acid sequences identical or similar, with
XX those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis
XX
XX SQ Sequence 14 AA;
    Query Match      100.0%; Score 72; DB 3; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1.2e-06;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPSAFQVDITID 14
Db 1 SNPSAFQVDITID 14

RESULT 3
ADG97913
```

---

```
ABP47086
ID ABP47086 standard; peptide; 10 AA.
XX
XX AC ABP47086;
XX
XX DT 19-AUG-2002 (first entry)
XX
XX DE Human BlyS binding scFv VH CDR3 SEQ ID 3097.
XX
XX KW BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX OS Homo sapiens.
XX
XX PN WO200202641-A1.
XX
XX PD 10-JAN-2002.
XX
XX PF 15-JUN-2001; 2001WO-US019110.
XX
XX PR 16-JUN-2000; 2000US-0212210P.
XX
XX PR 17-OCT-2000; 2000US-0240816P.
XX
XX PR 16-MAR-2001; 2001US-0276248P.
XX
XX PR 21-MAR-2001; 2001US-0277379P.
XX
XX PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX
XX WPI; 2002-114799/15.
XX
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX and so may be used to detect and quantitate the presence of BlyS in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of BlyS. They may also be
XX administered to treat diseases associated with aberrant BlyS expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX
XX SQ Sequence 10 AA;
    Query Match      38.9%; Score 28; DB 5; Length 10;
    Best Local Similarity 50.0%; Pred. No. 1.8e+02;
    Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9
Db 3 SPYDAFDI 10

RESULT 4
ADG97913
```

ID ADG97913 standard; peptide; 10 AA.  
 AC ADG97913;  
 XX  
 DT  
 XX  
 DE 11-MAR-2004 (first entry)  
 XX  
 DE scFV VHCDR3 peptide that immunospecifically binds BlyS SeqID 3097.  
 XX  
 KW antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;  
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;  
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003055979-A2.  
 XX  
 PD 10-JUL-2003.  
 XX  
 PF 14-NOV-2002; 2002WO-US036496.  
 XX  
 PR 16-NOV-2001; 2001US-0331469P.  
 PR 19-DEC-2001; 2001US-0340817P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;  
 XX  
 DR WPI; 2003-505530/47.  
 XX  
 PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
 PT (BlyS), useful for detecting and treating diseases or disorders e.g.  
 PT rheumatoid arthritis, asthma and leukemia.  
 XX  
 PS Example 1; SEQ ID NO 3097; 394pp; English.  
 XX  
 CC This invention relates to novel antibodies that immunospecifically bind  
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to  
 CC chromosome 13q34 and encodes a protein that is a member of the tumour  
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
 CC proliferation and differentiation. Specifically, it refers to single  
 CC chain antibody molecules (scFvs) derived, preferably, from the variable  
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
 CC fragment thereof, of either human, murine, rat or monkey BLYS. The  
 CC present invention refers to the use of such antibodies in various methods  
 CC for the detection, diagnosis and prognosis of diseases related to the  
 CC aberrant expression or inappropriate function of BlyS or its receptor. As  
 CC such, these compositions are useful for identifying immune disorders  
 CC including myasthenia gravis and multiple sclerosis, inflammatory  
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
 CC lymphoma. Accordingly, they can be described as exhibiting various  
 CC activities such as antirheumatic, antiarthritic, neuroprotective,  
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This  
 CC peptide sequence is a single chain antibody variable heavy CDR3 peptide  
 CC that immunospecifically binds BlyS of the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 38.9%; Score 28; DB 7; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 NPYSAFQV 9  
 :|||:  
 DB 3 SPYDAFDI 10  
 RESULT 5  
 AAB10012  
 ID AAB10012 standard; protein; 13 AA.  
 XX

AC AAB10012;  
 XX  
 DT 01-NOV-2000 (first entry)  
 XX  
 DE H. pylori beta-urease-binding antibody heavy chain CDR3 protein #2.  
 XX  
 KW Acid-resistant microorganism; detection; faecal; intestine; infection;  
 KW monoclonal antibody; heavy chain; complementarity determining region;  
 KW CDR; beta-urease.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200026671-A1.  
 XX  
 PD 11-MAY-2000.  
 XX  
 PF 29-OCT-1999; 99WO-EP008212.  
 XX  
 PR 29-OCT-1998; 98EP-00120517.  
 PR 06-NOV-1998; 98EP-00120687.  
 XX  
 PA (CONN-) CONNEX GMBH.  
 XX  
 PI Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;  
 PI Ringels A;  
 XX  
 DR WPI; 2000-365747/31.  
 DR N-PSDB; AAA40168.  
 XX  
 PT Detecting infection by acid-fast microbes for diagnosis of Helicobacter  
 PT pylori, comprises reacting a fecal sample with two binding reagents for  
 PT antigens that survive intestinal passage.  
 XX  
 PS Claim 26; Page 22; 84pp; German.  
 XX  
 CC This invention describes a novel method for the detection of a mammalian  
 CC infection by an acid-resistant microorganism (A) by treating a faecal  
 CC sample with at least two different monoclonal antibodies (MAB) for their  
 CC fragments or derivatives) or aptamers (collectively (I)) and detecting  
 CC formation of a complex (C) between (I) and the corresponding antigen of  
 CC (A). The first and second (I) bind to epitopes of different antigens  
 CC (Ag). These epitopes are present, after passage through the intestines,  
 CC in at least some mammals, and have either: (i) their native structure; or  
 CC (ii) a structure against which an antibody is produced by an animal  
 CC infected or immunized with (A), or its extract, lysate, derived protein  
 CC or fragment, or with a synthetic peptide. Practically all mammals display  
 CC at least one of the specified epitopes. The method is used to detect  
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,  
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M.  
 CC tuberculosis, C. jejuni and C. pylori. (I) may also be used  
 CC therapeutically. The method is direct and non-invasive, and provides an  
 CC inexpensive and easily standardizable diagnosis, despite possible  
 CC degradation of antigens during passage through the intestines. This  
 CC sequence represents a fragment of a H. pylori beta-urease-binding  
 CC antibody heavy chain complementarity determining region CDR3 which is  
 CC used to illustrate the method of the invention  
 XX  
 SQ Sequence 13 AA;  
 Query Match 38.9%; Score 28; DB 3; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SNPYS 5  
 :|||:  
 DB 6 SNPYS 10  
 RESULT 6  
 AAB86092  
 ID AAB86092 standard; peptide; 13 AA.  
 XX  
 AC AAB86092;

XX 17-JUL-2001 (first entry)  
 XX H. pylori beta-urease derived antibody light chain CDR3 #1.  
 DE Catalase; beta-urease; antibody; antigen; detection; infection; epitope;  
 XX acid-resistant microorganism; complementarity determining region; CDR;  
 KW feces; heavy chain; light chain.  
 KW Unidentified.  
 XX WO200127612-A2.  
 XX 19-APR-2001.  
 XX 12-OCT-2000; 2000WO-EP010057.  
 XX 12-OCT-1999; 99EP-00120351.  
 PR 16-MAR-2000; 2000EP-00105592.  
 PR 31-MAR-2000; 2000EP-00107028.  
 PR 10-MAY-2000; 2000EP-00110110.  
 XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.  
 PA Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;  
 XX WPI; 2001-282086/29.  
 DR N-PSDB; AAF88119.  
 XX Detecting infections by acid-resistant microorganisms, particularly for  
 PT diagnosing Helicobacter pylori, comprises immunochromatographic detection  
 PT of antigen in feces.  
 XX Claim 27; Page 27; 90pp; German.  
 XX This invention describes a novel method for detecting infection by an  
 CC acid-resistant microorganism (A), in a mammal, using  
 CC immunochromatography. The method is used to diagnose infection by an acid  
 CC resistant microorganism (A), in a mammal, such as Helicobacter,  
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),  
 CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,  
 CC inexpensive and non-invasive, and may indicate the stage of infection. A  
 CC test strip used in the method may include a filter to eliminate particles  
 CC present in the sample and only a single receptor provides a reasonably  
 CC secure diagnosis, with specificity and selectivity improved by detecting  
 CC several epitopes (of catalase) or different antigens (catalase and beta-  
 CC urease). The method can be automated. This sequence represents a  
 CC complementarity determining region (CDR) from an antibody raised against  
 CC the H. pylori catalase or beta-urease antigen which is used to illustrate  
 CC the method of the invention  
 XX Sequence 13 AA;  
 SQ Query Match 38.9%; Score 28; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SNPS 5  
 Db |||||  
 6 SNPS 10  
 RESULT 7  
 ID AAB86060 standard; peptide; 13 AA.  
 XX AAB86060;  
 XX 17-JUL-2001 (first entry)  
 DT H. pylori beta-urease derived antibody light chain CDR3 #1.  
 DE Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;  
 XX

KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;  
 KW antibacterial; complementarity determining region.  
 XX Unidentified.  
 OS WO200127613-A2.  
 XX 19-APR-2001.  
 XX 12-OCT-2000; 2000WO-EP010058.  
 XX 12-OCT-1999; 99EP-00120351.  
 PR 16-MAR-2000; 2000EP-00105592.  
 PR 31-MAR-2000; 2000EP-00107028.  
 PR 10-MAY-2000; 2000EP-00110110.  
 XX (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.  
 PA Reiter C, Cullmann G, Heppner P, Ringels A, Mueller H, Haindl E;  
 XX WPI; 2001-282087/29.  
 DR N-PSDB; AAF88062.  
 XX Detecting infections by acid-resistant microorganisms, particularly for  
 PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal  
 PT sample.  
 XX Claim 23; Page 17; 89pp; German.  
 XX This invention describes a novel method for detecting, in a mammal,  
 CC infection by an acid-resistant microorganism (A) which comprises reacting  
 CC a fecal sample with: (i) a receptor (R) such that a complex is formed  
 CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part  
 CC complex is formed with Ag, and the formation of a complex detected. R are  
 CC specific for an Ag which, after passage through the intestines, at least  
 CC in some mammals, retains a native (or corresponding) structure against  
 CC which the mammal produces antibodies (when immunized or infected with  
 CC (A), or its extracts, lysates or derived proteins (or fragments) or  
 CC synthetic peptides). The products of the invention have antibacterial  
 CC activity. The method is used to diagnose infection by Helicobacter,  
 CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),  
 CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the  
 CC progress of treatment. Receptors, particularly antibodies, directed  
 CC against Ag can be used therapeutically for treatment of infections. The  
 CC method requires only one R to provide a reasonably secure diagnosis  
 CC (although use of two R improves sensitivity), so is relatively  
 CC inexpensive and more easily standardized. Also it is direct, non-  
 CC invasive, suitable for automation and may indicate the stage of an  
 CC infection. This sequence represents a complementarity determining region  
 CC (CDR) from an antibody generated against a Helicobacter pylori antigen  
 CC (catalase or beta-urease) which is used to illustrate the method of the  
 CC invention  
 XX Sequence 13 AA;  
 SQ Query Match 38.9%; Score 28; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-02;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SNPS 5  
 Db |||||  
 6 SNPS 10  
 RESULT 8  
 ID ADH48572 standard; peptide; 10 AA.  
 XX ADH48572;  
 XX 25-MAR-2004 (first entry)  
 DT ATP-dependent Clp proteinase (clpL) epitopic peptide #SEQ ID 12.  
 XX

XX Antimicrobial; immunostimulant; gene therapy;  
KW ATP-dependent Clp proteinase; proline dipeptidase; chorismate mutase;  
KW aminotransferase; serine hydroxymethyltransferase;  
KW O-acetylserine sulphydrolase B; translocase; tRNA methyltransferase;  
KW 3-dehydroquinate synthase.  
XX Staphylococcus aureus.  
OS WO2003025005-A2.  
XX 27-MAR-2003.  
PD 20-SEP-2002; 2002WO-CA001426.  
XX 21-SEP-2001; 2001US-0324135P.  
PR 21-SEP-2001; 2001US-0324139P.  
PR 27-SEP-2001; 2001US-0325332P.  
PR 28-SEP-2001; 2001US-0325836P.  
PR 25-OCT-2001; 2001US-0338235P.  
PR 25-OCT-2001; 2001US-0343758P.  
PR 26-OCT-2001; 2001US-0340531P.  
PR 30-OCT-2001; 2001US-0340945P.  
PR 06-NOV-2001; 2001US-0333281P.  
PR 31-JUL-2002; 2002US-0399926P.  
XX (AFFI-) AFFINIUM PHARM INC.  
PA Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;  
PI Canadien V, Domagala M, Kanagarajah D, Li Q, Mansoury K, Necakov S;  
PI Netherly K, Ng I, Pinder B, Sheldrick B, Vallee F, Viola C;  
PI Wrezel O;  
XX WPI; 2003-371794/35.  
DR New crystallized recombinant polypeptides and polynucleotides encoding  
XX them, useful in developing antimicrobial agents for treating or  
PT preventing infection or contamination, or for inducing an immunological  
PT response.  
XX Disclosure; SEQ ID NO 12; 172pp; English.  
PS The invention relates to a novel crystallised recombinant polypeptide  
XX (I). The polypeptide of the invention has at least one biological  
CC activity of ATP-dependent Clp proteinase, proline dipeptidase, chorismate  
CC mutase homology, branched-chain amino acid aminotransferase or serine  
CC hydroxymethyltransferase from Staphylococcus aureus, O-acetylserine  
CC sulhydrylase B from Escherichia coli, preprotein translocase secretion  
CC protein or tRNA methyltransferase from Helicobacter pylori, or 3-  
CC dehydroquinate synthase from Streptococcus pneumoniae. Nucleic acids  
CC encoding polypeptides of the invention are useful in antisense therapy,  
CC as diagnostic agents to detect the presence of the target DNA or RNA  
CC sequences to which the specifically bind, and in producing recombinant  
CC polypeptides. The polypeptides are useful for producing specific  
CC antibodies which protect against invasion of bacteria, in identifying  
CC compounds which modulate the action of the polypeptides, and in  
CC developing antimicrobial agents for treating or preventing infection or  
CC contamination. The nucleic acids and polypeptides may also be used for  
CC inducing an immunological response. Sequences given in ADH48561-ADH48641  
CC represent polypeptides and polynucleotides that are identified in the  
CC scope of the invention as microbial target sequences, peptide fragments  
CC of the proteins, and primers used for their amplification.  
XX Sequence 10 AA;  
SQ

Query Match 37.5%; Score 27; DB 7; Length 10;  
Best Local Similarity 55.6%; Pred. No. 2.8e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
QY 2 NPYSAFQVD 10  
DB 2 NPYSVILFD 10

RESULT 9  
ABP46828  
ID ABP46828 standard; peptide; 11 AA.  
XX AC ABP46828;  
XX 19-AUG-2002 (first entry)  
XX Human Blys binding scFv VH CDR3 SEQ ID 2839.  
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;  
KW antiAIDS; vaccine; immune; autoimmune disorder; immunodeficiency;  
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
KW common variable immunodeficiency; acquired immunodeficiency syndrome.  
XX Homo sapiens.  
OS WO200202641-A1.  
PN 10-JAN-2002.  
PD 15-JUN-2001; 2001WO-US019110.  
PF 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.  
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
PI WPI; 2002-114799/15.  
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the  
PT diagnosis and treatment of cancers and immune disorders.  
PT Claim 2; Page 3062; 3148pp; English.  
XX This invention describes novel antibodies that immunospecifically bind to  
CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the  
CC tumour necrosis factor (TNF) super family and induces B cell  
CC proliferation and differentiation. The antibodies of the invention have  
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
CC antirheumatic and antiAIDS activity and can be used in vaccines to  
CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
CC and so may be used to detect and quantitate the presence of Blys in  
CC biological samples and may be used in this way to diagnose disease  
CC associated with aberrant expression of Blys. They may also be  
CC administered to treat diseases associated with aberrant Blys expression  
CC and activity such as cancer, immune, and autoimmune disorders and  
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,  
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX Sequence 11 AA;  
SQ

Query Match 37.5%; Score 27; DB 5; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 PYSAFQV 9  
DB 5 PYDAFDI 11

RESULT 10  
ADG97655  
ID ADG97655 standard; peptide; 11 AA.  
XX  
AC ADG97655;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE scFV VHCDR3 peptide that immunospecifically binds Blys SeqID 2839.  
XX  
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;  
KW B cell proliferation; differentiation; scFv; myasthenia gravis;  
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;  
KW antiinflammatory; antiaesthatic; antiallergic; cytostatic.  
XX  
OS Unidentified.  
XX  
PN WO2003055979-A2.  
XX  
PD 10-JUL-2003.  
XX  
PF 14-NOV-2002; 2002WO-US036496.  
XX  
PR 16-NOV-2001; 2001US-0331469P.  
PR 19-DEC-2001; 2001US-0340817P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;  
XX  
DR WPI; 2003-505530/47.  
XX  
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
PT (Blys), useful for detecting and treating diseases or disorders e.g.  
PT rheumatoid arthritis, asthma and leukemia.  
XX  
PS Example 1; SEQ ID NO 2839; 394pp; English.  
XX  
CC This invention relates to novel antibodies that immunospecifically bind  
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to  
CC chromosome 13q34 and encodes a protein that is a member of the tumour  
CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
CC proliferation and differentiation. Specifically, it refers to single  
CC chain antibody molecules (scFvs) derived, preferably, from the variable  
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
CC fragment thereof, of either human, murine, rat or monkey Blys. The  
CC present invention refers to the use of such antibodies in various methods  
CC for the detection, diagnosis and prognosis of diseases related to the  
CC aberrant expression or inappropriate function of Blys or its receptor. As  
CC such, these compositions are useful for identifying immune disorders  
CC including myasthenia gravis and multiple sclerosis, inflammatory  
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
CC lymphoma. Accordingly, they can be described as exhibiting various  
CC activities such as antirheumatic, antiallergic and neuroprotective.  
CC antiinflammatory, antiaesthatic, antiallergic and cytostatic. This  
CC peptide sequence is a single chain antibody variable heavy CDR3 peptide  
CC that immunospecifically binds Blys of the invention.  
XX  
SQ Sequence 11 AA;  
Query Match 37.5%; Score 27; DB 7; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 PYSAFQV 9  
DB 5 PYDAFDI 11  
RESULT 11  
ADG44449  
ID ADG44449 standard; peptide; 12 AA.  
XX  
AC ADG44449;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Endothelial cell binding peptide SEQ ID NO:177.  
XX  
KW endothelial cell binding protein; EGBP; anti-tumour; cytostatic;  
KW vasotropic; antiporiatic; dermatological; ophthalmological;  
KW antidiabetic; antiarthritic; vulnary; antileucemic; antineoplastic;  
KW antibacterial; gynaecological; angiogenesis.  
XX  
OS Synthetic.  
XX  
PN WO2003037172-A2.  
XX  
PD 08-MAY-2003.  
XX  
PF 01-NOV-2002; 2002WO-US035258.  
XX  
PR 01-NOV-2001; 2001US-0334822P.  
XX  
PA (GPCB-) GPC BIOTECH INC.  
XX  
PI Gyuris J, Lamphere L, Morris AJ, Tsaion K;  
XX  
DR WPI; 2003-482072/45.  
XX  
PT Novel synthetic or recombinant polypeptide useful for promoting, reducing  
PT proliferation and/or migration of endothelial cells, and for modulating  
PT angiogenesis, has endothelial cell binding protein sequences.  
XX  
PS Claim 3; SEQ ID NO 177; 126pp; English.  
XX  
CC The invention relates to a novel isolated, synthetic or recombinant  
CC peptide or polypeptide which includes one or more endothelial cell  
CC binding protein (EGBP) sequences. A peptide of the invention has anti-  
CC tumour, cytostatic, vasotropic, antiporiatic, dermatological,  
CC ophthalmological, antidiabetic, antiarthritic, vulnary, antileucemic,  
CC antineoplastic, antibacterial, and gynaecological activity. The peptide  
CC is useful for promoting, reducing the proliferation and/or migration of  
CC endothelial cells, by treating the cells with an EGBP agonist, which is  
CC preferably the peptide, to promote proliferation and/or migration of the  
CC treated cells, and for reducing or promoting angiogenesis, by treating  
CC the cells with an EGBP antagonist, which is preferably the peptide of the  
CC invention. A peptide of the invention is also useful for manufacturing a  
CC medicament for promoting angiogenesis, by admixing an EGBP agonist or  
CC EGBP antagonist to promote or reduce angiogenesis at one or more sites in  
CC a treated mammal. The medicament is useful for promoting or reducing  
CC angiogenesis. EGBP sequences are useful to alter the infectivity spectrum  
CC of a viral particle. The present sequence represents an EGBP of the  
CC invention.  
XX  
SQ Sequence 12 AA;  
Query Match 37.5%; Score 27; DB 7; Length 12;  
Best Local Similarity 83.3%; Pred. No. 3.4e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SNFYSA 6  
DB 1 SNFWSA 6  
RESULT 12  
AAR67117  
ID AAR67117 standard; peptide; 14 AA.  
XX  
AC AAR67117;  
XX  
DT 25-MAR-2003 (revised)  
DT 30-JUN-1995 (first entry)



KW allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;  
 KW glomerulonephritis; food hypersensitivity; malaria.  
 XX Unidentified.  
 XX WO9961916-A1.  
 XX 02-DEC-1999.  
 XX 28-MAY-1999; 99WO-US012066.  
 XX 29-MAY-1998; 98US-0087192P.  
 XX (EPIM-) EPIMMUNE INC.  
 XX Sette A, Southwood S, Sidney J;  
 XX WPI; 2000-097143/08.  
 XX New compositions containing immunogenic peptide epitopes for various HLA  
 XX class II DR molecules useful for inducing helper T cell response.  
 XX Claim 1; Page 46; 60pp; English.

CC The present invention relates to a new pharmaceutical composition  
 CC comprising a unit dose form of a peptide, or analogue, comprising an  
 CC epitope selected from those represented by peptides AAY9812-Y99339 which  
 CC are derived from various antigens for various human leucocyte antigen  
 CC class DR molecules, representative of the world wide population. The  
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
 CC helper T cell response. The pharmaceutical focuses the immune response  
 CC towards selected determinants and could therefore be used in cases of  
 CC chronic viral diseases and cancer. Examples of diseases that can be  
 CC treated using the peptide containing pharmaceutical include autoimmune  
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
 CC gravis), allograft rejection, allergies, lyme disease, hepatitis, post-  
 CC streptococcal endocarditis or glomerulonephritis and food  
 CC hypersensitivities. The peptide epitopes can be used to enhance immune  
 CC responses against other immunogens administered with the peptides.  
 CC Diseases which can be treated using immunogenic mixtures include prostate  
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
 CC used to make monoclonal antibodies useful as potential diagnostic or  
 CC therapeutic agents. The peptides may also be useful as diagnostic  
 CC reagents, for example, to determine the susceptibility of an individual  
 CC to a treatment regimen. Also, the peptides may be used to predict which  
 CC individuals will be at substantial risk of developing chronic infection.  
 CC The selection of appropriate T and B cell epitopes should allow the  
 CC development of epitope based vaccines particularly towards conserved  
 CC epitopes of pathogens which are characterized by high sequence  
 CC variability such as HIV, HCV and Malaria

XX Sequence 14 AA;

Query Match 37.5%; Score 27; DB 3; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDITIT 13  
 DB 1 YAAFSQTTTL 10

RESULT 15

AY99305  
 ID AAY99305 standard; peptide; 14 AA.

XX AAY99305;

XX 07-AUG-2000 (first entry)

DE HLA class II binding antigen epitope peptide #494.

XX Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical;  
 KW immune response; chronic viral disease; cancer; autoimmune disease;  
 KW rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS;  
 KW allograft rejection; allergy; lyme disease; hepatitis; prostate cancer;  
 KW glomerulonephritis; food hypersensitivity; malaria.  
 XX Unidentified.  
 XX WO9961916-A1.  
 XX 02-DEC-1999.  
 XX 28-MAY-1999; 99WO-US012066.  
 XX 29-MAY-1998; 98US-0087192P.  
 XX (EPIM-) EPIMMUNE INC.  
 XX Sette A, Southwood S, Sidney J;  
 XX WPI; 2000-097143/08.

PT New compositions containing immunogenic peptide epitopes for various HLA  
 PT class II DR molecules useful for inducing helper T cell response.  
 PS Claim 1; Page 48; 60pp; English.

CC The present invention relates to a new pharmaceutical composition  
 CC comprising a unit dose form of a peptide, or analogue, comprising an  
 CC epitope selected from those represented by peptides AAY9812-Y99339 which  
 CC are derived from various antigens for various human leucocyte antigen  
 CC class DR molecules, representative of the world wide population. The  
 CC peptide/analogue binds to an HLA class II molecule at an IC-50 of less  
 CC than or equal to 1,000 nM. The pharmaceutical can be used to induce a  
 CC helper T cell response. The pharmaceutical focuses the immune response  
 CC towards selected determinants and could therefore be used in cases of  
 CC chronic viral diseases and cancer. Examples of diseases that can be  
 CC treated using the peptide containing pharmaceutical include autoimmune  
 CC diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia  
 CC gravis), allograft rejection, allergies, lyme disease, hepatitis, post-  
 CC streptococcal endocarditis or glomerulonephritis and food  
 CC hypersensitivities. The peptide epitopes can be used to enhance immune  
 CC responses against other immunogens administered with the peptides.  
 CC Diseases which can be treated using immunogenic mixtures include prostate  
 CC cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical  
 CC carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be  
 CC used to make monoclonal antibodies useful as potential diagnostic or  
 CC therapeutic agents. The peptides may also be useful as diagnostic  
 CC reagents, for example, to determine the susceptibility of an individual  
 CC to a treatment regimen. Also, the peptides may be used to predict which  
 CC individuals will be at substantial risk of developing chronic infection.  
 CC The selection of appropriate T and B cell epitopes should allow the  
 CC development of epitope based vaccines particularly towards conserved  
 CC epitopes of pathogens which are characterized by high sequence  
 CC variability such as HIV, HCV and Malaria

XX Sequence 14 AA;

Query Match 37.5%; Score 27; DB 3; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDITIT 13  
 DB 1 YAAFSQTTTL 10

Search completed: November 14, 2004, 13:44:59  
 Job time : 112.5 secs



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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:17:28 ; Search time 122.5 Seconds  
(without alignments)  
65.757 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72

Sequence: 1 SNPSAFQVDITID 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 6764

Minimum DB seq length: 0

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_eprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	28	38.9	9	2 Q7RA82	Q7ra82 plasmodium
2	26	36.1	13	2 Q79A22	Q79a22 borrelia bu
3	25	34.7	10	2 Q76NM5	Q76nm5 eurypharynx
4	25	34.7	10	2 BAB87140	Bab87140 euryphary
5	25	34.7	11	2 Q7M154	Q7m154 bacillus th
6	25	34.7	12	2 Q7XB05	Q7xb05 zea mays (m
7	25	34.7	13	2 Q7X761	Q7x761 zea mays (m
8	25	34.7	14	2 P81801	P81801 streptomyce
9	25	34.7	14	2 Q9R5I8	Q9r5i8 vibrio algi
10	24	33.3	8	2 Q9IU19	Q9iu19 influenza a
11	24	33.3	8	2 Q9IU21	Q9iu21 influenza a
12	24	33.3	12	2 Q9S550	Q9s550 streptococ
13	23	31.9	10	2 Q76MK9	Q76mk9 eurypharynx
14	23	31.9	10	2 Q9FS93	Q9fs93 silene pent
15	23	31.9	10	2 BAB87148	Bab87148 euryphary
16	23	31.9	10	2 BAB87156	Bab87156 euryphary
17	23	31.9	10	2 BAB87164	Bab87164 euryphary
18	23	31.9	13	2 Q9FS94	Q9fs94 silene pent
19	23	31.9	13	2 Q9FSA8	Q9fsa8 silene bacc
20	23	31.9	14	2 Q9FS91	Q9fs91 silene sedo
21	23	31.9	14	2 Q9FS95	Q9fs95 silene pent
22	23	31.9	14	2 Q9RSB1	Q9rsb1 silene aega
23	22	30.6	8	1 ALL3_CYDPO	P82154 cydia pomon
24	22	30.6	12	1 VESP_VESMA	Q7m3t3 vespa manda
25	22	30.6	14	2 Q55326	Q55326 synchococ
26	21	29.2	7	1 ALL5_CARMA	P81808 carcinus ma
27	21	29.2	13	2 Q7M0L4	Q7m0l4 bacillus ce
28	21	29.2	14	2 O85576	O85576 chlamydia t
29	21	29.2	14	2 Q9S3K6	Q9s3k6 chlamydia t
30	21	29.2	14	2 Q9S3K8	Q9s3k8 chlamydia t
31	21	29.2	14	2 Q9R8E6	Q9r8e6 chlamydia t

#### ALIGNMENTS

##### RESULT 1

Q7RA82 PRELIMINARY; PRT; 9 AA.  
AC Q7RA82; Q9R8E7 14 2 Q9R8E7 chlamydia t  
DT 01-MAR-2004 (Tremblrel. 26, Created) Q9R8E8 14 2 Q9R8E8 chlamydia t  
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update) Q9R8E9 14 2 Q9R8E9 chlamydia t  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update) Q9R8F0 14 2 Q9R8F0 chlamydia t  
DE Hypothetical protein (Fragment). Q9R8F2 14 2 Q9R8F2 chlamydia t  
GN Name=PY06620; Q9R8F5 14 2 Q9R8F5 chlamydia t  
OS Plasmodium yoelii yoelii. Q9R8F7 14 2 Q9R8F7 chlamydia t  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. Q9R8F9 14 2 Q9R8F9 chlamydia t  
OX NCBI\_taxid=73239; Q9R8G1 14 2 Q9R8G1 chlamydia t  
RN [1] Q9R8G3 14 2 Q9R8G3 chlamydia t  
RP SEQUENCE FROM N.A. Q9R8G4 14 2 Q9R8G4 chlamydia t  
RC STRAIN=17XNL; Q9R8G6 14 2 Q9R8G6 chlamydia t  
RX PubMed=12368865; Q9R8G8 14 2 Q9R8G8 chlamydia t  
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M., Q9R8H0 14 2 Q9R8H0 chlamydia t  
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,  
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,  
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,  
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
Carucci D.J.;  
RT "Genome sequence and comparative analysis of the model rodent malaria  
parasite Plasmodium yoelii yoelii.";  
RL Nature 419:512-519(2002).  
CC Nature 419:512-519(2002).  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
DR EMBL; AABL01002263; EAA18865.1; -.  
KW Hypothetical protein.  
FT NON\_TER  
SQ SEQUENCE 9 AA; 1001 MW; 4687A5AB476455B7 CRC64;

Query Match 38.9%; Score 28; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPS 5

DB 3 SNPS 7

##### RESULT 2

Q79A22 PRELIMINARY; PRT; 13 AA.  
AC Q79A22; Q9R8E7 14 2 Q9R8E7 chlamydia t  
DT 05-JUL-2004 (Tremblrel. 27, Created) Q9R8E8 14 2 Q9R8E8 chlamydia t  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update) Q9R8E9 14 2 Q9R8E9 chlamydia t  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update) Q9R8F0 14 2 Q9R8F0 chlamydia t  
DE MoxR protein (fragment).

GN Name=moxR;  
 OS Borrelia burgdorferi (Lyme disease spirochete).  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=212;  
 RA Old I.G.;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X95668; CAA64970.1; -.  
 FT NON\_TER 13 13  
 SQ SEQUENCE 13 AA; 1484 MW; C7C2DF4CFD83A046 CRC64;  
 Query Match 36.1%; Score 26; DB 2; Length 13;  
 Best Local Similarity 40.0%; Pred. No. 9.2e+02;  
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 SAFQVDITD 14  
 Db |||: :  
 3 SGFQIDSEVE 12  
 RESULT 3  
 Q76MM5 PRELIMINARY; PRT; 10 AA.  
 AC Q76MM5;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE NADH dehydrogenase subunit 2 (Fragment).  
 GN Name=ND2;  
 OS Eurypharynx pelicanoides (pelican eel).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
 OC Eurypharyngidae; Eurypharynx.  
 OX NCBI\_TaxID=55117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22967687; PubMed=12949142;  
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
 "Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels."; Mol. Biol. Evol. 20:1917-1924(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
 Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB046477; BAB87140.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 NPYSAFQV 9  
 Db |||: :  
 2 NPYVMFLV 9  
 RESULT 4  
 BAB87140 PRELIMINARY; PRT; 10 AA.  
 AC BAB87140;  
 DT 02-MAR-2004 (TREMBLrel. 27, Created)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)  
 DE NADH dehydrogenase subunit 2 (Fragment).  
 GN ND2.  
 OS Eurypharynx pelicanoides (pelican eel).

OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
 OC Eurypharyngidae; Eurypharynx.  
 OX NCBI\_TaxID=55117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A;  
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
 "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels."; Mol. Biol. Evol. 20:1917-1924(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A;  
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
 Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB046477; BAB87140.1; -.  
 KW Mitochondrion.  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+03;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 NPYSAFQV 9  
 Db |||: :  
 2 NPYVMFLV 9  
 RESULT 5  
 Q7M154 PRELIMINARY; PRT; 11 AA.  
 AC Q7M154;  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Parasporal crystal protein, wax moth-specific (Fragment).  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE.  
 RA Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,  
 Stepanov V.M.;  
 "Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxins differing strongly in primary structure and entomocidal activity."; FEBS Lett. 232:249-251(1988).  
 RL PIR; S00616; S00616.  
 DR NON\_TER 1 1  
 FT NON\_TER 11 11  
 SQ SEQUENCE 11 AA; 1237 MW; C6FF9BD64764444D CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 1.2e+03;  
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 QY 1 SNPYS 5  
 Db |||: :  
 5 NNPYS 9  
 RESULT 6  
 Q7XB05 PRELIMINARY; PRT; 12 AA.  
 AC Q7XB05;  
 DT 01-OCT-2003 (TREMBLrel. 25, Created)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Phytoene synthase 2 (Fragment).  
 GN Name=psy2;

OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JCM4673 / KCC-S-0673;  
 RX STRAIN=JCM4673 / KCC-S-0673;  
 RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;  
 RA "Purification and characterization of a puromycin-hydrolyzing enzyme  
 RT from blastidin S-producing Streptomyces morookaensis.";  
 RT J. Biochem. 123:247-252(1998).  
 RL Plant Cell 15:1795-1806(2003).  
 DR EMBL; AY300568; AAP5307.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 12 12  
 SQ SEQUENCE 12 AA; 1335 MW; 9B1E0AA0869C325 CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 12;  
 Best Local Similarity 54.5%; Pred. No. 1.3e+03;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SNPYSAFQVDI 11  
 Db :|:|:|  
 1 SDTVSKFPVDI 11  
 RESULT 7  
 QY7X761 PRELIMINARY; PRT; 13 AA.  
 ID Q7X761;  
 AC Q7X761;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Phytoene synthase 2 (Fragment).  
 GN Name=psy2;  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=JCM4673 / KCC-S-0673;  
 RX STRAIN=JCM4673 / KCC-S-0673;  
 RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;  
 RA "Purification and characterization of a puromycin-hydrolyzing enzyme  
 RT from blastidin S-producing Streptomyces morookaensis.";  
 RT J. Biochem. 123:247-252(1998).  
 RL Plant Cell 15:1795-1806(2003).  
 DR EMBL; AY300568; AAP5307.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 12 12  
 SQ SEQUENCE 13 AA; 1449 MW; 9B1E0AA05615C325 CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 13;  
 Best Local Similarity 54.5%; Pred. No. 1.4e+03;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SNPYSAFQVDI 11  
 Db :|:|:|  
 2 SDTVSKFPVDI 12  
 RESULT 8  
 P81801 PRELIMINARY; PRT; 14 AA.  
 ID P81801;  
 AC P81801;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Puromycin-hydrolyzing enzyme (EC 3.-.-.-) (fragment).  
 OS Streptomyces morookaensis.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1970;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=JCM4673 / KCC-S-0673;  
 RX STRAIN=JCM4673 / KCC-S-0673;  
 RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;  
 RA "Purification and characterization of a puromycin-hydrolyzing enzyme  
 RT from blastidin S-producing Streptomyces morookaensis.";  
 RT J. Biochem. 123:247-252(1998).  
 RL J. Biochem. 123:247-252(1998).  
 RN [2]  
 RP CHARACTERIZATION, AND FUNCTION.  
 RA Nishimura M., Matsuo H., Sugiyama M.;  
 RA "Blastidin S-producing Streptomyces morookaensis possesses an enzyme  
 RT activity with hydrolyzes puromycin.";  
 RT FEMS Microbiol. Lett. 132:95-100(1995).  
 CC -!- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF  
 CC THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-  
 CC TYROSINE MOETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL  
 CC TEMPERATURE IS 45 DEGREES CELSIUS.  
 CC -!- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.  
 CC -!- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC  
 CC ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND  
 CC N-ETHYLMALIMIDE. PARTIALLY INHIBITED BY COBALT ION.  
 CC -!- SUBUNIT: MONOMER.  
 CC -!- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.  
 DR GO; GO:0004177; F:aminopeptidase activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 KW Aminopectidase; Hydrolase.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 PYSAPQVDI 11  
 Db :|:|:|  
 5 PYGAWQSPDI 13  
 RESULT 9  
 QY9R518 PRELIMINARY; PRT; 14 AA.  
 ID Q9R518;  
 AC Q9R518;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE L-2,4-diaminobutyrate decarboxylase (Fragment).  
 OS Vibrio alginolyticus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=663;  
 RN [1]  
 RP SEQUENCE.  
 RA MEDLINE=92381494; PubMed=1512577;  
 RA Yamamoto S., Tsuzaki Y., Tougou K., Shinoda S.;  
 RA "Purification and characterization of L-2,4-diaminobutyrate  
 RT decarboxylase from Acinetobacter calcoaceticus.";  
 RL J. Gen. Microbiol. 138:1461-1465(1992).  
 DR PIR; B44854; B44854.  
 SQ SEQUENCE 14 AA; 1643 MW; 9F1B13DD35168ABA CRC64;  
 Query Match 34.7%; Score 25; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 SAFQVDITI 13  
 Db :|:|:|  
 2 TAFEVDSNI 10

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RESULT 10
Q91U19
ID Q91U19 PRELIMINARY; PRT; 8 AA.
AC Q91U19;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nuclear export protein NS2 (Fragment).
OS Influenza A virus (A/Hong Kong/503/97 (H5N1)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H5N1 subtype.
OX NCBI_TaxID=155224;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Hong Kong/503/97;
RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y.,
RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
RA Subbarao K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256192; AAK49326.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 869 MW; D9D9D5A5A2D1A455 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPSAFQ 8
DB ||| |
1 SNTVSSFQ 8

RESULT 11
Q91U21
ID Q91U21 PRELIMINARY; PRT; 8 AA.
AC Q91U21;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Nuclear export protein NS2 (Fragment).
OS Influenza A virus (A/Hong Kong/491/97 (H5N1)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A; H5N1 subtype.
OX NCBI_TaxID=155223;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/Hong Kong/491/97;
RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Krauss S.L., Guan Y.,
RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,
RA Subbarao K.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF256191; AAK49324.1; -.
FT NON_TER 1
FT NON_TER 8
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Best Local Similarity 62.5%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPSAFQ 8
DB ||| |
1 SNTVSSFQ 8

RESULT 12
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ID Q9S550 PRELIMINARY; PRT; 12 AA.
AC Q9S550;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

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DE DexB (Fragment).
GN Name=dexB;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D39;
RX MEDLINE=99214122; PubMed=10198036;
RA Iannelli F., Pearce B.J., Pozzi G.;
RT "The type 2 capsule locus of Streptococcus pneumoniae.";
RL J. Bacteriol. 181:2652-2654 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D39;
RA Pearce B.J., Iannelli F., Pozzi G.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026471; AAD10169.1; -.
FT NON_TER 1
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SQ SEQUENCE 12 AA; 1405 MW; 90A979D2B2B9CDDA CRC64;

Query Match 33.3%; Score 24; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQVDI 11
DB ||| |
3 PWDAPFCVEL 11

RESULT 13
Q76MK9
ID Q76MK9 PRELIMINARY; PRT; 10 AA.
AC Q76MK9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN Name=ND2;
OS Eurypharynx pelecanoides (pelican eel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22967687; PubMed=12949142;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
RT scale gene rearrangements originated within the eels.";
RL Mol. Biol. Evol. 20:1917-1924 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046485; BAB87156.1; -.
DR EMBL; AB046489; BAB87164.1; -.
DR EMBL; AB046481; BAB87148.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

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QY 2 NPSYAF 7
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2 NPYVMF 7

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RESULT 14  
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 ID Q9FS93 PRELIMINARY; PRT; 10 AA.  
 AC Q9FS93;  
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 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
 DE RNA polymerase II (Fragment).  
 GN Name=rpb2;  
 OS Silene pentelica.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllaceae; Silene.  
 OX NCBI\_TaxID=49735;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21419634; PubMed=11527472;  
 RA Popp M., Oxelman B.;  
 RT "Inferring the history of the polyploid Silene aegaea  
 RT (Caryophyllaceae) using plastid and homoeologous nuclear DNA  
 RT sequences.";  
 RL Mol. Phylogenet. Evol. 20:474-481(2001).  
 DR EMBL; AJ296133; CAC13025.1; --  
 FT NON\_TER 1  
 FT NON\_TER 10  
 FT NON\_TER 10  
 SQ SEQUENCE 10 AA; 1108 MW; CFIAB6D1B2CAB1A9 CRC64;  
  
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 Best Local Similarity 60.0%; Pred. No. 2.5e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 10 DITID 14  
 Db 5 DVTVD 9  
  
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 AC BAB87148;  
 DT 02-MAR-2004 (TRENBLrel. 27, Created)  
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)  
 DE NADH dehydrogenase subunit 2 (Fragment).  
 GN ND2.  
 OS Eurypharynx pelecanoides (pelican eel).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
 OC Eurypharyngidae; Eurypharynx.  
 OX NCBI\_TaxID=55117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B;  
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
 RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-  
 RT Scale Gene Rearrangements Originated Within the Eels.";  
 RL Mol. Biol. Evol. 20:1917-1924(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=B;  
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB046481; BAB87148.1; --  
 KW Mitochondrion.  
 FT NON\_TER 10  
 FT NON\_TER 10  
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 Query Match 31.9%; Score 23; DB 2; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;  
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QY 2 NPYSAP 7  
 Db 2 NPYVWF 7

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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	32	44.4	15	14	US-10-014-340-802
5	32	44.4	15	17	US-10-700-330-264
6	29	40.3	15	14	US-10-285-394-332
7	29	40.3	20	14	US-10-162-538-25
8	29	40.3	22	9	US-09-864-761-43921
9	28	38.9	10	10	US-09-880-748-3097
10	28	38.9	10	14	US-10-293-418-3097
11	28	38.9	13	11	US-09-842-776A-30
12	28	38.9	19	14	US-10-230-880-125
13	28	38.9	23	15	US-10-211-462-91

14	27	37.5	11	10	US-09-880-748-2839	Sequence 2839, Ap
15	27	37.5	11	14	US-10-293-418-2839	Sequence 2839, Ap
16	27	37.5	12	14	US-10-286-457-177	Sequence 177, App
17	27	37.5	18	10	US-09-880-748-2736	Sequence 2736, Ap
18	27	37.5	18	14	US-10-293-418-2736	Sequence 2736, Ap
19	27	37.5	18	16	US-10-481-180-685	Sequence 685, App
20	27	37.5	19	9	US-09-864-761-43613	Sequence 43613, A
21	27	37.5	19	15	US-10-424-599-201443	Sequence 201443, A
22	27	37.5	19	16	US-10-481-180-692	Sequence 692, App
23	27	37.5	21	14	US-10-350-405-151	Sequence 151, App
24	27	37.5	23	16	US-10-481-180-714	Sequence 714, App
25	26.5	36.8	10	14	US-10-151-882-26	Sequence 26, Appl
26	26	36.1	7	9	US-09-927-180-3	Sequence 3, Appl
27	26	36.1	9	14	US-10-334-726-118	Sequence 118, App
28	26	36.1	9	14	US-10-334-726-220	Sequence 220, App
29	26	36.1	15	10	US-09-983-802-437	Sequence 437, App
30	26	36.1	15	10	US-09-984-490-437	Sequence 437, App
31	26	36.1	15	11	US-09-973-278-566	Sequence 566, App
32	26	36.1	15	14	US-10-411-120-102	Sequence 102, App
33	26	36.1	20	10	US-09-171-432A-70	Sequence 70, Appl
34	26	36.1	22	14	US-10-106-698-7411	Sequence 7411, A
35	26	36.1	22	14	US-10-029-386-31493	Sequence 31493, A
36	25	34.7	7	14	US-10-400-991-50	Sequence 50, Appl
37	25	34.7	9	10	US-09-995-529-83	Sequence 83, Appl
38	25	34.7	9	11	US-09-995-529-83	Sequence 83, Appl
39	25	34.7	10	10	US-09-572-404B-2428	Sequence 2428, Ap
40	25	34.7	10	16	US-10-327-598-519	Sequence 519, App
41	25	34.7	11	9	US-09-966-871-70	Sequence 70, Appl
42	25	34.7	11	13	US-10-039-645-70	Sequence 70, Appl
43	25	34.7	11	14	US-10-133-084-70	Sequence 70, Appl
44	25	34.7	11	15	US-10-458-860-70	Sequence 70, Appl
45	25	34.7	11	17	US-10-625-047-8	Sequence 8, Appl

#### ALIGNMENTS

#### RESULT 1

US-09-071-838-173  
; Sequence 173, Application US/09071838  
; Patent No. US20020152501A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; NUMBER OF SEQUENCES: 324  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,838  
; FILING DATE: 01-MAY-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-086100US  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 173:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-071-838-173

Query Match 51.4%; Score 37; DB 9; Length 17;  
Best Local Similarity 50.0%; Pred. No. 9.1;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDITD 14  
||| | : : ||  
Db 3 SNPYRKFKTNYTKD 16

## RESULT 2

US-10-213-512-173  
; Sequence 173, Application US/10213512  
; Publication No. US20030110536A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; FILE REFERENCE: 023070-086110US  
; CURRENT APPLICATION NUMBER: US/10/213,512  
; CURRENT FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: US/09/177,206  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: US 09/071,838  
; PRIOR FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 173  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-10-213-512-173

Query Match 51.4%; Score 37; DB 14; Length 17;  
Best Local Similarity 50.0%; Pred. No. 9.1;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDITD 14  
||| | : : ||  
Db 3 SNPYRKFKTNYTKD 16

## RESULT 3

US-09-988-493-305  
; Sequence 305, Application US/09988493  
; Publication No. US20030064419A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyansele Athula Chandrasiri  
; APPLICANT: O'Hare, Michael John  
; APPLICANT: Page, Martin John  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Waterfield, Michael Derek  
; TITLE OF INVENTION: Proteins, Genes, and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Breast Cancer  
; FILE REFERENCE: 2543-1-024  
; CURRENT APPLICATION NUMBER: US/09/988,493  
; CURRENT FILING DATE: 2002-05-21

; PRIOR APPLICATION NUMBER: PCT/GB01/01219  
; PRIOR FILING DATE: 2001-03-20  
; PRIOR APPLICATION NUMBER: GB 0006695.1  
; PRIOR FILING DATE: 2000-03-20  
; PRIOR APPLICATION NUMBER: GB 0007265.2  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 305  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-988-493-305

Query Match 44.4%; Score 32; DB 10; Length 15;  
Best Local Similarity 60.0%; Pred. No. 64;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITD 14  
| | | : : |  
Db 5 SGFQIEETD 14

## RESULT 4

US-10-014-340-802  
; Sequence 802, Application US/10014340  
; Publication No. US20030064411A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, et al  
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including  
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease  
; FILE REFERENCE: 9195-078  
; CURRENT APPLICATION NUMBER: US/10/014,340  
; CURRENT FILING DATE: 2001-12-10  
; NUMBER OF SEQ ID NOS: 823  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 802  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-014-340-802

Query Match 44.4%; Score 32; DB 14; Length 15;  
Best Local Similarity 60.0%; Pred. No. 64;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITD 14  
| | | : : |  
Db 5 SGFQIEETD 14

## RESULT 5

US-10-700-330-264  
; Sequence 264, Application US/10700330  
; Publication No. US20040203022A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Mudiyansele Athula Chandrasiri Herath  
; APPLICANT: Page, Martin John  
; TITLE OF INVENTION: Proteins and Genes For Diagnosis And Treatment of ErbB2-Related (c  
; FILE REFERENCE: 2543-1-031  
; CURRENT APPLICATION NUMBER: US/10/700,330  
; CURRENT FILING DATE: 2003-11-03  
; PRIOR APPLICATION NUMBER: GB 0110886.9  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: GB 0128183.1  
; PRIOR FILING DATE: 2001-11-23  
; NUMBER OF SEQ ID NOS: 269  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 264  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-700-330-264



Query Match 44.4%; Score 32; DB 17; Length 15;  
Best Local Similarity 60.0%; Pred. No. 64;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITID 14  
| | | | |  
| | | | |  
Db 5 SGFOIBETID 14

RESULT 6  
US-10-285-394-332  
; Sequence 332, Application US/10285394  
; Publication No. US20030228583A1  
; GENERAL INFORMATION:  
; APPLICANT: FASULO, DAVID E.  
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI  
; APPLICANT: HOLT, GORDON DUANE  
; APPLICANT: STIGER, THOMAS R.  
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE  
; FILE REFERENCE: POA-003.01  
; CURRENT APPLICATION NUMBER: US/10/285,394  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/335,964  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 412  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 332  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-285-394-332

Query Match 40.3%; Score 29; DB 14; Length 15;  
Best Local Similarity 54.5%; Pred. No. 2.3e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 YSAFOVDITID 14  
| | | | |  
| | | | |  
Db 2 YPGSQDJLID 12

RESULT 7  
US-10-162-538-25  
; Sequence 25, Application US/10162538  
; Publication No. US20030113749A1  
; GENERAL INFORMATION:  
; APPLICANT: Brent, Roger  
; McCoy, John M.  
; Jessen, Timm H.  
; Xu, Chanxing Wilson  
; TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING  
; PROTEIN  
; INTERACTIONS  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02110-2804  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/162,538  
; FILING DATE: 04-Jun-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/630,052  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/504,538  
FILING DATE: July 20, 1995  
APPLICATION NUMBER: 08/276,082  
FILING DATE: July 20, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Karen F. Lech  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/311001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. US20030113749A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-10-162-538-25

Query Match 40.3%; Score 29; DB 14; Length 20;  
Best Local Similarity 62.5%; Pred. No. 3.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFOVD 10  
| | | | |  
| | | | |  
Db 13 PHSVFNVVD 20

RESULT 8  
US-09-864-761-43921  
; Sequence 43921, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aemica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43921
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006227.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.86
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61
US-09-864-761-43921

Query Match      40.3%; Score 29; DB 9; Length 22;
Best Local Similarity 54.5%; Pred. No. 3.5e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 SNPSAFQVDI 11
DB      1 STPSSAFSVSL 11

RESULT 9
US-09-880-748-3097
; Sequence 3097, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3097
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3097

Query Match      38.9%; Score 28; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
DB      3 SPYDAFDI 10

RESULT 10
US-10-293-418-3097
; Sequence 3097, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3097
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3097

Query Match      38.9%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
DB      3 SPYDAFDI 10

RESULT 11
US-09-842-776A-30
; Sequence 30, Application US/09842776A
; Publication No. US2004002316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR3) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-30

Query Match      38.9%; Score 28; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNPYS 5
DB      6 SNPYS 10
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RESULT 12  
US-10-230-880-125  
; Sequence 125, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306  
; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 125  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-125

Query Match 38.9%; Score 28; DB 14; Length 19;  
Best Local Similarity 42.9%; Pred. No. 4.5e+02;  
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDITD 14  
DB 6 SNNYATFYAMSVKD 19

RESULT 13  
US-10-211-462-91  
; Sequence 91, Application US/10211462  
; Publication No. US20040033495A1  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Richard  
; APPLICANT: Glynn, Richard  
; APPLICANT: Watson, Susan R.  
; APPLICANT: Aziz, Nataasha  
; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
; FILE REFERENCE: 018501-006200US  
; CURRENT APPLICATION NUMBER: US/10/211,462  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 230  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 91  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-211-462-91

Query Match 38.9%; Score 28; DB 15; Length 23;  
Best Local Similarity 50.0%; Pred. No. 5.6e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVD 10

Db 3 SIPYTVFQTN 12  
RESULT 14  
US-09-880-748-2839  
; Sequence 2839, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2839  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-2839

Query Match 37.5%; Score 27; DB 10; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.7e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQV 9  
DB 5 PYDAFDI 11

RESULT 15  
US-10-293-418-2839  
; Sequence 2839, Application US/10293418  
; Publication No. US2003023996A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS  
; FILE REFERENCE: PF523P2  
; CURRENT APPLICATION NUMBER: US/10/293,418  
; CURRENT FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: 60/331,469  
; PRIOR FILING DATE: 2001-11-16  
; PRIOR APPLICATION NUMBER: 60/340,817  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 09/880,748  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 3247  
; SEQ ID NO 2839  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-293-418-2839

Query Match 37.5%; Score 27; DB 14; Length 11;  
Rest Local Similarity 57.1%; Pred. No. 3.7e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PYSAFQV 9  
||| :  
Db 5 PYDAFDI 11

Search completed: November 14, 2004, 12:26:59  
Job time : 33.0638 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 40.5106 Seconds  
(without alignments)  
123.973 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72

Sequence: 1 SNPYSAFQVDITD 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 23Sep04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	14	3 AAY92951	Aay92951 Transform
2	72	100.0	14	3 AAY93099	Aay93099 Transform
3	65	90.3	15	3 AAY92948	Aay92948 Transform
4	65	90.3	15	3 AAY93066	Aay93066 Transform
5	53	73.6	15	3 AAY93059	Aay93059 Transform
6	37	51.4	15	3 AAY93067	Aay93067 Transform
7	32	44.4	15	4 AAU68498	Aau68498 Human Bre
8	32	44.4	15	6 ABP99093	Abp99093 Erxb2 cel
9	32	44.4	15	6 ADA24180	Ada24180 Alzheimer
10	32	44.4	17	2 AAR42489	Aar42489 Canine ho
11	32	44.4	17	2 AAR67769	Aar67769 Peptide f
12	32	44.4	17	2 AAY23572	Aay23572 Peptide f
13	32	44.4	21	2 AAR34228	Aar34228 HTLV-I gp
14	32	44.4	22	2 AAY17925	Aay17925 Synthetic
15	30	41.7	15	8 ADL70819	Adl70819 pTP1B pho
16	30	41.7	15	8 ADL70903	Adl70903 pTP1B pho
17	30	41.7	15	8 ADL70907	Adl70907 pTP1B pho
18	30	41.7	15	8 ADL70906	Adl70906 pTP1B pho
19	30	41.7	15	8 ADL70908	Adl70908 pTP1B pho
20	30	41.7	17	7 ADD26370	Add26370 Staphyloc
21	30	41.7	20	2 AAU42169	Aau42169 T-cell ep
22	29	40.3	15	6 ABR75594	Abr75594 Liver res
23	29	40.3	15	7 ADN07473	Adn07473 Liver res
24	29	40.3	15	8 ADK90209	Adk90209 Human 191
25	29	40.3	20	2 AAW32131	Aaw32131 Interacti

26	29	40.3	20	4 AAB50335	Aab50335 Adeno-ass
27	29	40.3	22	4 AAM32954	Aam32954 Peptide #
28	29	40.3	22	4 AAM72723	Aam72723 Human: bon
29	29	40.3	22	4 AAM60111	Aam60111 Human bra
30	29	40.3	22	4 ABG54421	Abg54421 Human liv
31	29	40.3	22	5 ABG42547	Abg42547 Human pep
32	29	40.3	23	2 AAW60840	Aaw60840 Peptide c
33	29	40.3	23	6 ABP71452	Abp71452 Amino aci
34	29	40.3	23	6 ABR63206	Abri63206 Clone T4-
35	29	40.3	23	6 ABP96132	Abp96132 Tumour an
36	29	40.3	23	6 ABR43783	Abri43783 Clone T4-
37	28	38.9	10	5 ABP47086	Abp47086 Human BLD
38	28	38.9	10	7 ADG97913	Adg97913 scFV VHCD
39	28	38.9	13	3 AAB10012	Aab10012 H. pylori
40	28	38.9	13	4 AAB86092	Aab86092 H. pylori
41	28	38.9	13	4 AAB86060	Aab86060 H. pylori
42	28	38.9	15	3 AAY93058	Aay93058 Transform
43	28	38.9	17	2 AAR31182	Aar31182 N-termina
44	28	38.9	17	5 ABG68025	Abg68025 Human ADP
45	28	38.9	18	2 AAW42229	Aaw42229 Biotinyla

ALIGNMENTS

RESULT 1

AAY92951  
ID AAY92951 standard; peptide; 14 AA.

XX AC

XX AAY92951;

DT 08-NOV-2000 (first entry)

XX Transforming growth factor inhibitory peptide #7.

XX Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;  
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
XX Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betal.  
XX useful for treatment of liver disease, especially cirrhosis, are partial  
XX sequences of the factor or its receptors.

XX Claim 8; Page 82; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
XX vivo which have partial amino acid sequences identical, or similar, with  
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
XX examples of the peptides of the invention. The peptides act by  
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
XX they are inhibitors of stimulation of collagen synthesis in liver cells  
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the  
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or  
XX expression systems) encoding the peptides are used for treatment of liver  
XX disease, specifically cirrhosis

```

XX SQ Sequence 14 AA;
Query Match 100.0%; Score 72; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPSAFQVDITID 14
Db 1 SNPSAFQVDITID 14

RESULT 2
AAY93099
ID AAY93099 standard; peptide; 14 AA.
XX AC AAY93099;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide P145.
XX KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-b1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX OS Homo sapiens.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX PI Borrás Cuesta F;
XX DR WPI; 2000-411935/35.
XX PT Peptides that antagonize binding of transforming growth factor beta1,
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.
XX PS Claim 5; Page 81; 86pp; Spanish.
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor beta1 (TGF-b1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis
XX SQ Sequence 15 AA;
Query Match 90.3%; Score 65; DB 3; Length 15;
Best Local Similarity 85.7%; Pred. No. 2.9e-05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPSAFQVDITID 14
Db 1 SNPSAFQVDITID 14

RESULT 4
AAY93066
ID AAY93066 standard; peptide; 15 AA.
XX AC AAY93066;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide P106.
XX KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-b1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

```



CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
CC examples of the peptides of the invention. The peptides act by  
CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis  
XX  
SQ Sequence 15 AA;

Query Match 51.4%; Score 37; DB 3; Length 15;  
Best Local Similarity 77.8%; Pred. No. 5.8;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 AFQVDITID 14  
| | | | | : |  
Db 1 AFQVDIIVD 9

## RESULT 7

AAU68498

ID AAU68498 standard; peptide; 15 AA.

XX AC

XX AAU68498;

XX DT

XX 16-JAN-2002 (first entry)

XX DE

XX Human Breast cancer-associated protein isoform, BPI-279 peptide #3.

XX KW

XX Human; Breast cancer-associated protein isoform; breast cancer;

XX KM

XX immunogen; cytostatic; BPI; tryptic digest peptide.

XX XX

XX OS

XX Homo sapiens.

XX PN

XX WO200171357-A2.

XX PD

XX 27-SEP-2001.

XX PF

XX 20-MAR-2001; 2001WO-GB001219.

XX PR

XX 20-MAR-2000; 2000GB-00006695.

XX PR

XX 24-MAR-2000; 2000GB-00007265.

XX XX

XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PI

XX Herath HMAC, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;

XX XX

XX WPI; 2001-611532/70.

XX PS

XX Claim 9; Page 53; 197pp; English.

CC The invention relates to diagnosing, determining the stage or severity,  
CC or identifying the risk of a subject developing cancer (especially breast  
CC cancer), or monitoring the effect of therapy on a subject with cancer,  
CC comprising analysing a test sample using two-dimensional electrophoresis  
CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The  
CC methods disclosed are used for the diagnosis and prognosis of breast  
CC cancer, for determining the severity of breast cancer, and for  
CC identifying a subject at risk of developing breast cancer, and monitoring  
CC the effect of therapy administered to a subject. Antibodies raised  
CC against the binding domain of a BPI, the binding domain of a BPI, a  
CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function  
CC of a BPI can be incorporated into a pharmaceutical composition for  
CC treating or preventing breast cancer. The methods use sensitive and  
CC specific biomarkers provide early diagnosis of breast cancer, and the  
CC compositions are more potent, specific, and has a more rapid effect with  
CC fewer side effects than other prior art methods. The present sequence is  
CC a tryptic digest peptide from a BPI of the invention

XX

SQ Sequence 15 AA;

Query Match 44.4%; Score 32; DB 4; Length 15;  
Best Local Similarity 60.0%; Pred. No. 51;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITID 14  
| | | | | : |  
Db 5 SGFQIEETID 14

## RESULT 8

ABP99093

ID ABP99093 standard; peptide; 15 AA.

XX AC

XX ABP99093;

XX XX

XX 18-MAR-2003 (first entry)

XX DE

XX ErbB2 cell overexpression EOPI-97 peptide SEQ ID NO:264.

XX KW

XX ErbB2; cancer; oncogene; ErbB2 overexpression-associated protein isoform;

XX KW

XX EOPI; EOPI; ErbB2 overexpression feature; cytostatic; vaccine;

XX KW

XX gene therapy.

XX XX

XX OS

XX Homo sapiens.

XX XX

XX WO200290991-A2.

XX PD

XX 14-NOV-2002.

XX PF

XX 02-MAY-2002; 2002WO-GB002047.

XX XX

XX 03-MAY-2001; 2001GB-00010886.

XX PR

XX 23-NOV-2001; 2001GB-00028183.

XX XX

XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX PA

XX Herath HMAC, Page MJ;

XX PI

XX WPI; 2003-103531/09.

XX DR

XX PT

XX PT

XX PT

XX PT

XX PT

XX PS

XX Claim 3; Page 21; 106pp; English.

XX CC

XX The present invention describes a method for screening or diagnosing

XX ErbB2-related cancer. The method comprises generating ErbB2

XX overexpression features (EOFs) from test samples of body fluid from the

XX subject by electrophoresis, and comparing the EOFs in the test sample

XX with that from normal subjects or with an expression reference feature

XX (ERF) in the test sample. Also described: (1) an antibody capable of

XX immunospecific binding to an ErbB2 overexpression protein isoform (EOPI);

XX (2) pharmaceutical compositions comprising an EOPI, a nucleic acid

XX encoding an EOPI, an amount of the above antibody or its fragment, and a

XX carrier; (3) a kit comprising one or more antibodies and/or EOPIs cited

XX above, other reagents and instructions for use; (4) methods of treating

XX or preventing ErbB2-related cancer; (5) methods of screening for or

XX identifying agents that interact with or modulate the expression or

XX activity of, one or more EOPIs, EOPI fragment, EOPI-related polypeptides,

XX or EOPI-fusion proteins; (6) a method for modulating the activity of one

XX or more of the ErbB2 EOPIs, comprising administering to a subject an

XX agent identified by the method of (5); and (7) a method for identifying

XX targets for therapeutic modulation of ErbB2-related cancer. EOPIs have

XX cytostatic activity and can be used in vaccines and gene therapy. The

XX method is useful in screening, diagnosing, preventing or treating ErbB2-

XX related cancer, determining the stage or severity of ErbB2-related

XX cancer, identifying a subject at risk of developing ErbB2-related cancer,

XX monitoring the effect of therapy administered to a subject with ErbB2-



CC related cancer, and for drug screening or drug development. The kit is  
 CC useful in carrying out the above methods. ABP98940 to ABP99206 represent  
 CC specifically claimed EOPIS from the present invention  
 XX  
 SQ Sequence 15 AA;

Query Match 44.4%; Score 32; DB 6; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 51;  
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITID 14  
 | : : : :  
 Db 5 SGFOIETID 14

## RESULT 9

ADA24180  
 ID ADA24180 standard; peptide; 15 AA.

XX AC ADA24180;

XX 20-NOV-2003 (first entry)

XX Alzheimer's disease-associated protein isoform tryptic peptide #789.  
 XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;  
 KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;  
 KW Alzheimer's disease-associated protein isoform; ADPI.

XX Homo sapiens.

XX US2003064411-A1.

XX 03-APR-2003.

XX 10-DEC-2001; 2001US-00014340.

XX 08-DEC-2000; 2000US-0254431P.

XX (HERA/) HERATH H M A C.

XX (PARE/) PAREKH R B.

XX (ROHL/) ROHLFF C.

XX Herath HMAC, Parekh RB, Rohlf C;

XX WPI; 2003-540784/51.

XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,  
 PT involves analyzing test sample of brain tissue from subject, and  
 PT comparing feature in test sample with that of person(s) free from  
 PT Alzheimer's disease.

XX Disclosure; SEQ ID NO 789; 115pp; English.

XX The invention relates to a method of screening or diagnosing Alzheimer's  
 CC disease in a subject. The method is useful for screening, diagnosis or  
 CC prognosis of Alzheimer's disease in a subject for determining the stage  
 CC of severity of Alzheimer's disease in a subject, for identifying a  
 CC subject at risk of developing Alzheimer's disease, or for monitoring the  
 CC effect of therapy administered to a subject having Alzheimer's disease.  
 CC The method is also useful in treating vascular dementia, Lewy body  
 CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or  
 CC depression. The inventive method identifies sensitive and specific  
 CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.  
 CC It provides therapeutic agents for Alzheimer's disease that works  
 CC quickly, potentially, specifically with fewer side effects. The present  
 CC sequence represents the amino acid sequence of a Alzheimer's disease-  
 CC associated protein isoform tryptic peptide.

XX Sequence 15 AA;

Query Match 44.4%; Score 32; DB 6; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 51;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 SAFOVDITID 14  
 | : : : :  
 Db 5 SGFOIETID 14

## RESULT 10

AAR42489  
 ID AAR42489 standard; protein; 17 AA.

XX AAR42489;

XX 25-MAR-2003 (revised)

DT 02-JUN-1994 (first entry)

XX Canine hookworm NIF tryptic fragment T24.

XX neutrophil inhibitory factor; NIF; glycoprotein; endoparasite; nematode;  
 KW parasitic worm; canine hookworm; peritoneal inflammation.

XX Ancylostoma caninum.

XX WO9323063-A1.

XX 25-NOV-1993.

XX 11-MAY-1993; 93WO-US0004502.

XX 11-MAY-1992; 92US-00881721.

XX 24-DEC-1992; 92US-00996972.

XX (CORV-) CORVAS INT INC.

XX Moyle M, Foster DL, Vlasuk GP;

XX WPI; 1993-386208/48.

XX New neutrophil inhibitory factor from parasitic worms - for preventing  
 PT and treating inflammation, also derived nucleic acid, vectors,  
 PT transformed hosts and antibodies.

XX Example 9; Fig 7; 114pp; English.

XX Neutrophil Inhibitory Factor was isolated from canine hookworms. The NIF  
 CC was digested with either endoproteinase AspN, LysC or trypsin and the  
 CC resulting proteolytic fragments were sequenced. See AAR42489- AAR42493  
 CC for the trypsin fragments. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 17 AA;

Query Match 44.4%; Score 32; DB 2; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 59;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFOVDIT 12  
 | : : : :  
 Db 1 SAFELDIT 8

## RESULT 11

AAR67769  
 ID AAR67769 standard; protein; 17 AA.

XX AAR67769;

XX 25-MAR-2003 (revised)

DT 27-FEB-1995 (first entry)

XX Peptide fragment of neutrophil inhibitory factor (NIF).

XX Primer; neutrophil inhibitory factor; NIF; inflammation; adhesion;  
 KW endothelial cells; inflammatory response.

```

XX OS Ancylostoma caninum.
XX PN WO9414973-A1.
XX PD 07-JUL-1994.
XX PF 23-DEC-1993; 93WO-US012626.
XX PR 24-DEC-1992; 92US-00996972.
XX PR 11-MAY-1993; 93US-00060433.
XX PR 10-NOV-1993; 93US-00151064.
XX PA (CORV-) CORVAS INT INC.
XX PI Moyle M, Foster DL, Vlasuk GP;
XX WI 1994-234706/28.
XX PT Neutrophil inhibitory factor peptide(s) - derived from nematodes, useful
XX for therapy of inflammatory responses.
XX PS Example 9; Fig 7; 239pp; English.
XX CC Neutrophil inhibitory factors can be used in compositions to inhibit
XX CC neutrophil activity e.g. adhesion to vascular endothelial cells, and
XX CC which are useful in the therapy of conditions which involve abnormal or
XX CC undesired inflammatory responses. This is a peptide fragment of a
XX CC neutrophil inhibitory factor from canine hookworm which was designated T-
XX CC 24 and obtained by trypsin digestion of the factor. (Updated on 25-MAR-
XX CC 2003 to correct PN field.)
XX SQ Sequence 17 AA;
Query Match 44.4%; Score 32; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 SAFQVDIT 12
DB 1 SAFELDIT 8
RESULT 12
AAY23572
ID AAY23572 standard; peptide; 17 AA.
XX AC AAY23572;
XX DT 03-SEP-1999 (first entry)
XX DE Peptide fragment of canine hookworm NIF.
XX KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
XX KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;
XX KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
XX KW inflammatory bowel disease; adult respiratory distress syndrome;
XX KW ischemia-reperfusion injury; acute inflammation; bacterial infection;
XX KW vaccine; parasitic worm infection; antihelminic.
XX OS Ancylostoma caninum.
XX PN US5919900-A.
XX PD 06-JUL-1999.
XX PF 26-MAY-1995; 95US-00450497.
XX PR 11-MAY-1992; 92US-00881721.
XX PR 24-DEC-1992; 92US-00996972.
XX PR 11-MAY-1993; 93US-00060433.
XX PR 10-NOV-1993; 93US-00151064.
XX PR 23-DEC-1993; 93US-00173510.
XX OS (CORV-) CORVAS INT INC.
XX PI Moyle M, Foster DL;
XX WI 1999-403975/34.
XX PT Mutant Neutrophil Inhibitory Factors useful for treating inflammatory
XX conditions and especially to prevent or decrease inflammatory responses.
XX PS Example 9; Fig 7A; 131pp; English.
XX CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
XX CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
XX CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln
XX CC residue. NIFs may be useful for treating shock, stroke, acute and chronic
XX CC allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
XX CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
XX CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury
XX CC following myocardial infarction, and acute inflammation caused by
XX CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
XX CC fragments may be used as vaccines against parasitic worm infection. Anti-
XX CC NIF antibodies may be useful for detecting infection of a mammalian host
XX CC by a parasitic worm, as antihelminic agents, and in the detection and
XX CC isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be
XX CC useful for the detection of NIF mimics or antagonists in other compounds.
XX CC Other NIF agonists and inhibitors may also be used as antihelminic
XX CC agents. AAY23572-90 represent peptide fragments of a canine hookworm NIF,
XX CC obtained after proteolytic digestion
XX SQ Sequence 17 AA;
Query Match 44.4%; Score 32; DB 2; Length 17;
Best Local Similarity 75.0%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 SAFQVDIT 12
DB 1 SAFELDIT 8
RESULT 13
AAR34228
ID AAR34228 standard; peptide; 21 AA.
XX AC AAR34228;
XX DT 25-MAR-2003 (revised)
XX DT 04-AUG-1993 (first entry)
XX DE HTLV-I gp46 external envelope glycoprotein fragment 4.
XX KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;
XX KW diagnosis; antibodies.
XX OS Synthetic.
XX PN WO9306843-A1.
XX PD 15-APR-1993.
XX PF 08-OCT-1992; 92WO-US008405.
XX PR 08-OCT-1991; 91US-00771553.
XX PA (UYDU-) UNIV DUKE.
XX PI Palker TJ, Haynes BF;
XX WI 1993-134125/16.
XX PT Antigenic determinant peptide(s) of HTLV envelope glyco:protein - useful
XX for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.

```

XX	Claim 4; Page 11; 50pp; English.
PS	
XX	
CC	The sequence of peptide 4 corresponds to residues 129-149 from the HTLV-I gp46 external envelope glycoprotein. When covalently linked to a carrier mol. the hydrophilic peptide can induce in a mammal the prodn. of high titres of antibodies to gp46 envelope glycoprotein from HTLV-I or -II. The peptide and carrier may be used in vaccines against HTLV-I or -II infection. The peptide may be used in a diagnostic assay to detect the presence and titre of anti-HTLV antibodies. See also AAR34225-57. (Updated on 25-MAR-2003 to correct PN field.)
CC	
XX	
SQ	Sequence 21 AA;
	Query Match 44.4%; Score 32; DB 2; Length 21;
	Best Local Similarity 54.5%; Pred. No. 77;
	Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY	1 SNPYSAFQVDI 11
	:       :
DB	1 SSPYWKQHDV 11
RESULT 14	
AAV17925	
ID	AAV17925 standard; peptide; 22 AA.
XX	
AC	AAV17925;
XX	
DT	30-JUL-1999 (first entry)
XX	
DE	Synthetic peptide derived from HTLV envelope sugar protein.
XX	
KW	Hydrophilic peptide; antigen determinant; envelope sugar protein; HTLV-I; HTLV-II; B lymphatic corpuscle; gp46; gp63; tetanus toxoid.
XX	
OS	Synthetic.
XX	Human lymphotropic virus type i.
XX	
PN	JF02209889-A.
XX	
PD	21-AUG-1990.
XX	
PF	08-FEB-1989; 89JP-00029551.
XX	
PR	08-FEB-1988; 88US-00153420.
XX	
PR	30-JAN-1989; 89US-00303436.
XX	
PA	(UYDU-) UNIV DUKE.
XX	
DR	WPI; 1990-344000/39.
XX	
PT	Synthetic hydrophilic peptide - comprises 25 unit aminoacid that corresponds to at least one antigen determinant of envelope sugar protein(s) of HTLV-I and HTLV-II.
XX	
PS	Claim 4; Page 1; 15pp; Japanese.
XX	
CC	The invention relates to new synthetic hydrophilic peptides (AAV17922-934) that correspond to at least one of antigen determinants of envelope sugar proteins of HTLV-I and HTLV-II identified in the B lymphatic corpuscle. When bonded covalently to a carrier molecule, the peptides can induce the production of an antibody having a high titre to the gp46 and gp63 envelope sugar proteins of HTLV-I and HTLV-II in mammals. The carrier molecule is preferably a tetanus toxoid and selected from the group of sequences shown in AAV17935-39. The carrier molecule is preferably bonded to the peptide through at least one spacer molecule (preferably a dipeptide glycine-glycine). The peptides form effectively immunological response to factors causing virus HTLV-I and HTLV-II. The method also provides an effective conjugate having the peptide
XX	
SQ	Sequence 22 AA;

Db           |:|:|  
             6 YNAYQVD 12

Search completed: November 14, 2004, 12:02:14  
Job time : 42.5106 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: November 14, 2004, 11:57:25 ; Search time 8.6383 Seconds  
(without alignments)  
155.938 Million cell updates/sec

Title: US-09-831-253F-7  
Perfect score: 72  
Sequence: 1 SNPSAFQVDITD 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	43.1	22	2	C39800
2	31	43.1	23	2	PS0446
3	30	41.7	23	2	A48968
4	27	37.5	16	2	S16376
5	27	37.5	21	2	S69371
6	26	36.1	17	2	A58946
7	26	36.1	22	2	S05236
8	25	34.7	11	2	S00616
9	25	34.7	14	2	B44854
10	23	31.9	13	2	A54326
11	22	30.6	12	2	A61360
12	22	30.6	14	2	PS0371
13	22	30.6	15	2	A61612
14	22	30.6	17	2	A61334
15	22	30.6	18	2	S43834
16	22	30.6	19	2	A61110
17	22	30.6	20	2	A85659
18	21.5	29.9	21	2	A35646
19	21	29.2	11	2	A40795
20	21	29.2	12	2	S36899
21	21	29.2	13	2	PC2369
22	21	29.2	16	2	A48301
23	21	29.2	20	2	S27351
24	21	29.2	23	2	PH1361
25	21	29.2	23	2	PH1729
26	20	27.8	9	2	S10784
27	20	27.8	11	2	PT0229
28	20	27.8	14	2	A59018
29	20	27.8	15	2	S08209

30 20 27.8 17 2 A48179  
31 20 27.8 18 2 A45138  
32 20 27.8 20 2 I79432  
33 20 27.8 22 2 B31174  
34 20 27.8 23 2 A44524  
35 19 26.4 9 2 S36898  
36 19 26.4 13 2 G22565  
37 19 26.4 14 2 PT0077  
38 19 26.4 14 2 A28018  
39 19 26.4 15 2 G24417  
40 19 26.4 17 2 PH1802  
41 19 26.4 18 2 A61392  
42 19 26.4 18 2 S59490  
43 19 26.4 19 2 D24417  
44 19 26.4 19 2 B26930  
45 19 26.4 20 2 A53875

methane monooxygen  
arsenite oxidase I  
MHC class II histo  
sormatin - sorghum  
pregnancy-specific  
ribosomal protein  
R-phycoerythrin ga  
proteochondroitin c  
very late antigen-  
interphotoreceptor  
T cell receptor al  
brain-associated s  
translation elonga  
interphotoreceptor  
ermG leader peptid  
creatine kinase (E

ALIGNMENTS

RESULT 1  
C39800

Calcium-activated potassium channel, alternate exon B - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 09-Jul-2004

C;Accession: C39800

R;Atkinson, N.S.; Robertson, G.A.; Ganetzky, B.

Science 253, 551-555, 1991

A;Title: A component of calcium-activated potassium channels encoded by the Drosophila

A;Reference number: A39800; MUID:91313401; PMID:1857984

A;Accession: C39800

A;Molecule type: mRNA

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A;Residues: 1-22 <ATK>

A;Cross-references: UNIPROT:Q03720

C;Genetics:

A;Gene: FlyBase:slo

A;Cross-references: FlyBase:FBgn0003429

Query Match 43.1%; Score 31; DB 2; Length 22;  
Best Local Similarity 44.4%; Pred. No. 35;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPSAFQV 9  
:|:|:|:|:  
Db 6 ANPYAGYQL 14

RESULT 2  
PS0446

potassium channel protein Slo 11 - fruit fly (Drosophila melanogaster) (fragment)

C;Species: Drosophila melanogaster

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004

C;Accession: PS0446

R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bon

Neuron 9, 209-216, 1992

A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.

A;Reference number: JH0697; MUID:92360298; PMID:1497890

A;Accession: PS0446

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-23 <ADE>

A;Cross-references: UNIPROT:Q03720

C;Comment: This potassium channel is activated by calcium.

C;Genetics:

A;Gene: FlyBase:slo

A;Cross-references: FlyBase:FBgn0003429

C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 43.1%; Score 31; DB 2; Length 23;  
Best Local Similarity 44.4%; Pred. No. 37;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFOV 9  
:||||: :|  
Db 7 ANPYAGYQL 15

RESULT 3  
A48968  
exo-poly-alpha-galacturonidase (EC 3.2.1.82) - Clostridium thermosaccharolyticum (frag  
N/Alternate names: exo-poly-alpha-galacturonate hydrolase  
C/Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum  
C/Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 06-Dec-1996  
C/Accession: A48968  
R/Van Rijssel, M.; Gervig, G.J.; Hansen, T.A.  
Appl. Environ. Microbiol. 59, 828-836, 1993  
A/Title: Isolation and characterization of an extracellular glycosylated protein complex  
A/Reference number: A48968; MUID:93243739; PMID:8481009  
A/Accession: A48968  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-23 <VAN>  
A/Note: sequence extracted from NCBI backbone (NCBIP:130462)  
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 41.7%; Score 30; DB 2; Length 23;  
Best Local Similarity 45.5%; Pred. No. 56; Mismatches 3; Indels 0; Gaps 0;  
Matches 5; Conservative 3

QY 4 YSAFOVDITD 14  
:||||: :|  
Db 3 YAAFEYDXTFN 13

RESULT 4  
S16376  
L-serine dehydratase beta chain - Peptostreptococcus asaccharolyticus  
C/Species: Peptostreptococcus asaccharolyticus  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C/Accession: S16376  
R/Grabowski, R.; Buckel, W.  
Eur. J. Biochem. 199, 89-94, 1991  
A/Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat  
A/Reference number: S16224; MUID:91293139; PMID:2065681  
A/Accession: S16376  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-16 <EUR>  
A/Cross-references: UNIPROT:P33074

Query Match 37.5%; Score 27; DB 2; Length 16;  
Best Local Similarity 83.3%; Pred. No. 1.3e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFOV 9  
:||||: :|  
Db 1 YSAFEV 6

RESULT 5  
S69371  
duodenase - bovine (fragment)  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004  
C/Accession: S69371  
R/Zamolodchikova, T.S.; Vorotyntseva, T.I.; Antonov, V.K.  
Eur. J. Biochem. 227, 866-872, 1995  
A/Title: Duodenase, a new serine protease of unusual specificity from bovine duodenal mu  
A/Reference number: S69371; MUID:95172075; PMID:7867648  
A/Accession: S69371  
A/Molecule type: protein  
A/Residues: 1-21 <ZAM>  
A/Cross-references: UNIPROT:Q9GLN2  
C/Superfamily: trypsin; trypsin homology

Query Match 37.5%; Score 27; DB 2; Length 21;  
Best Local Similarity 71.4%; Pred. No. 1.8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAF 7  
:||||: :|  
Db 11 SRPYMAF 17

RESULT 6  
A58946  
formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum) chain C - Methanobacterium t  
N/Alternate names: formylmethanofuran dehydrogenase (molybdenum) chain B [misidentificat  
C/Species: Methanobacterium thermoautotrophicum  
C/Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 04-Feb-2000  
C/Accession: A58946  
R/Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.  
Eur. J. Biochem. 234, 910-920, 1995  
A/Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoautot  
A/Reference number: S63519; MUID:96163477; PMID:8575452  
A/Accession: A58946  
A/Molecule type: protein  
A/Residues: 1-17 <HOC>  
A/Note: the authors identify this peptide as the amino terminus of chain B, but it appea  
C/Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin; oxidoreduct

Query Match 36.1%; Score 26; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 PYSAFOVDITD 14  
:||||: :|  
Db 6 PTSDFOIGLEAD 17

RESULT 7  
S05236  
exoenzyme C3 - Clostridium botulinum (fragment)  
C/Species: Clostridium botulinum  
C/Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C/Accession: S05236  
R/Torata, S.; Yokosawa, N.; Yokosawa, H.; Ishii, S.I.; Oguma, K.  
FEBS Lett. 252, 83-87, 1989  
A/Title: Immuno-crossreactivity between botulinum neurotoxin type C1 or D and exoenzyme  
A/Reference number: S05236; MUID:89338716; PMID:2474453  
A/Accession: S05236  
A/Molecule type: protein  
A/Residues: 1-22 <TOR>  
A/Cross-references: UNIPROT:Q7M0L1

Query Match 36.1%; Score 26; DB 2; Length 22;  
Best Local Similarity 45.5%; Pred. No. 2.8e+02;  
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFOVDI 11  
:||||: :|  
Db 3 SNTYQEFNTNI 13

RESULT 8  
S00616  
paraspore crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleria  
N/Alternate names: delta-endotoxin; parasporal crystal protein positive chain  
C/Species: Bacillus thuringiensis  
C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: S00616  
R/Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.  
FEBS Lett. 232, 249-251, 1988  
A/Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxi  
A/Reference number: S00615  
A/Accession: S00616  
A/Molecule type: protein

A;Residues: 1-11 <CHE>  
A;Cross-references: UNIPROT:Q7M154  
C;Comment: This toxin is effective against the larvae of *Galleria melonella* (greater wax moth)  
C;Superfamily: parasporal crystal protein  
C;Keywords: delta-endotoxin

Query Match 34.7%; Score 25; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5  
Db 5 NNPYS 9

RESULT 9  
B44854  
L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.1) - *Vibrio alginolyticus* (fragment)  
C;Species: *Vibrio alginolyticus*  
C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: B44854; B41817  
R;Yamamoto, S.; Tsuzaki, Y.; Tougou, K.; Shinoda, S.  
J. Gen. Microbiol. 138, 1461-1465, 1992  
A;Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from *V. alginolyticus*  
A;Reference number: A44854; MUID:92381494; PMID:1512577  
A;Accession: B44854  
A;Molecule type: protein  
A;Residues: 1-14 <YAM>  
A;Cross-references: UNIPROT:Q9R5I8  
A;Note: sequence extracted from NCBI backbone (NCBIP:112332)  
C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 34.7%; Score 25; DB 2; Length 14;  
Best Local Similarity 55.6%; Pred. No. 2.6e+02;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SAFOVDITI 13  
Db 2 TAPEVDSNI 10

RESULT 10  
A54326  
glandular kallikrein-1 - human (fragment)  
C;Species: *Homo sapiens* (man)  
C;Date: 29-Aug-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995  
C;Accession: A54326  
R;Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.  
Mol. Cell. Endocrinol. 76, 181-190, 1991  
A;Title: Identification and androgen-regulated expression of two major human glandular kallikreins  
A;Reference number: A54326; MUID:92324494; PMID:1726490  
A;Accession: A54326  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: nucleic acid  
A;Residues: 1-13 <RIE>  
A;Experimental source: prostate  
A;Note: sequence extracted from NCBI backbone (NCBIP:108060)

Query Match 31.9%; Score 23; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 5.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5  
Db 2 SHPYS 6

RESULT 11  
A61360  
vespakinin M - hornet (*Vespa mandarinia*)  
C;Species: *Vespa mandarinia*  
C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C;Accession: A61360

R;Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
Chem. Pharm. Bull. 24, 2896-2897, 1976  
A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the venom of *Vespa mandarinia*  
A;Reference number: A61360; MUID:77114342; PMID:1017116  
A;Accession: A61360  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <KIS>  
A;Cross-references: UNIPROT:Q7M3T3  
C;Superfamily: unassigned animal peptides  
C;Keywords: hydroxyproline; venom  
F;4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 30.6%; Score 22; DB 2; Length 12;  
Best Local Similarity 42.9%; Pred. No. 7.7e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10  
Db 6 FSPFRID 12

RESULT 12  
PS0371  
hypothetical protein (psaC region) - *Synechococcus* sp. (fragment)  
C;Species: *Synechococcus* sp.  
C;Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 08-Oct-1999  
C;Accession: PS0371  
R;Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.  
Gene 112, 123-128, 1992  
A;Title: The psaC genes of *Synechococcus* sp. PCC7002 and *Cyanophora paradoxa*: cloning and characterization  
A;Reference number: JS0694; MUID:92201692; PMID:1551590  
A;Accession: PS0371  
A;Molecule type: DNA  
A;Residues: 1-14 <RHI>  
A;Cross-references: GB:M86238; NID:GL54574; PIDN:AAA27351.1; PID:G552030

Query Match 30.6%; Score 22; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 9.2e+02;  
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 FQVDIT 12  
Db 4 FKLDVT 9

RESULT 13  
A61612  
allatostatin - tobacco hornworm  
C;Species: *Manduca sexta* (tobacco hornworm)  
C;Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: A61612  
R;Kramer, S.J.; Toschi, A.; Miller, C.A.; Katsoka, H.; Quistad, G.B.; Li, J.P.; Carney, P.  
Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991  
A;Title: Identification of an allatostatin from the tobacco hornworm *Manduca sexta*.  
A;Reference number: A61612; MUID:92052112; PMID:1946359  
A;Accession: A61612  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-15 <KRA>  
A;Cross-references: UNIPROT:P42559  
C;Keywords: neuropeptide; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 30.6%; Score 22; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 9.9e+02;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPVSF 7  
Db 10 NPISCF 15

## RESULT 14

A61334  
trypsin (EC 3.4.21.4) 1 - starfish (*Dermasterias imbricata*) (fragment)  
C:Species: *Dermasterias imbricata*  
C>Date: 17-Jul-1994 #sequence\_revision 17-Jul-1994 #text\_change 09-Jul-2004  
C:Accession: A61334  
R:Estell, D.A.; Laskowski Jr., M.  
Biochemistry 19, 124-131, 1980  
A:Title: *Dermasterias imbricata* trypsin 1: an enzyme which rapidly hydrolyzes the reaction  
A:Reference number: A61334; MUID:80109692; PMID:7352972  
A:Accession: A61334  
A:Molecule type: protein  
A:Residues: 1-17 <EST>  
A:Cross-references: UNIPROT:O7M433  
C:Comment: This isoform is novel in that it readily dissociates from bovine pancreatic B  
inhibited.  
C:Superfamily: trypsin; trypsin homology  
C:Keywords: hydrolase; protein digestion; serine proteinase

Query Match 30.6%; Score 22; DB 2; Length 17;  
Best Local Similarity 66.7%; Pred. No. 1.1e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSA 6  
| | | | |  
DB 11 SRPYQA 16

## RESULT 15

S43834  
DNA topoisomerase (EC 5.99.1.2) - *Klebsiella* sp. (ATCC 15380) (fragment)  
C:Species: *Klebsiella* sp.  
A:Variety: ATCC 15380  
C>Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 07-May-1999  
C:Accession: S43834  
R:lynnch, A.S.; Tyrrell, R.; Smerdon, S.J.; Briggs, G.S.; Wilkinson, A.J.  
Biochem. J. 299, 129-136, 1994  
A:Title: Characterization of the CysB protein of *Klebsiella aerogenes*: direct evidence  
A:Reference number: S43834; MUID:94220019; PMID:8166630  
A:Accession: S43834  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-18 <LVN>  
A:Experimental source: ATCC 15380  
C:Genetics:  
C:Gene: topI  
C:Function:  
A:Description: catalyzes ATP-independent transient breakage of DNA phosphodiester bonds  
rejoining; this reaction will lead to the conversion of one topological isomer of DNA to  
C:Superfamily: bacterial type I DNA topoisomerase  
C:Keywords: DNA binding; DNA replication; isomerase; zinc finger

Query Match 30.6%; Score 22; DB 2; Length 18;  
Best Local Similarity 57.1%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10  
: | | | : |  
DB 4 WSAFFID 10

Search completed: November 14, 2004, 12:03:13  
Job time : 8.6383 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 11.0213 Seconds  
(without alignments)  
84.242 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72  
Sequence: 1 SNPYSAFQVDITID 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	51.4	17	3	US-09-177-249-173
2	32	44.4	17	1	US-08-173-510B-63
3	32	44.4	17	1	US-08-458-218-61
4	32	44.4	17	2	US-08-450-497-63
5	32	44.4	17	4	US-08-060-433C-13
6	32	44.4	22	1	US-08-116-733-5
7	29	40.3	20	3	US-08-630-052-25
8	28	38.9	21	4	US-09-270-767-56843
9	27	37.5	14	2	US-08-934-222-110
10	27	37.5	14	2	US-08-933-402-110
11	27	37.5	14	2	US-09-207-621-110
12	27	37.5	14	2	US-08-532-818-110
13	27	37.5	14	3	US-09-231-797-110
14	27	37.5	14	3	US-08-934-224-110
15	27	37.5	14	3	US-08-933-843-110
16	27	37.5	14	3	US-08-934-223-110
17	27	37.5	14	3	US-09-413-492-110
18	27	37.5	17	1	US-08-435-925C-7
19	27	37.5	17	1	US-08-435-925C-8
20	27	37.5	21	1	US-08-290-373B-7
21	27	37.5	21	1	US-08-127-499A-18
22	27	37.5	21	1	US-08-482-847-18
23	26	36.1	7	1	US-08-281-193-3
24	26	36.1	7	1	US-08-422-106-3
25	26	36.1	7	2	US-08-735-716-3
26	26	36.1	7	2	US-08-555-568B-3
27	26	36.1	7	3	US-09-519-223-3

28 36.1 7 4 US-09-927-180-3  
29 36.1 7 5 PCT-US95-08069-3  
30 36.1 15 3 US-09-227-357-437  
31 36.1 22 1 US-08-399-696-89  
32 34.7 8 3 US-08-444-818-304  
33 34.7 8 3 US-08-444-818-305  
34 34.7 15 5 PCT-US91-09422-27  
35 34.7 16 3 US-08-847-844A-75  
36 34.7 18 4 US-09-250-609-39  
37 34.7 18 4 US-09-250-611-39  
38 34.7 20 3 US-08-612-973-56  
39 34.7 20 3 US-08-927-597-56  
40 34.7 20 4 US-08-635-886C-15  
41 34.7 20 4 US-08-974-690C-15  
42 34.7 20 4 US-08-974-685-15  
43 34.7 20 4 US-08-861-153A-10  
44 34.7 21 3 US-08-907-468-11  
45 24.5 34.0 17 3 US-08-652-877-1

## ALIGNMENTS

RESULT 1  
US-09-177-249-173  
; Sequence 173, Application US/09177249  
; Patent No. 6229064  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
; FILE REFERENCE: 023070-086120US  
; CURRENT APPLICATION NUMBER: US/09/177,249  
; CURRENT FILING DATE: 1998-10-22  
; EARLIER APPLICATION NUMBER: US 09/071,838  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 173  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-177-249-173

Query Match 51.4%; Score 37; DB 3; Length 17;  
Best Local Similarity 50.0%; Pred. No. 1.9;  
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVDITID 14  
||| | : :  
Db 3 SNPYRKFQNTYKD 16

RESULT 2  
US-08-173-510B-63  
; Sequence 63, Application US/08173510B  
; Patent No. 5747296  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW MOYLE, ET AL.  
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,510B  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOV-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 205/073  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 63:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-173-510B-63

Query Match 44.4%; Score 32; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFQVDIT 12  
|||:|  
Db 1 SAFELDIT 8

RESULT 3  
US-08-458-218-61  
Sequence 61, Application US/08458218  
Patent No. 5789178  
GENERAL INFORMATION:  
APPLICANT: MATTHEW MOYLE ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 102  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,218  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOVEMBER-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 203/226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-458-218-61

Query Match 44.4%; Score 32; DB 1; Length 17;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFQVDIT 12  
|||:|  
Db 1 SAFELDIT 8

RESULT 4  
US-08-450-497-63  
Sequence 63, Application US/08450497  
Patent No. 591900  
GENERAL INFORMATION:  
APPLICANT: MATTHEW MOYLE, ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,497  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/173,510  
FILING DATE: 23-DEC-1993  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOV-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 205/073

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
US-08-450-497-63

Query Match 44.4%; Score 32; DB 2; Length 17;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFQVDIT 12  
|||:||||  
Db 1 SAFELDIT 8

RESULT 5  
US-08-060-433C-13  
; Sequence 13, Application US/08060433C  
; Patent No. 6756211  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW MOYLE ET AL.  
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
; NUMBER OF SEQUENCES: 41  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44  
; MEDIUM TYPE: Mb storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/060,433C  
; FILING DATE: 11 May 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/881,721  
; FILING DATE: 11 May 1992  
; APPLICATION NUMBER: 07/996,972  
; FILING DATE: 24 December 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 200/271  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
US-08-060-433C-13

Query Match 44.4%; Score 32; DB 4; Length 17;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFQVDIT 12

Db 1 SAFELDIT 8  
|||:||||

RESULT 6  
US-08-116-733-5  
; Sequence 5, Application US/08116733  
; Patent No. 5516632  
; GENERAL INFORMATION:  
; APPLICANT: PALKER, Thomas J.  
; APPLICANT: HAYNES, Barton F.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/116,733  
; FILING DATE: 07-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 1579-33  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; TELEX: 200797 NIXN UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 22 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-116-733-5

Query Match 44.4%; Score 32; DB 1; Length 22;  
Best Local Similarity 54.5%; Pred. No. 22;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11  
|||:||||  
Db 1 SSPYWKQHDV 11

RESULT 7  
US-08-630-052-25  
; Sequence 25, Application US/08630052  
; Patent No. 639296  
; GENERAL INFORMATION:  
; APPLICANT: Brent, Roger  
; APPLICANT: McCoy, John M.  
; APPLICANT: Jessen, Timm H.  
; APPLICANT: Xu, Chanxing Wilson  
; TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson, P.C.  
; STREET: 225 Franklin Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,052  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/504,538  
FILING DATE: July 20, 1995  
APPLICATION NUMBER: 08/278,082  
FILING DATE: July 20, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Karen F. Lech  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/311001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-052-25

Query Match 40.3%; Score 29; DB 3; Length 20;  
Best Local Similarity 62.5%; Pred. No. 71;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10  
|:|:|:  
Db 13 PHSVFND 20

RESULT 8  
US-09-270-767-56843  
Sequence 56843, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 56843  
LENGTH: 21  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-56843

Query Match 38.9%; Score 28; DB 4; Length 21;  
Best Local Similarity 27.3%; Pred. No. 1.2e+02;  
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDITD 14  
|:|:|:|:  
Db 7 YXKENIDVSLN 17

RESULT 9  
US-08-934-222-110  
Sequence 110, Application US/08934222  
Patent No. 5928896

GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
CURRENT APPLICATION DATA:  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,222  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-222-110

Query Match 37.5%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
|:|:|:  
Db 1 NPWTVFQ 7

RESULT 10  
US-08-933-402-110  
Sequence 110, Application US/08933402  
Patent No. 5948887  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
CURRENT APPLICATION DATA:  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,402  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-402-110

Query Match 37.5%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPVSAFQ 8  
Db 1 NPWTVFQ 7

## RESULT 11

US-09-207-621-110  
Sequence 110, Application US/09207621  
Patent No. 5952465  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/207,621  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148

INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-207-621-110

Query Match 37.5%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPVSAFQ 8  
Db 1 NPWTVFQ 7

## RESULT 12

US-08-532-818-110  
Sequence 110, Application US/08532818  
Patent No. 5965698  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-532-818-110

Query Match 37.5%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPVSAFQ 8  
Db 1 NPWTVFQ 7

## RESULT 13

US-09-231-797-110

; Sequence 110, Application US/09231797  
; Patent No. 6084066

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/231,797

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; APPLICATION NUMBER: PCT/US94/04294

; FILING DATE: 21-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Isaacson, John P.

; REGISTRATION NUMBER: 33,751

; REFERENCE/DOCKET NUMBER: 040433/0148

; INFORMATION FOR SEQ ID NO: 110:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-09-231-797-110

Query Match

Best Local Similarity 37.5%; Score 27; DB 3; Length 14;

Mismatches 2; Conservative 2; Indels 1; Gaps 0;

QY 2 NPYSAFQ 8

Db 1 NPWTVFQ 7

RESULT 14

US-08-934-224-110

; Sequence 110, Application US/08934224

; Patent No. 6100044

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/934,224

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; APPLICATION NUMBER: PCT/US94/04294

; FILING DATE: 21-APR-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Isaacson, John P.

; REGISTRATION NUMBER: 33,751

; REFERENCE/DOCKET NUMBER: 040433/0148

; INFORMATION FOR SEQ ID NO: 110:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; US-08-934-224-110

Query Match

Best Local Similarity 37.5%; Score 27; DB 3; Length 14;

Mismatches 2; Conservative 2; Indels 1; Gaps 0;

QY 2 NPYSAFQ 8

Db 1 NPWTVFQ 7

RESULT 15

US-08-933-843-110

; Sequence 110, Application US/08933843

; Patent No. 6111069

; GENERAL INFORMATION:

; APPLICANT: EVANS, Herbert J.

; APPLICANT: KINI, R. Manjunatha

; TITLE OF INVENTION: Polypeptides That Include Conformation-

; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction

; NUMBER OF SEQUENCES: 153

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: Suite 500, 3000 K Street NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20007

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/933,843

; FILING DATE: 19-SEPT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/532,818

; FILING DATE: 03-MAY-1996

; APPLICATION NUMBER: U.S. 08/143,364

; FILING DATE: 29-OCT-1993

; ATTORNEY/AGENT INFORMATION:

; APPLICATION NUMBER: U.S. 08/051,741

; FILING DATE: 23-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Isacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-843-110

Query Match 37.5%; Score 27; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred.No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||:|  
Db 1 NPWTVFQ 7

Search completed: November 14, 2004, 12:08:49  
Job time : 11.0213 secs

**This Page Blank (uspto)**



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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:32:59 ; Search time 27 Seconds  
(without alignments)  
34.387 Million cell updates/sec

Title: US-09-831-253F-7

Perfect score: 72  
Sequence: 1 SNPSAFOVDITID 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 145874

Minimum DB seq length: 0  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
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2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	37.5	14	2 US-08-934-222-110	Sequence 110, Appl
2	27	37.5	14	2 US-08-933-402-110	Sequence 110, Appl
3	27	37.5	14	2 US-09-207-621-110	Sequence 110, Appl
4	27	37.5	14	2 US-08-532-818-110	Sequence 110, Appl
5	27	37.5	14	3 US-09-231-797-110	Sequence 110, Appl
6	27	37.5	14	3 US-08-934-224-110	Sequence 110, Appl
7	27	37.5	14	3 US-08-933-843-110	Sequence 110, Appl
8	27	37.5	14	3 US-08-934-223-110	Sequence 110, Appl
9	27	37.5	14	3 US-09-413-492-110	Sequence 110, Appl
10	26	36.1	7	1 US-08-281-193-3	Sequence 3, Appl
11	26	36.1	7	1 US-08-422-106-3	Sequence 3, Appl
12	26	36.1	7	2 US-08-735-716-3	Sequence 3, Appl
13	26	36.1	7	2 US-08-555-568B-3	Sequence 3, Appl
14	26	36.1	7	3 US-09-519-223-3	Sequence 3, Appl
15	26	36.1	7	4 US-09-927-180-3	Sequence 3, Appl
16	26	36.1	7	5 PCT-US95-08069-3	Sequence 304, Appl
17	25	34.7	8	3 US-08-444-818-304	Sequence 305, Appl
18	25	34.7	8	3 US-08-444-818-305	Sequence 99, Appl
19	23	31.9	11	2 US-08-621-803-99	Sequence 99, Appl
20	23	31.9	11	2 US-08-598-873-39	Sequence 99, Appl
21	23	31.9	11	3 US-08-605-430-39	Sequence 99, Appl
22	23	31.9	11	3 US-09-217-352-99	Sequence 99, Appl
23	23	31.9	11	4 US-09-717-054-39	Sequence 33, Appl
24	23	31.9	14	4 US-09-517-439-33	Sequence 33, Appl
25	23	31.9	14	4 US-09-517-439-36	Sequence 36, Appl
26	23	31.9	14	4 US-09-517-439-39	Sequence 39, Appl
27	22.5	31.2	12	1 US-08-190-788A-70	Sequence 70, Appl

ALIGNMENTS

RESULT 1

US-08-934-222-110  
; Sequence 110, Application US/08934222  
; Patent No. 5928896  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,222  
; FILING DATE: 19-SEPT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-934-222-110

Query Match 37.5%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
||: ||  
Db 1 NPWTVPQ 7

## RESULT 2

US-08-933-402-110  
; Sequence 110, Application US/08933402  
; Patent No. 5948887  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,402  
; FILING DATE: 19-SEPT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-933-402-110

Query Match 37.5%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
||: ||  
Db 1 NPWTVPQ 7

## RESULT 3

US-09-207-621-110  
; Sequence 110, Application US/09207621  
; Patent No. 5952465  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW

; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/207,621  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-207-621-110

Query Match 37.5%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
||: ||  
Db 1 NPWTVPQ 7

## RESULT 4

US-08-532-818-110  
; Sequence 110, Application US/08532818  
; Patent No. 5965658  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/532,818  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-532-818-110

Query Match 37.5%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||: ||  
Db 1 NPWTVFQ 7

## RESULT 5

US-09-231-797-110  
Sequence 110, Application US/09231797  
Patent No. 6084066  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/231,797  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-231-797-110

Query Match 37.5%; Score 27; DB 3; Length 14;

Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||: ||  
Db 1 NPWTVFQ 7

## RESULT 6

US-08-934-224-110  
Sequence 110, Application US/08934224  
Patent No. 6100044  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,224  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-224-110

Query Match 37.5%; Score 27; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||: ||  
Db 1 NPWTVFQ 7

## RESULT 7

US-08-933-843-110  
Sequence 110, Application US/08933843  
Patent No. 6111069  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-



; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-413-492-110

Query Match 37.5%; Score 27; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||:|:  
Db 1 NPWTVFQ 7

RESULT 10  
US-08-281-193-3  
; Sequence 3, Application US/08281193  
; Patent No. 546595  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 15  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/281,193  
; FILING DATE:  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-281-193-3

Query Match 36.1%; Score 26; DB 1; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||:|:  
Db 1 NPHSGFR 7

RESULT 11  
US-08-422-106-3  
; Sequence 3, Application US/08422106  
; Patent No. 5589170  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 15  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,106  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/281,193  
; FILING DATE: 27-JUL-1994

; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-422-106-3

Query Match 36.1%; Score 26; DB 1; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||:|:  
Db 1 NPHSGFR 7

RESULT 12  
US-08-735-716-3  
; Sequence 3, Application US/08735716  
; Patent No. 5840511  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 15  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/735,716  
; FILING DATE: 23-OCT-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/281,193  
; FILING DATE: 27-JUL-1994  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-735-716-3

Query Match 36.1%; Score 26; DB 2; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||:|:  
Db 1 NPHSGFR 7

RESULT 13  
US-08-555-568B-3  
; Sequence 3, Application US/08555568B  
; Patent No. 5976854  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts

COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/555,568B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-555-568B-3

Query Match 36.1%; Score 26; DB 2; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
Db 1 NPHSGFR 7

RESULT 14  
US-09-519-223-3  
; Sequence 3, Application US/09519223  
; Patent No. 6274140  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids

TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-09-519-223-3

Query Match 36.1%; Score 26; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
Db 1 NPHSGFR 7

RESULT 15  
US-09-927-180-3  
; Sequence 3, Application US/09927180  
; Patent No. 6645736  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
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; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
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; APPLICATION NUMBER: US/09/519,223  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/555,568  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids

QY 2 NPYSAPQ 8  
Db 1 NPHSGFR 7

Search completed: November 14, 2004, 13:46:48  
Job time : 28.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:45:09 ; Search time 94.5 Seconds  
(without alignments)  
52.418 Million cell updates/sec

Title: US-09-831-253F-7  
Perfect score: 72  
Sequence: 1 SNPSAFQVDITD 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 222219

Minimum DB seq length: 0  
Maximum DB seq length: 14

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA.\*
- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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  - 8: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
  - 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
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  - 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	38.9	10	10	US-09-880-748-3097
2	28	38.9	10	14	US-10-293-418-3097
3	28	38.9	13	11	US-09-842-776A-30
4	27	37.5	11	10	US-09-880-748-2839
5	27	37.5	11	14	US-10-293-418-2839
6	27	37.5	12	14	US-10-286-457-177
7	26.5	36.8	10	14	US-10-151-882-26
8	26	36.1	7	9	US-09-927-180-3
9	26	36.1	9	14	US-10-334-726-118
10	26	36.1	9	14	US-10-334-726-220
11	25	34.7	7	14	US-10-400-991-50
12	25	34.7	9	10	US-09-995-529-83
13	25	34.7	9	11	US-09-995-529-83

14	25	34.7	10	10	US-09-572-404B-2428	Sequence 2428, Ap
15	25	34.7	10	16	US-10-327-598-519	Sequence 519, Appl
16	25	34.7	11	9	US-09-966-871-70	Sequence 70, Appl
17	25	34.7	11	13	US-10-039-645-70	Sequence 70, Appl
18	25	34.7	11	14	US-10-139-084-70	Sequence 70, Appl
19	25	34.7	11	15	US-10-458-860-70	Sequence 70, Appl
20	25	34.7	11	17	US-10-625-047-8	Sequence 8, Appl
21	25	34.7	12	14	US-10-073-118-30	Sequence 30, Appl
22	25	34.7	12	16	US-10-128-520-34	Sequence 34, Appl
23	25	34.7	13	12	US-09-855-604-602	Sequence 602, Appl
24	25	34.7	13	12	US-09-855-604-792	Sequence 792, Appl
25	25	34.7	14	14	US-10-355-738-15	Sequence 15, Appl
26	24	33.3	8	15	US-10-182-452A-319	Sequence 319, Appl
27	24	33.3	8	15	US-10-182-452A-1072	Sequence 1072, Ap
28	24	33.3	8	15	US-10-182-452A-1073	Sequence 1073, Ap
29	24	33.3	8	15	US-10-182-452A-1074	Sequence 1074, Ap
30	24	33.3	8	15	US-10-182-452A-1085	Sequence 1085, Ap
31	24	33.3	8	15	US-10-182-452A-1086	Sequence 1086, Ap
32	24	33.3	8	15	US-10-182-452A-1087	Sequence 1087, Ap
33	24	33.3	8	15	US-10-182-452A-1104	Sequence 1104, Ap
34	24	33.3	8	15	US-10-182-452A-1105	Sequence 1105, Ap
35	24	33.3	8	15	US-10-182-452A-1106	Sequence 1106, Ap
36	24	33.3	8	15	US-10-182-452A-1112	Sequence 1112, Ap
37	24	33.3	8	15	US-10-182-452A-1113	Sequence 1113, Ap
38	24	33.3	8	15	US-10-182-452A-1282	Sequence 1282, Ap
39	24	33.3	10	10	US-09-572-404B-2193	Sequence 2193, Ap
40	24	33.3	10	14	US-10-200-708-99	Sequence 99, Appl
41	24	33.3	11	14	US-10-014-340-453	Sequence 453, Appl
42	24	33.3	12	16	US-10-652-407-11	Sequence 11, Appl
43	24	33.3	14	10	US-09-880-748-2619	Sequence 2619, Ap
44	24	33.3	14	14	US-10-293-418-2619	Sequence 2619, Ap
45	23.5	32.6	10	15	US-10-149-138-4377	Sequence 4377, Ap

ALIGNMENTS

RESULT 1

US-09-880-748-3097  
; Sequence 3097, Application US/09880748  
; Publication No. US20030059937A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
; FILE REFERENCE: PF523  
; CURRENT APPLICATION NUMBER: US/09/880,748  
; CURRENT FILING DATE: 2001-05-15  
; PRIOR APPLICATION NUMBER: 60/212,210  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 60/240,816  
; PRIOR FILING DATE: 2000-10-17  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/277,379  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 3239  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3097  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-880-748-3097

Query Match 38.9%; Score 28; DB 10; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.2e+02;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 NPYSAFQV 9

DB 3 SPYDAFDI 10

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RESULT 2
US-10-293-418-3097
; Sequence 3097, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3097
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3097

Query Match      38.9%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
DB      3 SPYDAFDI 10

RESULT 3
US-09-842-776A-30
; Sequence 30, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR3) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
US-09-842-776A-30

Query Match      38.9%; Score 28; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 SNPYS 5
DB      6 SNPYS 10

RESULT 4
US-09-880-748-2839
; Sequence 2839, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2839

Query Match      37.5%; Score 27; DB 10; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 PYSAFQV 9
DB      5 PYDAFDI 11

RESULT 5
US-10-293-418-2839
; Sequence 2839, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
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## US-10-293-418-2839

Query Match 37.5%; Score 27; DB 14; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.7e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PYSAFQV 9  
||| :  
Db 5 PYDAFDI 11

## RESULT 6

US-10-286-457-177  
; Sequence 177, Application US/10286457  
; Publication No. US20030166004A1  
; GENERAL INFORMATION:  
; APPLICANT: JENO GYURIS et al.  
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY  
; FILE REFERENCE: GPCI-POI-178  
; CURRENT APPLICATION NUMBER: US/10/286,457  
; CURRENT FILING DATE: 2002-11-01  
; PRIOR APPLICATION NUMBER: 60/334822  
; PRIOR FILING DATE: 2001-11-01  
; NUMBER OF SEQ ID NOS: 684  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 177  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based  
; OTHER INFORMATION: ability to selectively bind to endothelial cells  
US-10-286-457-177

Query Match 37.5%; Score 27; DB 14; Length 12;  
Best Local Similarity 83.3%; Pred. No. 4.1e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPWSA 6  
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Db 1 SNPWSA 6

## RESULT 7

US-10-151-882-26  
; Sequence 26, Application US/10151882  
; Publication No. US20030059862A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRII)  
; FILE REFERENCE: PF554  
; CURRENT APPLICATION NUMBER: US/10/151,882  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: 60/293,100  
; PRIOR FILING DATE: 2001-05-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 26  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-151-882-26

Query Match 36.8%; Score 26.5; DB 14; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.1e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 SNP-YSAFQV 9  
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Db 1 SNPQYDAFDI 10

## RESULT 8

## US-09-927-180-3

; Sequence 3, Application US/09927180  
; Patent No. US20020106364A1  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; ; Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genetics Institute, Inc.  
; STREET: 87 CambridgePark Drive  
; CITY: Cambridge  
; STATE: Massachusetts  
; COUNTRY: U.S.A.  
; ZIP: 02140

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/927,180  
; FILING DATE: 09-Aug-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/519,223  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Scott A.  
; REGISTRATION NUMBER: 32,724  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 498-8224  
; TELEFAX: (617) 876-5851  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-927-180-3

Query Match 36.1%; Score 26; DB 9; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.4e+06;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NPYSAFQ 8  
||| :  
Db 1 NPHSGFR 7

## RESULT 9

US-10-334-726-118  
; Sequence 118, Application US/10334726  
; Publication No. US20030211521A1  
; GENERAL INFORMATION:  
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE  
; TITLE OF INVENTION: BREAST CANCER ANTIGEN  
; FILE REFERENCE: 1090-36  
; CURRENT APPLICATION NUMBER: US/10/334,726  
; CURRENT FILING DATE: 2003-01-02  
; PRIOR APPLICATION NUMBER: US/09/645,446  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: PCT/GB99/00866  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: GB 9805877.9  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 118  
; LENGTH: 9

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:predicted  
; OTHER INFORMATION: peptide  
US-10-334-726-118

Query Match 36.1%; Score 26; DB 14; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAF 7  
Db 3 NPNYLF 8

RESULT 10  
US-10-334-726-220  
; Sequence 220, Application US/10334726  
; Publication No. US20030211521A1  
; GENERAL INFORMATION:  
; APPLICANT: TAYLOR-PAPADIMITROU, JOYCE  
; TITLE OF INVENTION: BREAST CANCER ANTIGEN  
; FILE REFERENCE: 1090-36  
; CURRENT APPLICATION NUMBER: US/10/334,726  
; PRIOR FILING DATE: 2003-01-02  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR FILING DATE: 1998-09-20  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 220  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:predicted  
; OTHER INFORMATION: peptide  
US-10-334-726-220

Query Match 36.1%; Score 26; DB 14; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAF 7  
Db 4 NPNYLF 9

RESULT 11  
US-10-400-991-50  
; Sequence 50, Application US/10400991  
; Publication No. US20030224417A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Glucksmann, Maria A.  
; APPLICANT: Weich, Nadine S.  
; APPLICANT: Hunter, John J.  
; APPLICANT: White, David  
; APPLICANT: MacBeth, Kyle J.  
; APPLICANT: Williamson, Mark J.  
; APPLICANT: Meyers, Rachel E.  
; APPLICANT: Chun, Miyoung  
; TITLE OF INVENTION: 1400, 2838, 14618, 15334, 14274, 32164,  
; TITLE OF INVENTION: 39404, 38911, 26904, 31237, 18057, 16405, 32705, 23224,  
; TITLE OF INVENTION: 27423, 32700, 32712 AND 12216, NOVEL SEVEN-TRANSMEMBRANE  
; TITLE OF INVENTION: PROTEINS/G-PROTEIN COUPLES RECEPTORS  
; FILE REFERENCE: NP103-024OWNIM  
; CURRENT APPLICATION NUMBER: US/10/400,991  
; CURRENT FILING DATE: 2003-03-27

; PRIOR APPLICATION NUMBER: US 10/190,469  
; PRIOR FILING DATE: 2002-07-05  
; PRIOR APPLICATION NUMBER: US 09/439,159  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: US 09/137,063  
; PRIOR FILING DATE: 1998-08-20  
; PRIOR APPLICATION NUMBER: US 10/167,192  
; PRIOR FILING DATE: 2002-06-11  
; PRIOR APPLICATION NUMBER: US 09/420,187  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: US 09/173,869  
; PRIOR FILING DATE: 1998-10-16  
; PRIOR APPLICATION NUMBER: US 10/339,056  
; PRIOR FILING DATE: 2003-01-09  
; PRIOR APPLICATION NUMBER: US 09/377,429  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: US 09/136,726  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: US 09/911,583  
; PRIOR FILING DATE: 2001-07-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 50  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Amino Acid Fragment  
US-10-400-991-50

Query Match 34.7%; Score 25; DB 14; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PYSAFQ 8  
Db 1 PYSLFE 6

RESULT 12  
US-09-995-529-83  
; Sequence 83, Application US/09995529  
; Publication No. US2003009655A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Tang, Ying  
; TITLE OF INVENTION: Humanized Collagen Antibodies and  
; FILE REFERENCE: P-IX 4976  
; CURRENT APPLICATION NUMBER: US/09/995,529  
; CURRENT FILING DATE: 2001-11-26  
; NUMBER OF SEQ ID NOS: 358  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 83  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic antibody mutation  
US-09-995-529-83

Query Match 34.7%; Score 25; DB 10; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5  
Db 5 SNPYT 9

RESULT 13

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US-09-995-529-83
; Sequence 83, Application US/09995529
; Publication No. US20040091482A9
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Tang, Ying
; TITLE OF INVENTION: Humanized Collagen Antibodies and
; TITLE OF INVENTION: Related Methods
; FILE REFERENCE: P-IX 4976
; CURRENT APPLICATION NUMBER: US/09/995,529
; CURRENT FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic antibody mutation
US-09-995-529-83

Query Match          34.7%; Score 25; DB 11; Length 9;
Best Local Similarity 80.0%; Pred.No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5
Db 5 SNPYT 9

RESULT 14
US-09-572-404B-2428
; Sequence 2428, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human Patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2428
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in API2 OR IAP2 OR MIHB at 171-180 and may inter
; OTHER INFORMATION: with Sequence 2427 in this patent.
US-09-572-404B-2428

Query Match          34.7%; Score 25; DB 10; Length 10;
Best Local Similarity 80.0%; Pred.No. 7.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5
Db 4 TNPYS 8

RESULT 15
US-10-327-598-519
; Sequence 519, Application US/10327598
; Publication No. US20040181039A1
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
```

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; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 519
; LENGTH: 10
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-519

Query Match          34.7%; Score 25; DB 16; Length 10;
Best Local Similarity 57.1%; Pred.No. 7.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAF 7
Db 3 SRPFNAF 9

Search completed: November 14, 2004, 14:01:10
Job time : 95.5 secs
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**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:46:55 ; Search time 188 Seconds  
(without alignments)  
27.545 Million cell updates/sec

Title: US-09-831-253F-5

Perfect score: 48

Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1598

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	39.6	8	2	O85406 coxiella bu
2	19	39.6	8	2	Q8NHL3
3	18	37.5	8	2	Q8IVK3
4	18	37.5	9	2	Q9H3Y3
5	18	37.5	9	2	Q38366
6	18	37.5	9	2	Q801K0
7	18	37.5	9	2	Q801K1
8	18	37.5	9	2	Q801K2
9	17	35.4	8	2	Q99MN0
10	17	35.4	9	2	Q71EB9
11	17	35.4	9	2	AAQ08824
12	16	33.3	8	2	Q86SL0
13	16	33.3	9	2	Q94VC6
14	16	33.3	9	2	Q9R5M1
15	16	33.3	9	2	Q8X4G1
16	15	31.2	6	1	E101 LITRU
17	15	31.2	7	1	WWA1_ACHFU
18	15	31.2	7	1	WWA2_ACHFU
19	15	31.2	7	1	WWA3_ACHFU
20	15	31.2	7	2	Q95945
21	15	31.2	8	2	Q70Y57
22	15	31.2	8	2	P77556
23	15	31.2	8	2	CAD45547
24	15	31.2	9	2	Q6LDP7
25	15	31.2	9	2	Q69100
26	15	31.2	9	2	AAA63501
27	14	29.2	7	2	Q8JEB1
28	14	29.2	8	1	C125 CYPDO
29	14	29.2	8	1	COW2_CONFU
30	14	29.2	8	2	Q94VC1
31	14	29.2	8	2	Q9SAY7

32 14 29.2 8 2 Q7M0L0  
33 14 29.2 8 2 Q6R7U6  
34 14 29.2 8 2 AAS09897  
35 14 29.2 8 2 AAS09898  
36 13 27.1 7 2 Q9BRV4  
37 13 27.1 8 2 Q7RBP6  
38 13 27.1 8 2 O18854  
39 13 27.1 8 2 Q7M124  
40 13 27.1 8 2 P79940  
41 13 27.1 8 2 Q98TU5  
42 13 27.1 8 2 AAB33374  
43 13 27.1 9 1 LITR\_PHYRO  
44 13 27.1 9 2 O95953  
45 13 27.1 9 2 Q15891

#### ALIGNMENTS

RESULT 1  
O85406 PRELIMINARY; PRT; 8 AA.  
AC O85406;  
DT 01-NOV-1998 (TREMELrel. 08, Created)  
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)  
DE Hypothetical protein (Fragment).  
OS Coxiella burnetii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;  
OC Coxiellaceae; Coxiella.  
OX NCBI\_TaxID=777;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Nine Mile Phase I;  
RX MEDLINE=9834842; PubMed=9683477;  
RA Willems H., Jaeger C., Baljer G.;  
RT "Physical and genetic map of the obligate intracellular bacterium  
Coxiella burnetii.";  
RL J. Bacteriol. 180:3816-3822(1998).  
DR EMBL; AF064963; AAD09947.1; -;  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 8 AA; 993 MW; 04655AA453772727 CRC64;  
Query Match 39.6%; Score 19; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 3 LMW 6  
DB 1 LLLW 4  
RESULT 2  
Q8NHL3 PRELIMINARY; PRT; 9 AA.  
AC Q8NHL3;  
DT 01-OCT-2002 (TREMELrel. 22, Created)  
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)  
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
DE Killer-cell immunoglobulin-like receptor KIR2DL5.3 (Fragment).  
GN Name=KIR2DL5;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20540100; PubMed=11086080;  
RA Vilches C., Gardiner C.M., Parham P.;  
RT "Gene structure and promoter variation of expressed and nonexpressed  
variants of the KIR2DL5 gene.";  
RL J. Immunol. 165:6416-6421(2000).

```
DR EMBL; AF260137; AAG38010.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 9
SQ SEQUENCE 9 AA; 968 MW; 9DEF85A2D2C69735 CRC64;

Query Match 39.6%; Score 19; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMWVSM 8
DB 2 SLMWVSM 8

RESULT 3
ID Q81VK3 PRELIMINARY; PRT; 8 AA.
AC Q81VK3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Steering2 (Fragment).
OS Homo sapiens (Human).
GN Name=STEERING2;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,
RA Geysen J.J.G.H.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ488208; CAD32561.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1030 MW; E8A7245417737726 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MTW 6
DB 1 MLW 3

RESULT 4
ID Q9H3Y3 PRELIMINARY; PRT; 9 AA.
AC Q9H3Y3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DJ839B11.1 (Novel protein with a Kunitz/Bovine pancreatic trypsin
DE inhibitor domain and WAP-type (Whey Acidic Protein) 'four-disulfide
DE core' domains) (Fragment).
GN Name=dJ461P17.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL121778; CAB76844.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

DR EMBL; AF260137; AAG38010.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 9
SQ SEQUENCE 9 AA; 968 MW; 9DEF85A2D2C69735 CRC64;

Query Match 39.6%; Score 19; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMWVSM 8
DB 2 SLMWVSM 8

RESULT 5
ID Q83366 PRELIMINARY; PRT; 9 AA.
AC Q83366;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E gene product (Fragment).
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP SEQUENCE FROM N.A.
RA Buckley K.J., Hayashi M.;
RL "Role of premature translational termination in the regulation of
RL expression of the phi X174 lysis gene.";
RL J. Mol. Biol. 198:599-607 (1987).
DR EMBL; X07809; CAA30668.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1207 MW; C093B37731B36412 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 4 WTL 6

RESULT 6
ID Q801K0 PRELIMINARY; PRT; 9 AA.
AC Q801K0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Illicura militaris (pin-tailed manakin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Illicura.
OX NCBI_TaxID=208056;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RL "A Multifaceted Approach to the Characterization of an Intergeneric
RL Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120 (2002).
DR EMBL; AV136617; AAN16894.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 7 WTL 9

RESULT 7
ID Q801K1 PRELIMINARY; PRT; 9 AA.
AC Q801K1;

us-09-831-253f-5.closed.rup
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DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Chiroxiphia caudata.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archoosauria; Aves; Neognathae; Passeriformes; Pipridae; Chiroxiphia.
OX NCBI_TaxID=196027;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL; AY136616; AAN16893.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 7 WTL 9

RESULT 8
Q801K2 ID Q801K2 PRELIMINARY; PRT; 9 AA.
AC Q801K2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Antilophia galeata (Helmeted manakin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archoosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Antilophia.
OX NCBI_TaxID=208054;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL; AY136615; AAN16892.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 37.5%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 7 WTL 9

RESULT 9
Q99MN0 ID Q99MN0 PRELIMINARY; PRT; 8 AA.
AC Q99MN0;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Adenosine deaminase tRNA-specific 1 (Fragment).
GN Name=Adat1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
EX MEDLINE=21231131; PubMed=11331948;
RA Maas S., Kim Y.G., Rich A.;
RT "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two
RT tRNA synthetases.";
RL Mamm. Genome 12:387-393(2001).
DR EMBL; AF328904; AAK19310.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 936 MW; F4D05B1AADC1B376 CRC64;

Query Match 35.4%; Score 17; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWT 7
DB 1 MWT 3

RESULT 10
Q71EB9 ID Q71EB9 PRELIMINARY; PRT; 9 AA.
AC Q71EB9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Tumor antigen CML66 short isoform (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14688378;
RA Yan Y., Phan L., Yang F., Talpaz M., Yang Y., Xiong Z., Ng B.,
RA Timchenko N.A., Wu C.J., Ritz J., Wang H., Yang X.-F.;
RT "A novel mechanism of alternative promoter and splicing regulates the
RT epitope generation of tumor antigen CML66-L.";
RL J. Immunol. 172:651-660(2004).
DR EMBL; AF521134; AAQ08824.1; -.
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1128 MW; 55BCA37866D73B57 CRC64;

Query Match 35.4%; Score 17; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8
DB 7 WSM 9

RESULT 11
AAQ08824 ID AAQ08824 PRELIMINARY; PRT; 9 AA.
AC AAQ08824;
DT 02-MAR-2004 (TReMBLrel. 27, Created)
DT 02-MAR-2004 (TReMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TReMBLrel. 27, Last annotation update)
DE Tumor antigen CML66 short isoform (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14688378;
RA Yan Y., Phan L., Yang F., Talpaz M., Yang Y., Xiong Z., Ng B.,
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RA Timchenko N.A., Wu C.J., Ritz J., Wang H., Yang X.-F.;  
 RT "A Novel Mechanism of Alternative Promoter and Splicing Regulates the  
 RL Epitope Generation of Tumor Antigen CML66-L.";  
 RL J. Immunol. 172:651-660(2004).  
 DR EMBL, AF521134; AAQ08824.1; -.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1128 MW; 55BCA37866D73B57 CRC64;

Query Match 35.4%; Score 17; DB 2; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WTM 8  
 |:  
 Db 7 WSM 9

## RESULT 12

Q86SLO PRELIMINARY; PRT; 8 AA.  
 AC Q86SLO; DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Flavocytochrome b-558 alpha polypeptide (Fragment).  
 GN Names=Cyba;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22615572; PubMed=12729892;  
 RA Moreno M.U., San Jose G., Orbe J., Paramo J.A., Beloqui O., Diez J.,  
 RA Zalba G.;  
 RT "Preliminary characterisation of the promoter of the human p22phox  
 RT gene: identification of a new polymorphism associated with  
 RT hypertension.";  
 RL FEBS Lett. 542:27-31(2003).  
 DR EMBL, AV128666; AAM96953.1; -.  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 965 MW; FF9DC37B1046D876 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 WTM 8  
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 Db 6 WAM 8

## RESULT 13

Q94VC6 PRELIMINARY; PRT; 9 AA.  
 AC Q94VC6; DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit I (Fragment).  
 GN Names=COI;  
 OS Varanus pilbarensis.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodactylidae; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.  
 OX NCBI\_TaxID=62048;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Aet J.C.;  
 RA "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";  
 RL Cladistics 17:211-226(2001).  
 DR EMBL, AF407518; AAL10108.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 1064 MW; 874CA5A36411A735 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SLMIWT 7  
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 Db 2 SLTRWS 7

## RESULT 14

Q9R5M1 PRELIMINARY; PRT; 9 AA.  
 AC Q9R5M1; DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 66 kDa cell surface adhesin for heparan sulfate (Fragment).  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
 OX NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=92176005; PubMed=1541563;  
 RA Liang O.D., Acencio F., Fransson L.A., Wadstrom T.;  
 RT "Binding of heparan sulfate to Staphylococcus aureus.";  
 RL Infect. Immun. 60:899-906(1992).  
 DR PIR; A43848; A43848.  
 FT NON\_TER 1 1  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 990 MW; 2289DDD7337861B3 CRC64;

Query Match 33.3%; Score 16; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WT 7  
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 Db 2 WT 3

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 AC Q8X4G1; DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 22947 protein.  
 GN OrderedLocusNames=z2947;  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";  
 RL Nature 409:529-533(2001).  
 DR EMBL; AE005411; AAG56883.1; -.  
 DR PIR; G85802; G85802.  
 KW Complete proteome.  
 SQ SEQUENCE 9 AA; 1107 MW; 8F6CB72699D1B841 CRC64;



Query Match 33.3%; Score 16; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred.No. 1.8e+06;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 4 MIWTNM 9  
| : |  
Db 1 MTYTFM 6

Search completed: November 14, 2004, 14:07:05  
Job time : 189 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 14:07:12 ; Search time 137 Seconds  
(without alignments)  
23.244 Million cell updates/sec

Title: US-09-831-253F-5  
Perfect score: 48  
Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 133040

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	54.2	9	US-09-796-744-10	Sequence 10, Appli
2	26	54.2	9	US-10-231-452-7	Sequence 7, Appli
3	25	52.1	8	US-08-979-847-170	Sequence 170, App
4	25	52.1	8	US-10-114-104-170	Sequence 170, App
5	25	52.1	9	US-10-182-252A-632	Sequence 632, App
6	25	52.1	9	US-10-182-252A-657	Sequence 657, App
7	24	50.0	5	US-10-441-626-35	Sequence 35, Appl
8	24	50.0	5	US-10-441-625-35	Sequence 35, Appl
9	24	50.0	6	US-10-441-626-38	Sequence 38, Appl
10	24	50.0	6	US-10-441-625-38	Sequence 38, Appl
11	24	50.0	7	US-10-651-165-170	Sequence 170, App
12	24	50.0	8	US-08-979-847-169	Sequence 169, App
13	24	50.0	8	US-10-114-104-169	Sequence 169, App

14	24	50.0	9	15	US-10-182-252A-3	Sequence 3, Appli
15	24	50.0	9	15	US-10-182-252A-215	Sequence 215, App
16	24	50.0	9	15	US-10-182-252A-617	Sequence 617, App
17	24	50.0	9	15	US-10-182-252A-631	Sequence 631, App
18	24	50.0	9	15	US-10-182-252A-656	Sequence 656, App
19	24	50.0	9	15	US-10-182-252A-658	Sequence 658, App
20	24	50.0	9	15	US-10-182-252A-685	Sequence 685, App
21	24	50.0	9	15	US-10-182-252A-1216	Sequence 1216, App
22	23	47.9	7	14	US-10-052-578-216	Sequence 216, App
23	23	47.9	7	14	US-10-053-520-216	Sequence 216, App
24	23	47.9	7	14	US-10-053-498B-216	Sequence 216, App
25	23	47.9	7	15	US-10-258-146A-74	Sequence 74, Appli
26	23	47.9	7	15	US-10-328-353-219	Sequence 219, App
27	23	47.9	7	16	US-10-258-144-109	Sequence 109, App
28	23	47.9	8	15	US-10-462-452-475	Sequence 475, App
29	23	47.9	8	15	US-10-601-953-604	Sequence 604, App
30	23	47.9	8	16	US-10-322-266-476	Sequence 476, App
31	23	47.9	9	10	US-09-845-042-27	Sequence 27, Appli
32	23	47.9	9	15	US-10-182-252A-630	Sequence 630, App
33	23	47.9	9	15	US-10-182-252A-655	Sequence 655, App
34	22	45.8	6	14	US-10-348-167-40	Sequence 40, Appl
35	22	45.8	8	8	US-08-979-847-171	Sequence 171, App
36	22	45.8	8	14	US-10-190-082-595	Sequence 595, App
37	22	45.8	8	14	US-10-114-104-171	Sequence 171, App
38	22	45.8	9	9	US-09-751-788-5	Sequence 5, Appli
39	22	45.8	9	9	US-09-751-788-6	Sequence 6, Appli
40	22	45.8	9	9	US-09-780-053-145	Sequence 145, App
41	22	45.8	9	9	US-09-766-889A-51	Sequence 51, Appl
42	22	45.8	9	9	US-09-766-889A-52	Sequence 52, Appl
43	22	45.8	9	10	US-09-995-529-133	Sequence 133, App
44	22	45.8	9	10	US-09-833-039-122	Sequence 122, App
45	22	45.8	9	11	US-09-995-529-133	Sequence 133, App

ALIGNMENTS

RESULT 1  
US-09-796-744-10  
; Sequence 10, Application US/09796744  
; Patent No. US20020098527A1  
; GENERAL INFORMATION:  
; APPLICANT: SHITARA, KENYA  
; APPLICANT: HANAI, NOBUO  
; APPLICANT: SHOJI, EMI  
; APPLICANT: SAKURADA, MIKKIKO  
; APPLICANT: FURUYA, AKIKO  
; APPLICANT: NAKAMURA, KAZUYASU  
; APPLICANT: NIWA, RINPEI  
; APPLICANT: SHIBATA, KENJI  
; APPLICANT: YAMASAKI, MOTOO  
; TITLE OF INVENTION: GENE RECOMBINANT ANTIBODY AND ANTIBODY FRAGMENT THEREOF  
; FILE REFERENCE: 249-170  
; CURRENT APPLICATION NUMBER: US/09/796,744  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: JP 2000-59508  
; PRIOR FILING DATE: 2000-03-03  
; PRIOR APPLICATION NUMBER: JP 2000-401563  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-796-744-10

Query Match 54.2%; Score 26; DB 9; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMIWT 7  
||: ||

Db 4 SLLFWT 9

RESULT 2

US-10-231-452-7

; Sequence 7, Application US/10231452

; Publication No. US20030175273A1

; GENERAL INFORMATION:

; APPLICANT: SHITARA, KENYA

; APPLICANT: NAKAMURA, KAZUYASU

; APPLICANT: HOSAKA, EMI

; APPLICANT: TANAKA, AKIKO

; APPLICANT: KOIKE, MASAMICHI

; TITLE OF INVENTION: HUMAN CDR GRAFTED ANTIBODY AND ANTIBODY FRAGMENT THEREOF

; FILE REFERENCE: 249-273

; CURRENT APPLICATION NUMBER: US/10/231,452

; CURRENT FILING DATE: 2003-04-18

; PRIOR APPLICATION NUMBER: JP 2001-265144

; PRIOR FILING DATE: 2001-08-31

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-231-452-7

Query Match 54.2%; Score 26; DB 14; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.4e+06;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMWT 7

Db 4 SLLFWT 9

RESULT 3

US-08-979-847-170

; Sequence 170, Application US/08979847

; Publication No. US20030039664A1

; GENERAL INFORMATION:

; APPLICANT: PERRON, HERVE

; APPLICANT: BESEME, FREDERIC

; APPLICANT: BEDIN, FREDERIC

; APPLICANT: PARANHOS-BACCALA, GLAUCIA

; APPLICANT: KOMURIAN-PRADEL, FLORENCE

; APPLICANT: JOLIVET-REYNAUD, COLETTE

; APPLICANT: MANDRAND, BERNARD

; APPLICANT: GARSON, JEREMY

; APPLICANT: TUKE, PHILIP

; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

; TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT

; TITLE OF INVENTION: THERAPEUTIC PURPOSES

; NUMBER OF SEQUENCES: 210

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE, PLC

; STREET: P.O. BOX 19928

; CITY: ALEXANDRIA

; STATE: VA

; COUNTRY: USA

; ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979,847

FILING DATE: 26-NOV-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

TELEPHONE: 703-836-6400

TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 78

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

; REFERENCE/DOCKET NUMBER: WPB 39046A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6400

; TELEFAX: 703-836-2787

; INFORMATION FOR SEQ ID NO: 170:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-979-847-170

Query Match 52.1%; Score 25; DB 8; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.4e+06;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 1 TSQLTWT 8

RESULT 4

US-10-114-104-170

; Sequence 170, Application US/10114104

; Publication No. US20030198647A1

; GENERAL INFORMATION:

; APPLICANT: PERRON, HERVE

; APPLICANT: BESEME, FREDERIC

; APPLICANT: BEDIN, FREDERIC

; APPLICANT: PARANHOS-BACCALA, GLAUCIA

; APPLICANT: KOMURIAN-PRADEL, FLORENCE

; APPLICANT: JOLIVET-REYNAUD, COLETTE

; APPLICANT: MANDRAND, BERNARD

; APPLICANT: GARSON, JEREMY

; APPLICANT: TUKE, PHILIP

; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

; TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACT

; TITLE OF INVENTION: THERAPEUTIC PURPOSES

; NUMBER OF SEQUENCES: 210

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF & BERRIDGE, PLC

; STREET: P.O. BOX 19928

; CITY: ALEXANDRIA

; STATE: VA

; COUNTRY: USA

; ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/114,104

FILING DATE: 03-Apr-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/979,847

FILING DATE: 26-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 39046A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6400

TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 170:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

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; SEQUENCE DESCRIPTION: SEQ ID NO: 170;
US-10-114-104-170

Query Match      52.1%; Score 25; DB 14; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
Db 1 TSOLTWTV 8
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US-10-182-252A-632
; Sequence 632, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; PRIOR FILING DATE: 2003-04-10
; PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 632
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-632

Query Match      52.1%; Score 25; DB 15; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIWTM 8
Db 3 AIVVWTL 9
   ::::|||

RESULT 6
US-10-182-252A-657
; Sequence 657, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
```

```
; SEQUENCE DESCRIPTION: SEQ ID NO: 170;
US-10-114-104-170

Query Match      52.1%; Score 25; DB 14; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
Db 1 TSOLTWTV 8
   ||| : |||

RESULT 5
US-10-182-252A-632
; Sequence 632, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; PRIOR FILING DATE: 2003-04-10
; PCT/PK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 632
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-632

Query Match      52.1%; Score 25; DB 15; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIWTM 8
Db 3 AIVVWTL 9
   ::::|||

RESULT 6
US-10-182-252A-657
; Sequence 657, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PCT/PK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
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; SEQUENCE DESCRIPTION: SEQ ID NO: 170;

US-10-114-104-170

Query Match            52.1%; Score 25; DB 14; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches      4; Conservative    2; Mismatches    2; Indels        0; Gaps          0;

QY     1 TSLMIWTM 8  
       |||:  
Db     1 TSOLTWTV 8

RESULT 5  
US-10-182-252A-632  
Sequence 632, Application US/10182252A  
Publication No. US20040072162A1  
GENERAL INFORMATION:  
APPLICANT: FOMSGAARD, ANDERS  
APPLICANT: BRUNAK, SOREN  
APPLICANT: BUUS, SOREN  
APPLICANT: CORBET, SYLVIE  
APPLICANT: LAUEMOLLER, SANNNE LISE  
APPLICANT: HANSEN, JAN  
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
FILE REFERENCE: 030307/0205  
CURRENT APPLICATION NUMBER: US/10/182,252A  
PRIORITY FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: PCT/DK01/00059  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: EP 00610017.6  
PRIOR FILING DATE: 2000-01-28  
PRIOR APPLICATION NUMBER: US 60/179,333  
PRIOR FILING DATE: 2000-01-31  
NUMBER OF SEQ ID NOS: 1388  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 632  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide

US-10-182-252A-632

Query Match            52.1%; Score 25; DB 15; Length 9;  
Best Local Similarity 28.6%; Pred. No. 1.4e+06;  
Matches      2; Conservative    5; Mismatches    0; Indels        0; Gaps          0;

QY     2 SLMIWTM 8  
       :::||  
Db     3 AIVVWTL 9

RESULT 6  
US-10-182-252A-657  
Sequence 657, Application US/10182252A  
Publication No. US20040072162A1  
GENERAL INFORMATION:  
APPLICANT: FOMSGAARD, ANDERS  
APPLICANT: BRUNAK, SOREN  
APPLICANT: BUUS, SOREN  
APPLICANT: CORBET, SYLVIE  
APPLICANT: LAUEMOLLER, SANNNE LISE  
APPLICANT: HANSEN, JAN  
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS  
FILE REFERENCE: 030307/0205  
CURRENT APPLICATION NUMBER: US/10/182,252A  
PRIORITY FILING DATE: 2003-04-10  
PRIOR APPLICATION NUMBER: PCT/DK01/00059  
PRIOR FILING DATE: 2001-01-29  
PRIOR APPLICATION NUMBER: EP 00610017.6  
PRIOR FILING DATE: 2000-01-28

; OTHER INFORMATION: BOX2  
US-10-441-625-35

Query Match 50.0%; Score 24; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6  
|||  
Db 2 LMIW 5  
|||

## RESULT 9

US-10-441-626-38  
; Sequence 38, Application US/10441626  
; Publication No. US20030186418A1  
; GENERAL INFORMATION:  
; APPLICANT: Gualfetti, Peter  
; APPLICANT: Mitchinson, Colin  
; APPLICANT: Phillips, Jay Ian  
; TITLE OF INVENTION: No. US20030186418A1el Variant EGIII-Like Cellulase  
; TITLE OF INVENTION: Compositions  
; FILE REFERENCE: GC631  
; CURRENT APPLICATION NUMBER: US/10/441,626  
; CURRENT FILING DATE: 2003-05-19  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: BOX2'  
US-10-441-626-38

Query Match 50.0%; Score 24; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6  
|||  
Db 3 LMIW 6  
|||

## RESULT 10

US-10-441-625-38  
; Sequence 38, Application US/10441625  
; Publication No. US20030203467A1  
; GENERAL INFORMATION:  
; APPLICANT: Gualfetti, Peter  
; APPLICANT: Mitchinson, Colin  
; APPLICANT: Phillips, Jay Ian  
; TITLE OF INVENTION: Novel Variant EGIII-Like Cellulase  
; TITLE OF INVENTION: Compositions  
; FILE REFERENCE: GC631  
; CURRENT APPLICATION NUMBER: US/10/441,625  
; CURRENT FILING DATE: 2003-05-19  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: BOX2'  
US-10-441-625-38

Query Match 50.0%; Score 24; DB 14; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6  
|||

Db 3 LMIW 6

## RESULT 11

US-10-651-165-170  
; Sequence 170, Application US/10651165  
; Publication No. US20040047877A1  
; GENERAL INFORMATION:  
; APPLICANT: LEROUX-ROELS, Geert  
; APPLICANT: DELEYS, Robert  
; APPLICANT: MAERTENS, Geert  
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C  
; TITLE OF INVENTION: VIRUS  
; FILE REFERENCE: 2551-94  
; CURRENT APPLICATION NUMBER: US/10/651,165  
; CURRENT FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US/08/974,690C  
; PRIOR FILING DATE: 1997-11-19  
; PRIOR APPLICATION NUMBER: PCT/EP94/03555  
; PRIOR FILING DATE: 1994-10-28  
; PRIOR APPLICATION NUMBER: EP 93402718.6  
; PRIOR FILING DATE: 1993-11-04  
; NUMBER OF SEQ ID NOS: 286  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 170  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
US-10-651-165-170

Query Match 50.0%; Score 24; DB 15; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTMM 9  
|||  
Db 2 MAWDMM 7  
|||

## RESULT 12

US-08-979-847-169  
; Sequence 169, Application US/08979847  
; Publication No. US20030039664A1  
; GENERAL INFORMATION:  
; APPLICANT: PERRON, HERVE  
; APPLICANT: BESEME, FREDERIC  
; APPLICANT: BEDIN, FREDERIC  
; APPLICANT: PARANHOS-BACCALA, GLAUCIA  
; APPLICANT: KOMURIAN-PRADEL, FLORENCE  
; APPLICANT: JOLIVET-REYNAUD, COLETTE  
; APPLICANT: MANDRAND, BERNARD  
; APPLICANT: GARSON, JEREMY  
; APPLICANT: TUKE, PHILIP  
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS  
; TITLE OF INVENTION: ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYLACTIC  
; TITLE OF INVENTION: THERAPEUTIC PURPOSES  
; NUMBER OF SEQUENCES: 210  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OLIFF & BERRIDGE, PLC  
; STREET: P.O. BOX 19928  
; CITY: ALEXANDRIA  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/979,847  
; APPLICATION NUMBER: US/08/979,847  
; FILING DATE: 26-NOV-1997  
; CLASSIFICATION: 435

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 39046A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-979-847-169

Query Match 50.0%; Score 24; DB 8; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
Db 2 TSQLTWT 8

RESULT 13
US-10-114-104-169
; Sequence 169, Application US/10114104
; Publication No. US20030198647A1
; GENERAL INFORMATION:
; APPLICANT: PERRON, HERVE
; BESEME, FREDERIC
; BEDIN, FREDERIC
; PARANHOS-BACCALA, GLAUCIA
; KOMURIAN-PRADEL, FLORENCE
; JOLIVET-REYNAUD, COLETTE
; MANDRAND, BERNARD
; GARSON, JEREMY
; TUKE, PHILIP
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
; THERAPEUTIC PURPOSES
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSER: OLIFF & BERRIDGE, PLC
; STREET: P.O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,104
; FILING DATE: 03-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/979,847
; FILING DATE: 26-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 39046A
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
; INFORMATION FOR SEQ ID NO: 169:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-114-104-169

Query Match 50.0%; Score 24; DB 8; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
Db 2 TSQLTWT 8

RESULT 14
US-10-182-252A-3
; Sequence 3, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-3

Query Match 50.0%; Score 24; DB 15; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIWTM 8
Db 3 AIVVWII 9

RESULT 15
US-10-182-252A-215
; Sequence 215, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
```

```
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 215
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-215
```

```
Query Match      50.0%; Score 24; DB 15; Length 9;
Best Local Similarity 28.6%; Pred. No. 1.4e+06;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 SLMIWTM 8
      :::||:
Db      3 AIVWTV 9
```

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Search completed: November 14, 2004, 14:18:57
Job time : 137 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:45:55 ; Search time 156 Seconds  
(without alignments)  
20.696 Million cell updates/sec

Title: US-09-831-253F-5

Perfect score: 48

Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 202273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 313949

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_213Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	3	AAY93096 Transform
2	48	100.0	9	3	AAY92949 Transform
3	28	58.3	9	8	ADK08459 Human pap
4	28	58.3	9	8	ADK08095 Human pap
5	27	56.2	9	6	ABU64837 Human NV-
6	26	54.2	8	8	ADK08449 Human pap
7	26	54.2	8	8	ADK08088 Human pap
8	26	54.2	9	4	AA67672 Complemen
9	26	54.2	9	6	ABR40267 Murine pe
10	26	54.2	9	7	AD227682 Mouse ant
11	26	54.2	9	8	ADK08458 Human pap
12	25	52.1	8	4	ABP14228 HIV A02 s
13	25	52.1	8	4	ABP19690 HIV B62 s
14	25	52.1	8	7	AD84465 MSRV-1 PO
15	25	52.1	8	8	ADG14911 MSRV-1 PO
16	25	52.1	9	4	AAW22772 HIV pept-i
17	25	52.1	9	4	AAW22747 HIV pept-i
18	25	52.1	9	4	ABP16598 HIV A24 s
19	25	52.1	9	4	ABP14239 HIV A02 s
20	25	52.1	9	4	ABP18424 HIV B58 s
21	25	52.1	9	4	ABP22273 HIV A03 m
22	25	52.1	9	4	ABP11937 HIV A01 s
23	25	52.1	9	4	ABP19680 HIV B62 s
24	24	50.0	5	3	AAB13397 EGIII-lik
25	24	50.0	5	5	AAU77443 BOX2 pept

26	24	50.0	5	5	AAU87811	Aau87811 Endogluca
27	24	50.0	6	3	AAI13398	Aabi3398 EGIII-lik
28	24	50.0	6	5	AAU77075	Aau77075 Endogluca
29	24	50.0	6	5	AAU77444	Aau77444 BOX2, pep
30	24	50.0	6	5	AAU87812	Aau87812 Endogluca
31	24	50.0	8	2	AAV33692	Aav33692 Maize 33k
32	24	50.0	8	4	ABP18425	Abp18425 HIV B58 s
33	24	50.0	8	4	ABP22274	Abp22274 HIV A03 m
34	24	50.0	8	4	ABP16588	Abp16588 HIV A24 s
35	24	50.0	8	4	ABP19683	Abp19683 HIV B62 s
36	24	50.0	8	4	ABP16597	Abp16597 HIV A24 s
37	24	50.0	8	4	ABP11934	Abp11934 HIV A01 s
38	24	50.0	8	4	ABP14227	Abp14227 HIV A02 s
39	24	50.0	8	4	AAJ00551	Aaj00551 Hepatitis
40	24	50.0	8	4	AAJ01013	Aaj01013 Hepatitis
41	24	50.0	8	4	AAJ01178	Aaj01178 Hepatitis
42	24	50.0	8	4	AAJ01692	Aaj01692 Hepatitis
43	24	50.0	8	7	ADB84464	Adb84464 MSRV-1 PO
44	24	50.0	8	7	ABW00710	Abw00710 Chrysoespo
45	24	50.0	8	8	ADG14910	Adg14910 MSRV-1 PO

## ALIGNMENTS

RESULT 1  
AAY93096  
ID AAY93096 standard; peptide; 9 AA.  
XX  
AC AAY93096;  
XX  
DT 08-NOV-2000 (first entry)  
XX  
DE Transforming growth factor inhibitory peptide P142.  
XX  
KW Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;  
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
XX  
OS Homo sapiens.  
XX  
PN WO200031135-A1.  
XX  
PD 02-JUN-2000.  
XX  
PF 23-NOV-1999; 99WO-ES000375.  
XX  
PR 24-NOV-1998; 98ES-00002465.  
XX  
PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
XX  
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
PI Borrás Cuesta F;  
XX  
DR WPI; 2000-411935/35.  
XX  
PT Peptides that antagonize binding of transforming growth factor betal,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.  
XX  
PS Disclosure; Page 31; 86pp; Spanish.  
XX  
CC The invention relates to synthetic peptides that antagonise the binding  
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
CC vivo which have partial amino acid sequences identical, or similar, with  
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
CC examples of the peptides of the invention. the peptides act by  
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis

```

XX SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
   |||||
Db 1 TSLMIWTMM 9

RESULT 2
AAY92949
ID AAY92949 standard; peptide; 9 AA.
XX AC AAY92949;
XX DT 08-NOV-2000 (first entry)
XX DE Transforming growth factor inhibitory peptide #5.
XX KW Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX KW extracellular matrix degradation inhibitor; mimotope; cirrhosis.
XX OS Homo sapiens.
XX PN WO200031135-A1.
XX PD 02-JUN-2000.
XX PF 23-NOV-1999; 99WO-ES000375.
XX PR 24-NOV-1998; 98ES-00002465.
XX SQ (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX PI Borras Cuesta F;
XX WPI; 2000-411935/35.
XX PT Peptides that antagonize binding of transforming growth factor beta1,
XX PT useful for treatment of liver disease, especially cirrhosis, are partial
XX PT sequences of the factor or its receptors.
XX PS Claim 6; Page 81; 86pp; Spanish.
XX CC The invention relates to synthetic peptides that antagonise the binding
XX CC of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
XX CC vivo which have partial amino acid sequences identical, or similar, with
XX CC those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX CC examples of the peptides of the invention. The peptides act by
XX CC competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
XX CC they are inhibitors of stimulation of collagen synthesis in liver cells
XX CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX CC expression systems) encoding the peptides are used for treatment of liver
XX CC disease, specifically cirrhosis
XX SQ Sequence 9 AA;
Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
   |||||
Db 1 TSLMIWTMM 9

RESULT 3
ADK08459
ID ADK08459 standard; peptide; 9 AA.
XX AC ADK08459;
XX DT 06-MAY-2004 (first entry)
XX DE Human papillomavirus peptide #514.
XX KW pathogenic virus; alternative reading frame; antigenic determinant;
XX KW virucide; vaccine; therapeutic agent; infection; HPV.
XX OS Human papillomavirus.
XX PN WO2004011650-A2.
XX PD 05-FEB-2004.
XX PF 24-JUL-2003; 2003WO-EP008112.
XX PR 24-JUL-2002; 2002AT-00001124.
XX PR 11-JUL-2003; 2003EP-00450171.
XX PA (INTE-) INTERCELL AG.
XX PI Mattner F, Schmidt W, Habel A;
XX WPI; 2004-169243/16.
XX PT New polypeptide encoded by an alternative reading frame of a pathogenic
XX PT virus comprising an antigenic determinant, useful for treating or
XX PT preventing an infection with the pathogenic virus.
XX PS Claim 18; Page 179; 220pp; English.
XX CC This invention relates to a novel polypeptide encoded by an alternative
XX CC reading frame of a pathogenic virus, where the polypeptide starts with a
XX CC methionine amino acid residue, which comprises an antigenic determinant
XX CC and more than 7 amino acid residues. The invention may be useful for the
XX CC production of compounds with a virucide activity or the development of a
XX CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
XX CC agent. It is also useful for the manufacture of a medicament for treating
XX CC or preventing an infection with the pathogenic virus. The present
XX CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
XX CC invention.
XX SQ Sequence 9 AA;
Query Match 58.3%; Score 28; DB 8; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.7e+06;
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMWTMM 9
   :|||:
Db 2 ALVLTLL 9

RESULT 4
ADK08095
ID ADK08095 standard; peptide; 9 AA.
XX AC ADK08095;
XX DT 06-MAY-2004 (first entry)
XX DE Human papillomavirus peptide #150.
XX KW pathogenic virus; alternative reading frame; antigenic determinant;
XX KW virucide; vaccine; therapeutic agent; infection; HPV.
XX OS Human papillomavirus.
XX PN WO2004011650-A2.

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XX PD 05-FEB-2004.  
 XX PF 24-JUL-2003; 2003WO-EF008112.  
 XX PR 24-JUL-2002; 2002AT-00001124.  
 XX PR 11-JUL-2003; 2003EP-00450171.  
 XX PA (INTE-) INTERCELL AG.  
 XX PI Mattner F, Schmidt W, Habel A;  
 XX DR WPI; 2004-169243/16.  
 XX PT New polypeptide encoded by an alternative reading frame of a pathogenic  
 PT virus comprising an antigenic determinant, useful for treating or  
 PT preventing an infection with the pathogenic virus.  
 XX PS Claim 18; Page 175; 220pp; English.  
 XX CC This invention relates to a novel polypeptide encoded by an alternative  
 CC reading frame of a pathogenic virus, where the polypeptide starts with a  
 CC methionine amino acid residue, which comprises an antigenic determinant  
 CC and more than 7 amino acid residues. The invention may be useful for the  
 CC production of compounds with a virucide activity or the development of a  
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
 CC agent. It is also useful for the manufacture of a medicament for treating  
 CC or preventing an infection with the pathogenic virus. The present  
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
 CC invention.  
 XX SQ Sequence 9 AA;  
 Query Match 58.3%; Score 28; DB 8; Length 9;  
 Best Local Similarity 37.5%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SLMIWTMM 9  
 Db 2 ALVLWTLL 9  
 RESULT 5  
 ABU64837.  
 ID ABU64837 standard; peptide; 9 AA.  
 AC ABU64837;  
 XX 14-MAY-2003 (first entry)  
 DE Human NY-ESO-1 HLA binding motif #21.  
 KW Human; antigen; NY-ESO-1; cancer; SEREX; cytostatic; immunosuppressive;  
 KW serological identification of antigens by recombinant expression cloning;  
 KW melanoma; hepatoma; lymphoma; breast cancer; prostate cancer;  
 KW lung cancer; ovarian cancer; thyroid cancer; bladder cancer; infection;  
 KW autoimmune disorder; cancer marker; CTL; cytolytic T cell line;  
 KW human leukocyte antigen; HLA binding motif.  
 XX OS Homo sapiens.  
 XX US2002164665-A1.  
 PD 07-NOV-2002.  
 XX 17-DEC-2001; 2001US-00023182.  
 XX 03-OCT-1996; 96US-00725182.  
 XX 15-SEP-1997; 97US-00937263.  
 XX 29-DEC-2000; 2000US-00751798.  
 XX (STOC/) STOCKERT E.  
 XX (JAGE/) JAGER E.

(CHEN/) CHEN Y.  
 (SCAN/) SCANLAN M.  
 (ALEX/) ALEXANDER K.  
 (OLDL/) OLD L J.  
 Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;  
 WPI; 2003-298695/29.  
 New antibody that binds to the cancer associated antigen NY-ESO-1, useful  
 for treating cancer, e.g. melanoma, hepatoma, lymphoma, or breast,  
 prostate, lung, ovarian, thyroid or bladder cancer, infections or  
 autoimmune disorders.  
 Example 13; Page 6; 18pp; English.  
 The invention relates to an isolated antibody or binding fragment of an  
 antibody, which binds with a protein that is encoded by an isolated  
 nucleic acid molecule the complementary sequence of which hybridises  
 under stringent conditions to a nucleic acid molecule comprising the  
 nucleotides 54-593 of the human cancer marker NY-ESO-1 cDNA appearing as  
 ABX96656. Also included are a hybridoma cell line producing the novel  
 monoclonal antibody, screening for cancer in a sample (by contacting the  
 sample with the isolated antibody, and determining binding of the novel  
 antibody to a target as an indicator of cancer), determining antibodies  
 against a cancer-associated antigen in a sample, determining  
 regression/progression/onset of a cancerous condition (by monitoring a  
 sample from a patient with the cancerous condition from parameters such  
 as NY-ESO-1 protein or a peptide derived from NY-ESO-1 protein, with the  
 antibody that binds to it, where the amount of the parameter is  
 indicative of progression, regression or onset of cancerous conditions),  
 and treating a subject afflicted with a cancerous condition by  
 administering to the subject an antibody that specifically binds to NY-  
 ESO-1 protein or to an ESO-1 derived peptide (e.g. a peptide identified  
 as stimulating a CTL (cytolytic T cell line) identified by SEREX  
 (serological identification of antigens by recombinant expression  
 cloning) expressed on a cancerous cell associated with the cancerous  
 condition) where the antibody is coupled to an anticancer agent. The  
 antibody is useful for treating cancer, e.g. melanoma, hepatoma,  
 lymphoma, or breast, prostate, lung, ovarian, thyroid or bladder cancer,  
 infections or autoimmune disorders. The present sequence represents an  
 HLA (human leukocyte antigen) binding peptide derived from human NY-ESO-1  
 Sequence 9 AA;  
 Query Match 56.2%; Score 27; DB 6; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SLMIWT 7  
 Db 4 SLLMWT 9  
 RESULT 6  
 ADK08449  
 ID ADK08449 standard; peptide; 8 AA.  
 XX ADK08449;  
 XX 06-MAY-2004 (first entry)  
 XX Human papillomavirus peptide #504.  
 XX pathogenic virus; alternative reading frame; antigenic determinant;  
 KW virucide; vaccine; therapeutic agent; infection; HPV.  
 XX Human papillomavirus.  
 OS WO2004011650-A2.  
 XX 05-FEB-2004.

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PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 178; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 8 AA;

Query Match 54.2%; Score 26; DB 8; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.7e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLMIWTM 8
DB :|:|:|:
2 ALVLWTL 8

RESULT 8
AAG67672
ID AAG67672 standard; peptide; 9 AA.
XX
AC AAG67672;
XX
XX
DT 26-NOV-2001 (first entry)
XX
DE Complementarity determining region 3 of light chain variable region.
XX
KW Gene recombinant antibody; CCR4; Th2-mediated immune disease;
KW blood cancer; bronchial asthma; atrophic dermatitis; leukemia.
XX
OS Mus musculus.
XX
PN WO200164754-A1.
XX
XX
PD 07-SEP-2001.
XX
XX
PF 02-MAR-2001; 2001WO-JP001656.
XX
PR 03-MAR-2000; 2000JP-00059508.
PR 28-DEC-2000; 2000JP-00401583.
XX
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Shitara K, Hanai N, Shoji E, Sakurada M, Furuya A, Nakamura K;
PI Niwa R, Shibata K, Yamasaki M;
XX
XX
DR WPI; 2001-565496/63.
XX
PT Gene-recombinant antibody, its fragment and encoded DNAs, applicable in
PT diagnosis and development of drugs for Th2-mediated immune diseases and
PT blood cancer, and in reducing or eliminating cells.
XX
XX
PS Claim 15; Page 101; 116pp; Japanese.
XX
CC The specification describes a gene recombinant antibody that can
CC specifically react with the extracellular domain of human CCR4. The
CC antibody and its fragment are applicable in diagnosis and development of
CC drugs for Th2-mediated immune diseases and blood cancer including
CC bronchial asthma, atrophic dermatitis and leukemia. The present sequence
CC represents a complementarity determining region (CDR) of the light chain
CC variable region of an antibody directed against human CCR4
XX
SQ Sequence 9 AA;

Query Match 54.2%; Score 26; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;

PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 178; 220pp; English.
XX
CC This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 8 AA;

Query Match 54.2%; Score 26; DB 8; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.7e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLMIWTM 8
DB :|:|:|:
2 ALVLWTL 8

RESULT 7
ADK08088
ID ADK08088 standard; peptide; 8 AA.
XX
AC ADK08088;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus peptide #143.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
XX
OS Human papillomavirus.
XX
XX
PN WO2004011650-A2.
XX
XX
PD 05-FEB-2004.
XX
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX

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XX WPI; 2004-169243/16.  
 XX New polypeptide encoded by an alternative reading frame of a pathogenic  
 PT virus comprising an antigenic determinant, useful for treating or  
 PT preventing an infection with the pathogenic virus.  
 PS Claim 18; Page 179; 220pp; English.  
 XX This invention relates to a novel polypeptide encoded by an alternative  
 CC reading frame of a pathogenic virus, where the polypeptide starts with a  
 CC methionine amino acid residue, which comprises an antigenic determinant  
 CC and more than 7 amino acid residues. The invention may be useful for the  
 CC production of compounds with a virucide activity or the development of a  
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
 CC agent. It is also useful for the manufacture of a medicament for treating  
 CC or preventing an infection with the pathogenic virus. The present  
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
 CC invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 54.2%; Score 26; DB 8; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SLMIWTM 8  
 Db 3 ALVLWTL 9  
 :|:|:  
 :|:|:  
 RESULT 12  
 ABP14228  
 ID ABP14228 standard; peptide; 8 AA.  
 XX  
 AC ABP14228;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV A02 super motif vpu peptide #11.  
 XX  
 XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
 KW vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US027766.  
 XX  
 PR 05-OCT-1999; 99US-00412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 159; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (AB125347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine

CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 8 AA;  
 Query Match 52.1%; Score 25; DB 4; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.7e+06;  
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SLMIWTMM 9  
 Db 1 AIVVWTV 8  
 :|:|:  
 :|:|:  
 RESULT 13  
 ABP19690  
 ID ABP19690 standard; peptide; 8 AA.  
 XX  
 AC ABP19690;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE HIV B62 super motif vpu peptide #28.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
 KW vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US027766.  
 XX  
 PR 05-OCT-1999; 99US-00412863.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Celis E, Kubo RT, Grey HM;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 272; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (AB125347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 8 AA;

Query Match 52.1%; Score 25; DB 4; Length 8;  
 Best Local Similarity 25.0%; Pred. No. 1.7e+06;  
 Matches 2; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIWTMM 9  
 : : : : : : : :  
 DB 1 AIVVTV 8

RESULT 14  
 ADB84465  
 ID ADB84465 standard; peptide; 8 AA.

AC ADB84465;

DT 04-DEC-2003 (first entry)

DE MSRV-1 POL2B octapeptide #27.

XX MSRV; multiple sclerosis; rheumatoid arthritis; gag; pol;  
 KW reverse transcriptase; ribonuclease H; antigen; immunogen.

XX Multiple sclerosis associated retrovirus.

XX US2003039664-A1.

PN 27-FEB-2003.

XX 26-NOV-1997; 97US-00979847.

XX 26-NOV-1996; 96US-00756429.

XX (PERR/) PERRON H.  
 PA (BESE/) BESEME F.  
 PA (BED/) BEDIN F.  
 PA (PAPA/) PARANHOS-BACCALA G.  
 PA (KOMU/) KOMURIAN-PRADEL F.  
 PA (JOLI/) JOLIVET-REYNAUD C.  
 PA (MAND/) MANDRAND B.  
 PA (GARS/) GARSON J A.  
 PA (TUK/) TUKE P W.

XX Perron H, Beseme F, Bedin F, Paranhos-Baccala G;  
 PI Komurian-Pradel F, Jollivet-Reynaud C, Mandrand B, Garson JA, Tuke PW;  
 XX WPI; 2003-512253/48.

XX New isolated or purified nucleic acid associated with multiple sclerosis  
 PT retrovirus, useful for detecting a virus associated with  
 PT multiple sclerosis or rheumatoid arthritis in a biological sample.

XX Example 11; Fig 31; 193pp; English.

XX The invention relates to an isolated or purified nucleic acid from a  
 CC virus associated with multiple sclerosis and/or rheumatoid arthritis,

CC multiple sclerosis-associated virus (MSRV)-1. The nucleic acids comprise  
 CC pol, gag or reverse transcriptase genes (or their fragments) encoding the  
 CC proteins or defined peptides (including immunodominant peptides,  
 CC antigenic peptides or conserved motifs). Also included are a process for  
 CC detecting a virus associated with multiple sclerosis or rheumatoid  
 CC arthritis in a biological sample, a nucleic acid probe for the detection  
 CC of a virus associated with multiple sclerosis or rheumatoid arthritis, a  
 CC primer for the amplification by polymerisation of a nucleic acid of a  
 CC viral material associated with multiple sclerosis or rheumatoid  
 CC arthritis, a polypeptide exhibiting an inhibitory activity on the  
 CC proteolytic, reverse transcriptase or ribonuclease H activity from MSRV,  
 CC and an antibody directed against the MSRV-1 virus obtained by  
 CC immunologically reacting a human or animal body or cells with an  
 CC immunogenic agent consisting of the antigenic polypeptide defined above.  
 CC The nucleic acids are useful for detecting a biological sample a virus  
 CC associated with multiple sclerosis or rheumatoid arthritis, or for  
 CC detecting in a biological sample, the presence of or exposure to a virus  
 CC associated with multiple sclerosis or rheumatoid arthritis. The present  
 CC sequence is an MSRV immunogenic or antigenic peptide (or a conserved  
 CC peptide motif). Note: The SEQ ID numbers for the sequences as displayed  
 CC in the main body of the patent do not match the SEQ ID numbers in the  
 CC sequence listing. Consequently those sequences mentioned in the claims  
 CC may not be the sequences the authors intended to claim.

XX Sequence 8 AA;

Query Match 52.1%; Score 25; DB 7; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 8  
 : : : : : : : :  
 DB 1 TSQLTWTV 8

RESULT 15

ADG14911

ID ADG14911 standard; peptide; 8 AA.

XX ADG14911;

XX 26-FEB-2004 (first entry)

XX MSRV-1 POL2B peptide #29.

DE pol gene; retrovirus; multiple sclerosis; rheumatoid arthritis.

XX Multiple sclerosis associated retrovirus.

XX US2003198647-A1.

XX 23-OCT-2003.

XX 03-APR-2002; 2002US-00114104.

XX 26-NOV-1996; 96US-00756429.

XX 26-NOV-1997; 97US-00979847.

XX (INNR ) BIO MERIEUX.

XX Perron H, Beseme F, Bedin F, Paranhos-Baccala G;  
 PI Komurian-Pradel F, Jollivet-Reynaud C, Mandrand B, Garson JA, Tuke PW;  
 XX WPI; 2004-032461/03.

XX New isolated nucleic acid and their fragments having the pol gene of a  
 PT retrovirus, useful for diagnosing, preventing and/or treating multiple  
 PT sclerosis and/or rheumatoid arthritis.

XX Disclosure; SEQ ID NO 170; 193pp; English.

XX The invention relates to an isolated nucleic acid which comprises the pol  
 CC gene of a retrovirus associated with multiple sclerosis or rheumatoid

CC arthritis. The methods and compositions of the present invention are  
CC useful for diagnosing, preventing and/or treating multiple sclerosis  
CC and/or rheumatoid arthritis. The present sequence is used in the  
CC exemplification of the invention.

XX

SQ Sequence 8 AA;

Query Match 52.1%; Score 25; DB 8; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TSLMIWTM 8

Db 1 TSQLTWTV 8

Search completed: November 14, 2004, 14:03:53  
Job time : 158 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 13:58:00 ; Search time 36 Seconds  
(without alignments)  
16.579 Million cell updates/sec

Title: US-09-831-253F-5  
Perfect score: 48  
Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 95011

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A-COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS-COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	52.1	8	US-08-979-847B-170	Sequence 170, Appl
2	24	50.0	5	US-09-632-570-35	Sequence 35, Appl
3	24	50.0	6	US-08-032-848C-20	Sequence 20, Appl
4	24	50.0	6	US-09-632-570-38	Sequence 38, Appl
5	24	50.0	7	US-08-635-886C-170	Sequence 170, Appl
6	24	50.0	7	US-08-974-690C-170	Sequence 170, Appl
7	24	50.0	7	US-08-974-685-170	Sequence 170, Appl
8	24	50.0	7	US-08-974-685-180	Sequence 180, Appl
9	24	50.0	8	US-08-641-314C-7	Sequence 7, Appl
10	24	50.0	8	US-09-548-938A-17	Sequence 17, Appl
11	24	50.0	8	US-08-979-847B-169	Sequence 169, Appl
12	24	50.0	9	US-08-466-601A-160	Sequence 160, Appl
13	22	45.8	6	US-08-134-231C-40	Sequence 40, Appl
14	22	45.8	7	US-09-258-754-385	Sequence 385, Appl
15	22	45.8	7	US-09-042-107-385	Sequence 385, Appl
16	22	45.8	7	US-09-722-250D-385	Sequence 385, Appl
17	22	45.8	7	US-09-676-475A-385	Sequence 385, Appl
18	22	45.8	8	US-08-979-847B-171	Sequence 171, Appl
19	22	45.8	9	US-09-183-931-43	Sequence 43, Appl
20	22	45.8	9	US-09-183-931-44	Sequence 44, Appl
21	22	45.8	9	US-09-359-503-5	Sequence 5, Appl
22	22	45.8	9	US-09-359-503-6	Sequence 6, Appl
23	22	45.8	9	US-09-062-422-5	Sequence 5, Appl
24	22	45.8	9	US-09-062-422-6	Sequence 6, Appl
25	22	45.8	9	US-08-937-263B-5	Sequence 5, Appl
26	22	45.8	9	US-08-937-263B-6	Sequence 6, Appl
27	22	45.8	9	US-09-166-448-81	Sequence 81, Appl

28	22	45.8	9	US-09-166-448-81	Sequence 81, Appl
29	22	45.8	9	US-09-705-160-43	Sequence 43, Appl
30	22	45.8	9	US-09-705-160-44	Sequence 44, Appl
31	22	45.8	9	US-09-440-621-2	Sequence 2, Appl
32	22	45.8	9	US-09-440-621-3	Sequence 3, Appl
33	22	45.8	9	US-09-440-621-6	Sequence 6, Appl
34	22	45.8	9	US-09-440-621-7	Sequence 7, Appl
35	22	45.8	9	US-09-440-621-8	Sequence 8, Appl
36	22	45.8	9	US-09-440-621-10	Sequence 10, Appl
37	22	45.8	9	US-09-697-884-80	Sequence 80, Appl
38	22	45.8	9	US-09-697-884-81	Sequence 81, Appl
39	22	45.8	9	US-09-670-456A-1	Sequence 1, Appl
40	22	45.8	9	US-09-751-798-5	Sequence 5, Appl
41	22	45.8	9	US-09-751-798-6	Sequence 6, Appl
42	22	45.8	9	US-09-344-040C-122	Sequence 122, App
43	22	45.8	9	US-09-344-040C-131	Sequence 131, App
44	22	45.8	9	US-09-344-040C-132	Sequence 132, App
45	22	45.8	9	US-09-574-749B-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-08-979-847B-170  
; Sequence 170, Application US/08979847B  
; Patent No. 6582703

GENERAL INFORMATION:

APPLICANT: PERRON, HERVE  
BESEME, FREDERIC  
BEDIN, FREDERIC  
PARANHOS-BACCALA, GLAUCIA  
KOMURIAN-PRADEL, FLORENCE  
JOLIVET-REYNAUD, COLETTE  
MANDRAND, BERNARD  
GARSON, JEREMY  
TUKES, PHILIP

TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS  
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL  
THERAPEUTIC PURPOSES

NUMBER OF SEQUENCES: 210

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE, PLC  
STREET: P.O. BOX 19928  
CITY: ALEXANDRIA  
STATE: VA  
COUNTRY: USA  
ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/979,847B

FILING DATE: 26-NO. 6582703-1997

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 39046A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6400

TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 170:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 170:

US-08-979-847B-170

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Query Match      52.1%; Score 25; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
   || : ||:
Db 1 TSQLTWTW 8

RESULT 2
US-09-632-570-35
; Sequence 35, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BOX2
US-09-632-570-35

Query Match      50.0%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
   ||||
Db 2 LMIW 5

RESULT 3
US-09-632-848C-20
; Sequence 20, Application US/08032848C
; Patent No. 5475101
; GENERAL INFORMATION:
; APPLICANT: Ward, Michael
; APPLICANT: Clarkson, Kathleen A.
; APPLICANT: Weiss, Geoffrey L.
; APPLICANT: Larenas, Edward
; APPLICANT: Lorch, Jeffrey D.
; TITLE OF INVENTION: Purification and Molecular Cloning of
; TITLE OF INVENTION: EG III Cellulase
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 180 Kimball Way
; CITY: South San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/032,848C
; FILING DATE: MAR 17 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Horn, Margaret A.
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; REGISTRATION NUMBER: 33,401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415 742-7356
; TELEFAX: 415 742-7217
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-032-848C-20

Query Match      50.0%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
   ||||
Db 2 LMIW 5

RESULT 4
US-09-632-570-38
; Sequence 38, Application US/09632570
; Patent No. 6623949
; GENERAL INFORMATION:
; APPLICANT: Gualfetti, Peter
; APPLICANT: Mitchinson, Colin
; APPLICANT: Phillips, Jay Ian
; TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
; TITLE OF INVENTION: Compositions
; FILE REFERENCE: GC631
; CURRENT APPLICATION NUMBER: US/09/632,570
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BOX2'
US-09-632-570-38

Query Match      50.0%; Score 24; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6
   ||||
Db 3 LMIW 6

RESULT 5
US-08-635-886C-170
; Sequence 170, Application US/08635886C
; Patent No. 6555114
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, Geert
; APPLICANT: DELEYS, Robert
; APPLICANT: MAERTENS, Geert
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; FILE REFERENCE: 2752-18
; CURRENT APPLICATION NUMBER: US/08/635,886C
; CURRENT FILING DATE: 1996-04-25
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 170
; LENGTH: 7
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-170

Query Match
Best Local Similarity 50.0%; Score 24; DB 4; Length 7;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTMM 9
Db 2 MAWDMM 7

RESULT 6
US-08-974-690C-170
; Sequence 170, Application US/08974690C
; Patent No. 6613333
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, GEERT
; APPLICANT: DELEYS, ROBERT
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; FILE REFERENCE: 2551-94
; CURRENT APPLICATION NUMBER: US/08/974,690C
; CURRENT FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: PCT/EP94/03555
; PRIOR FILING DATE: 1994-10-28
; PRIOR APPLICATION NUMBER: EP 93402718.6
; PRIOR FILING DATE: 1993-11-04
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 7
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-974-690C-170

Query Match
Best Local Similarity 50.0%; Score 24; DB 4; Length 7;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTMM 9
Db 2 MAWDMM 7

RESULT 7
US-08-974-685-170
; Sequence 170, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, GEERT
; APPLICANT: DELEYS, ROBERT
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
; HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
; THERAPEUTIC COMPOSITIONS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,685
; FILING DATE: 19-NO. 6689368-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: single
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:

; SEQ ID NO 170
; LENGTH: 7
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-08-635-886C-170

Query Match
Best Local Similarity 50.0%; Score 24; DB 4; Length 7;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTMM 9
Db 2 MAWDMM 7

RESULT 8
US-08-974-685-180
; Sequence 180, Application US/08974685
; Patent No. 6689368
; GENERAL INFORMATION:
; APPLICANT: LEROUX-ROELS, GEERT
; APPLICANT: DELEYS, ROBERT
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: IMMUNODOMINANT HUMAN T CELL EPITOPES OF
; HEPATITIS C VIRUS STRUCTURAL PROTEINS, PROPHYLACTIC AND
; THERAPEUTIC COMPOSITIONS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 181
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,685
; FILING DATE: 19-NO. 6689368-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BYRNE, THOMAS E.
; REGISTRATION NUMBER: 32,205
; REFERENCE/DOCKET NUMBER: 1487-11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: single
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 180:
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US-08-974-685-180

Query Match 50.0%; Score 24; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MIWTMM 9  
Db 2 MAWDMM 7

## RESULT 9

US-08-641-314C-7  
; Sequence 7; Application US/08641314C  
; Patent No. 5977440

## ; GENERAL INFORMATION:

; APPLICANT: LUTHE, DAWN S.

; APPLICANT: WILLIAMS, W. P.

; APPLICANT: BINGHUA, JIANG

; APPLICANT: PECHAN, TIBOR

; TITLE OF INVENTION: DNA MOLECULE ENCODING A 33 KD CYSTEINE

; TITLE OF INVENTION: PROTEINASE AND ITS USE IN TRANSFORMING PLANTS TO PROVIDE

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER &amp; NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

## ; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/641,314C

; FILING DATE: 30-APR-1996

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: KELBER, STEVEN B.

; REGISTRATION NUMBER: 30,073

; REFERENCE/DOCKET NUMBER: 2343-045-27

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-641-314C-7

Query Match 50.0%; Score 24; DB 2; Length 8;  
Best Local Similarity 60.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SLMIW 6  
Db 1 SVMVW 5

## RESULT 10

US-09-548-938A-17

; Sequence 17; Application US/09548938A

; Patent No. 6573086

; GENERAL INFORMATION:

; APPLICANT: EMALFARB, MARK AARON

; APPLICANT: BURLINGAME, RICHARD PAUL

; APPLICANT: OLSON, PHILIP TERRY  
; APPLICANT: SINITSYN, ARKADY PANTELEIMONOVICK  
; APPLICANT: PARRICHE, MARTINE  
; APPLICANT: BOUSSON, JEAN CHRISTOPHE  
; APPLICANT: PUNNONEN, CHRISTINE MARIE  
; APPLICANT: PUNT, PETER JAN

; APPLICANT: VAN-ZEIJL, CORNELIA MARIA JOHANNA

; TITLE OF INVENTION: TRANSFORMATION SYSTEM IN THE FIELD OF FILAMENTOUS FUNGI

; FILE REFERENCE: 3123-4001

; CURRENT APPLICATION NUMBER: US/09/548,938A

; CURRENT FILING DATE: 2000-04-13

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Chrysosporium sp.

US-09-548-938A-17

Query Match 50.0%; Score 24; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LMIW 6  
Db 5 LMIW 8

## RESULT 11

US-08-979-847B-169

; Sequence 169; Application US/08979847B

; Patent No. 6582703

; GENERAL INFORMATION:

; APPLICANT: PERRON, HERVE

; BESEME, FREDERIC

; BEDIN, FREDERIC

; PARANHOS-BACCALA, GLAUCIA

; KOMURIAN-PRADEL, FLORENCE

; JOLIVET-REYNAUD, COLETTE

; MANDRAND, BERNARD

; GARSON, JEREMY

; TUKER, PHILIP

; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

; ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL

; THERAPEUTIC PURPOSES

; NUMBER OF SEQUENCES: 210

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OLIFF &amp; BERRIDGE, PLC

; STREET: P.O. BOX 19928

; CITY: ALEXANDRIA

; STATE: VA

; COUNTRY: USA

; ZIP: 22320

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/979,847B

; FILING DATE: 26-NO. 6582703-1997

; CLASSIFICATION: &lt;Unknown&gt;

; ATTORNEY/AGENT INFORMATION:

; NAME: BERRIDGE, WILLIAM P.

; REGISTRATION NUMBER: 30,024

; REFERENCE/DOCKET NUMBER: WPB 39046A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6400

; TELEFAX: 703-836-2787

; INFORMATION FOR SEQ ID NO: 169:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-08-979-847B-169
Query Match 50.0%; Score 24; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
DB 2 TSQLTWT 8

RESULT 12
US-08-466-601A-160
; Sequence 160, Application US/08466601A
; Patent No. 6572864
; GENERAL INFORMATION:
; APPLICANT: BUKH, J., MILLER, R.H. AND
; TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF THE ENVELOPE 1 GENE
; TITLE OF INVENTION: OF 51 ISOLATES OF HEPATITIS C AND THE USE
; TITLE OF INVENTION: OF REAGENTS DERIVED FROM THESE SEQUENCES IN
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND VACCINES
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,601A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/086,428
; FILING DATE: 29-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4070US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-08-466-601A-160
Query Match 50.0%; Score 24; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTMM 9
DB 4 MAWDM 9

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-08-979-847B-169
Query Match 50.0%; Score 24; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
DB 2 TSQLTWT 8

RESULT 13
US-08-134-231C-40
; Sequence 40, Application US/08134231C
; Patent No. 6562596
; GENERAL INFORMATION:
; APPLICANT: Silbiger, Scott M.
; Koski, Raymond A.
; TITLE OF INVENTION: Tissue Inhibitor Metalloproteinase Type
; Three (TIMP-3) Composition and Methods
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/134,231C
; FILING DATE: 06-Oct-1993
; CLASSIFICATION: <Unknown>
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:
US-08-134-231C-40
Query Match 45.8%; Score 22; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IWTMM 9
DB 2 IWTDM 6

RESULT 14
US-09-258-754-385
; Sequence 385, Application US/09258754
; Patent No. 6174887
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 385
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-385
Query Match 45.8%; Score 22; DB 3; Length 7;
Best Local Similarity 60.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 5 IWTMM 9  
| | | | :  
Db 1 IWTVV 5

RESULT 15  
US-09-042-107-385  
; Sequence 385, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 385  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-385

Query Match 45.8%; Score 22; DB 3; Length 7;  
Best Local Similarity 60.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9  
| | | | :  
Db 1 IWTVV 5

Search completed: November 14, 2004, 14:08:30  
Job time : 36 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 7.08511 Seconds  
(without alignments)  
84.242 Million cell updates/sec

Title: US-09-831-253F-5  
Perfect score: 48  
Sequence: 1 TSLMWTMM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	58.3	11	4	US-09-149-476-551
2	28	58.3	12	1	US-08-241-054-50
3	28	58.3	12	1	US-08-241-054-53
4	28	58.3	12	1	US-08-241-054-61
5	28	58.3	12	1	US-08-390-156A-22
6	28	58.3	12	1	US-08-390-156A-57
7	28	58.3	12	1	US-08-390-156A-61
8	28	58.3	12	1	US-08-439-817-30
9	28	58.3	12	1	US-08-439-817-33
10	28	58.3	12	1	US-08-439-817-41
11	28	58.3	12	1	US-08-485-508-50
12	28	58.3	12	1	US-08-485-508-53
13	28	58.3	12	1	US-08-485-508-61
14	27	56.2	21	3	US-08-905-223-20
15	27	56.2	21	3	US-08-247-155-20
16	27	56.2	21	4	US-09-663-600A-20
17	27	56.2	21	4	US-09-621-976-2
18	27	56.2	21	4	US-09-513-999C-2
19	26	54.2	20	1	US-08-241-054-81
20	26	54.2	20	1	US-08-390-156A-38
21	26	54.2	20	1	US-08-439-817-61
22	26	54.2	20	1	US-08-485-508-81
23	25	52.1	8	4	US-08-979-847B-170
24	25	52.1	12	1	US-08-241-054-55
25	25	52.1	12	1	US-08-241-054-95
26	25	52.1	12	1	US-08-241-054-98
27	25	52.1	12	1	US-08-390-156A-45

28	52.1	12	1	US-08-390-156A-58	Sequence 58, Appl
29	52.1	12	1	US-08-390-156A-87	Sequence 87, Appl
30	52.1	12	1	US-08-439-817-35	Sequence 35, Appl
31	52.1	12	1	US-08-439-817-75	Sequence 75, Appl
32	52.1	12	1	US-08-439-817-78	Sequence 78, Appl
33	52.1	12	1	US-08-439-817-200	Sequence 200, Appl
34	52.1	12	1	US-08-485-508-55	Sequence 55, Appl
35	52.1	12	1	US-08-485-508-95	Sequence 95, Appl
36	52.1	12	1	US-08-485-508-98	Sequence 98, Appl
37	52.1	12	4	US-09-428-082B-151	Sequence 151, Appl
38	52.1	12	4	US-09-419-381-21	Sequence 21, Appl
39	52.1	16	3	US-09-180-100-25	Sequence 25, Appl
40	52.1	20	3	US-08-826-964-3	Sequence 3, Appl
41	52.1	22	4	US-09-205-258-896	Sequence 896, Appl
42	50.0	5	4	US-09-632-570-35	Sequence 35, Appl
43	50.0	6	1	US-08-032-848C-20	Sequence 20, Appl
44	50.0	6	4	US-09-632-570-38	Sequence 38, Appl
45	50.0	7	4	US-08-635-886C-170	Sequence 170, Appl

## ALIGNMENTS

## RESULT 1

US-09-149-476-551  
; Sequence 551, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,583  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23

1	EARLIER	FILING DATE:	1997-08-22	
2	EARLIER	APPLICATION NUMBER:	60/056,894	
3	EARLIER	FILING DATE:	1997-08-22	
4	EARLIER	APPLICATION NUMBER:	60/056,911	
5	EARLIER	FILING DATE:	1997-08-22	
6	EARLIER	APPLICATION NUMBER:	60/056,636	
7	EARLIER	FILING DATE:	1997-08-22	
8	EARLIER	APPLICATION NUMBER:	60/056,874	
9	EARLIER	FILING DATE:	1997-08-22	
10	EARLIER	APPLICATION NUMBER:	60/056,910	
11	EARLIER	FILING DATE:	1997-08-22	
12	EARLIER	APPLICATION NUMBER:	60/056,864	
13	EARLIER	FILING DATE:	1997-08-22	
14	EARLIER	APPLICATION NUMBER:	60/056,631	
15	EARLIER	FILING DATE:	1997-08-22	
16	EARLIER	APPLICATION NUMBER:	60/056,845	
17	EARLIER	FILING DATE:	1997-08-22	
18	EARLIER	APPLICATION NUMBER:	60/056,892	
19	EARLIER	FILING DATE:	1997-08-22	
20	EARLIER	APPLICATION NUMBER:	60/057,761	
21	EARLIER	FILING DATE:	1997-08-22	
22	EARLIER	APPLICATION NUMBER:	60/047,595	
23	EARLIER	FILING DATE:	1997-05-23	
24	EARLIER	APPLICATION NUMBER:	60/047,599	
25	EARLIER	FILING DATE:	1997-05-23	
26	EARLIER	APPLICATION NUMBER:	60/047,588	
27	EARLIER	FILING DATE:	1997-05-23	
28	EARLIER	APPLICATION NUMBER:	60/047,585	
29	EARLIER	FILING DATE:	1997-05-23	
30	EARLIER	APPLICATION NUMBER:	60/047,586	
31	EARLIER	FILING DATE:	1997-05-23	
32	EARLIER	APPLICATION NUMBER:	60/047,590	
33	EARLIER	FILING DATE:	1997-05-23	
34	EARLIER	APPLICATION NUMBER:	60/047,594	
35	EARLIER	FILING DATE:	1997-05-23	
36	EARLIER	APPLICATION NUMBER:	60/047,589	
37	EARLIER	FILING DATE:	1997-05-23	
38	EARLIER	APPLICATION NUMBER:	60/047,593	
39	EARLIER	FILING DATE:	1997-05-23	
40	EARLIER	APPLICATION NUMBER:	60/047,614	
41	EARLIER	FILING DATE:	1997-05-23	
42	EARLIER	APPLICATION NUMBER:	60/043,578	
43	EARLIER	FILING DATE:	1997-04-11	
44	EARLIER	APPLICATION NUMBER:	60/043,576	
45	EARLIER	FILING DATE:	1997-04-11	
46	EARLIER	APPLICATION NUMBER:	60/047,501	
47	EARLIER	FILING DATE:	1997-05-23	
48	EARLIER	APPLICATION NUMBER:	60/043,670	
49	EARLIER	FILING DATE:	1997-04-11	
50	EARLIER	APPLICATION NUMBER:	60/056,632	
51	EARLIER	FILING DATE:	1997-08-22	
52	EARLIER	APPLICATION NUMBER:	60/056,664	
53	EARLIER	FILING DATE:	1997-08-22	
54	EARLIER	APPLICATION NUMBER:	60/056,876	
55	EARLIER	FILING DATE:	1997-08-22	
56	EARLIER	APPLICATION NUMBER:	60/056,881	
57	EARLIER	FILING DATE:	1997-08-22	
58	EARLIER	APPLICATION NUMBER:	60/056,909	
59	EARLIER	FILING DATE:	1997-08-22	
60	EARLIER	APPLICATION NUMBER:	60/056,875	
61	EARLIER	FILING DATE:	1997-08-22	
62	EARLIER	APPLICATION NUMBER:	60/056,862	
63	EARLIER	FILING DATE:	1997-08-22	
64	EARLIER	APPLICATION NUMBER:	60/056,887	
65	EARLIER	FILING DATE:	1997-08-22	
66	EARLIER	APPLICATION NUMBER:	60/056,908	
67	EARLIER	FILING DATE:	1997-08-22	
68	EARLIER	APPLICATION NUMBER:	60/048,964	
69	EARLIER	FILING DATE:	1997-06-06	
70	EARLIER	APPLICATION NUMBER:	60/057,650	
71	EARLIER	FILING DATE:	1997-09-05	
72	EARLIER	APPLICATION NUMBER:	60/056,884	
73	EARLIER	FILING DATE:	1997-08-22	



; EARLIER APPLICATION NUMBER: 60/057,669  
; EARLIER FILING DATE: 1997-09-05  
; EARLIER APPLICATION NUMBER: 60/049,610  
; EARLIER FILING DATE: 1997-06-13  
; EARLIER APPLICATION NUMBER: 60/061,060  
; EARLIER FILING DATE: 1997-10-02

Query Match 58.3%; Score 28; DB 4; Length 11;  
Best Local Similarity 42.9%; Pred. No. 66;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWTMM 9  
|:|:|:|:  
Db 1 LLLWTL 7

RESULT 2  
US-08-241-054-50  
; Sequence 50, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; APPLICATION DATA:  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gerald F. Swiss  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-002  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-241-054-50

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MIWTMM 9  
|:|:|:|:  
Db 6 MLANNM 11

RESULT 3  
US-08-241-054-53  
; Sequence 53, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; APPLICATION DATA:  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gerald F. Swiss  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-002  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-241-054-53

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9  
|:|:|:|:  
Db 7 LWTMM 11

RESULT 4  
US-08-241-054-61  
; Sequence 61, Application US/08241054  
; Patent No. 5643873

GENERAL INFORMATION:  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice  
TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
TITLE OF INVENTION: Molecule 1  
NUMBER OF SEQUENCES: 169  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: 699 Prince Street  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22313  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Gerald F. Swiss  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-002  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-241-054-61

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9  
DB 7 LWTMM 11

RESULT 5  
US-08-190-156A-22  
Sequence 22, Application US/08390156A  
Patent No. 5648458  
GENERAL INFORMATION:  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
TITLE OF INVENTION: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.

STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-156A-22

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MIWTMM 9  
DB 6 MLWNMM 11

RESULT 6  
US-08-390-156A-57  
Sequence 57, Application US/08390156A  
Patent No. 5648458  
GENERAL INFORMATION:  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
TITLE OF INVENTION: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295

; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 1023.1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 57:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-390-156A-57

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IWTMM 9  
Db 7 LWTMM 11

RESULT 7  
US-08-390-156A-61  
; Sequence 61, Application US/08390156A  
; Patent No. 5648458  
; GENERAL INFORMATION:  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Dower, William J.  
; TITLE OF INVENTION: Peptides and Compounds That Bind to  
; TITLE OF INVENTION: ELAM-1  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, N.V.  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/390,156A  
; FILING DATE: 16-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Swiss, Gerald F.  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 1023.1A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid

; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-390-156A-61

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IWTMM 9  
Db 7 LWTMM 11

RESULT 8  
US-08-439-817-30  
; Sequence 30, Application US/08439817  
; Patent No. 5728802  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I (ELAM-1)  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,817  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-439-817-30

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 72;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MIWTMM 9  
|:|:|  
Db 6 MLWNMM 11

RESULT 9  
US-08-439-817-33  
; Sequence 33, Application US/08439817  
; Patent No. 5728802  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I (ELAM-1)  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,817  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-439-817-33

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9  
|:|:|  
Db 7 LWTMM 11

RESULT 10  
US-08-439-817-41  
; Sequence 41, Application US/08439817  
; Patent No. 5728802  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I (ELAM-1)  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,817  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-439-817-41

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9  
|:|:|  
Db 7 LWTMM 11

RESULT 11  
US-08-485-508-50  
; Sequence 50, Application US/08485508  
; Patent No. 5786322  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.

APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice  
TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule I  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, NV  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,508  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 000324-002/1056  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-485-508-50

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 86.7%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 MIWTMM 9  
Db 6 MLNNMM 11

RESULT 12  
US-08-485-508-53  
Sequence 53, Application US/08485508  
Patent No. 5786322  
GENERAL INFORMATION:  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice  
TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule I  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, NV  
STREET: 4001 Miranda Ave.

TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule I  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, NV  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,508  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 000324-002/1056  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-485-508-53

Query Match 58.3%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 72;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9  
Db 7 LWTMM 11

RESULT 13  
US-08-485-508-61  
Sequence 61, Application US/08485508  
Patent No. 5786322  
GENERAL INFORMATION:  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice  
TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule I  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, NV  
STREET: 4001 Miranda Ave.

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; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,508
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-002/1056
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-485-508-61

Query Match 58.3%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 72;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 INTMM 9
DB 7 LWTMM 11

RESULT 14
US-08-905-223-20
; Sequence 20, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTE FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
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; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..21
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-08-905-223-20

Query Match 56.2%; Score 27; DB 3; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
DB 13 SALVIWT 19

RESULT 15
US-09-247-155-20
; Sequence 20, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 20
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..21
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.5
; OTHER INFORMATION: seq SFLPSALVIWTS/AF
US-09-247-155-20

Query Match 56.2%; Score 27; DB 3; Length 21;
Best Local Similarity 57.1%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWT 7
DB 13 SALVIWT 19
```

Db 13 SALVINT 19

Search completed: November 14, 2004, 12:08:48  
Job time : 8.08511 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 26.0426 Seconds  
(without alignments)  
123.973 Million cell updates/sec

Title: US-09-831-253F-5

Perfect score: 48

Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	3 AAY93096	Aay93096 Transform
2	48	100.0	9	3 AAY92949	Aay92949 Transform
3	36.5	76.0	12	3 AAY92947	Aay92947 Transform
4	36.5	76.0	12	3 AAY93008	Aay93008 Transform
5	35	72.9	11	3 AAY93094	Aay93094 Transform
6	35	72.9	12	3 AAY93009	Aay93009 Transform
7	35	72.9	12	3 AAY93010	Aay93010 Transform
8	31	64.6	18	4 AAB89123	Aab89123 HIV gp120
9	31	64.6	18	4 AAB89121	Aab89121 HIV gp120
10	31	64.6	18	4 AAB89122	Aab89122 HIV gp120
11	28	58.3	9	8 ADK08459	Adk08459 Human pap
12	28	58.3	9	8 ADK08095	Adk08095 Human pap
13	28	58.3	10	8 ADG94446	Adg94446 Human JAM
14	28	58.3	10	8 ADI46844	Adi46844 Permeabil
15	28	58.3	10	8 ADP87021	Adp87021 Junctiona
16	28	58.3	11	2 AAW74952	Aaw74952 Human sec
17	28	58.3	11	5 ABG95411	Abg95411 Human nov
18	28	58.3	11	6 ABO34605	Ab034605 Region of
19	28	58.3	11	7 ADI23266	Adi23266 Novel hum
20	28	58.3	11	8 ADH74268	Adh74268 Human sec
21	28	58.3	12	2 AAR86068	Aar86068 Anti-ELAM
22	28	58.3	12	2 AAR86065	Aar86065 Anti-ELAM
23	28	58.3	12	2 AAW26904	Aaw26904 ELAM-1 bi
24	28	58.3	12	2 AAW26900	Aaw26900 ELAM-1 bi
25	28	58.3	12	2 AAW26865	Aaw26865 ELAM-1 bi

26	28	58.3	12	2 AAW63875	Aaw63875 ELAM-1 pe
27	28	58.3	12	2 AAW63886	Aaw63886 ELAM-1 pe
28	28	58.3	12	2 AAW63878	Aaw63878 ELAM-1 pe
29	28	58.3	20	2 AAY17756	Aay17756 Target si
30	28	58.3	20	6 ABU93298	Abu93298 Single ch
31	28	58.3	21	4 ABB41629	Abb41629 Peptide #
32	28	58.3	21	4 AAM35422	Aam35422 Peptide #
33	28	58.3	21	4 AAM75309	Aam75309 Human bon
34	28	58.3	21	4 AAM62500	Aam62500 Human bra
35	27.5	57.3	14	3 AAY93098	Aay93098 Transform
36	27.5	57.3	14	3 AAY92950	Aay92950 Transform
37	27	56.2	9	6 ABU64837	Abu64837 Human NY-
38	27	56.2	10	8 ADK08116	Adk08116 Human pap
39	27	56.2	10	8 ADK08482	Adk08482 Human pap
40	27	56.2	20	4 AAM13980	Aam13980 Peptide #
41	27	56.2	20	4 ABB32925	Abb32925 Peptide #
42	27	56.2	20	4 AAM26386	Aam26386 Peptide #
43	27	56.2	20	4 ABB27754	Abb27754 Human pep
44	27	56.2	20	4 ABB18404	Abb18404 Protein #
45	27	56.2	20	4 AAM66109	Aam66109 Human bon

## ALIGNMENTS

## RESULT 1

AAY93096  
ID AAY93096 standard; peptide; 9 AA.

XX AAY93096;

XX AC

XX 08-NOV-2000 (first entry)

XX Transforming growth factor inhibitory peptide P142.

XX Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;

XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;

XX extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Exquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

XX Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betal,

XX useful for treatment of liver disease, especially cirrhosis, are partial

XX sequences of the factor or its receptors.

XX Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding

XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in

XX vivo which have partial amino acid sequences identical, or similar, with

XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent

XX examples of the peptides of the invention. The peptides act by

XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.

XX they are inhibitors of stimulation of collagen synthesis in liver cells

XX and inhibitors of synthesis of proteolytic enzymes able to degrade the

XX extracellular matrix. The peptides, their mimetopes and/or DNA (or

XX expression systems) encoding the peptides are used for treatment of liver

XX disease, specifically cirrhosis

```

XX
SQ Sequence 9 AA;
  Query Match      100.0%; Score 48; DB 3; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.7e+06;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
  |||||
Db 1 TSLMIWTMM 9

RESULT 2
AAY92949
ID AAY92949 standard; peptide; 9 AA.
AC AAY92949;
XX
AC AAY92949;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #5.
XX
KW Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borras Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Claim 6; Page 81; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis
XX
XX Sequence 9 AA;
  Query Match      100.0%; Score 48; DB 3; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.7e+06;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
  |||||
Db 1 TSLMIWTMM 9

RESULT 3
AAY92949
ID AAY92949 standard; peptide; 9 AA.
AC AAY92949;
XX
AC AAY92949;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide #5.
XX
KW Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Homo sapiens.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borras Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Claim 6; Page 81; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis
XX
XX Sequence 9 AA;
  Query Match      100.0%; Score 48; DB 3; Length 9;
  Best Local Similarity 100.0%; Pred. No. 1.7e+06;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9
  |||||
Db 1 TSLMIWTMM 9

RESULT 4
AAY93008
ID AAY93008 standard; peptide; 12 AA.
XX
AC AAY93008;
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P54.
XX
KW Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX

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OS Rattus sp.  
 XX WO200031135-A1.  
 XX  
 XX 02-JUN-2000.  
 XX  
 XX 23-NOV-1999; 99WO-ES000375.  
 XX  
 XX 24-NOV-1998; 98ES-00002465.  
 XX  
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 XX  
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borras Cuesta F;  
 XX WPI; 2000-411935/35.  
 XX  
 XX Peptides that antagonize binding of transforming growth factor betal.  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 XX  
 XX Disclosure; Page 27; 86pp; Spanish.  
 XX  
 XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 XX Sequence 12 AA;  
 SQ

Query Match 76.0%; Score 36.5; DB 3; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 3.9;  
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 1 TSL---MIWTMM 9  
 DB 1 TSLDATMIWTMM 12  
 ||| |||||  
 ||| |||||

RESULT 5  
 AAY93094  
 ID AAY93094 standard; peptide; 11 AA.  
 XX  
 XX AAY93094;  
 AC  
 XX 08-NOV-2000 (first entry)  
 DT  
 XX Transforming growth factor inhibitory peptide P140.  
 DE  
 XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200031135-A1.  
 XX  
 XX 02-JUN-2000.  
 PD  
 XX 23-NOV-1999; 99WO-ES000375.  
 XX  
 XX 24-NOV-1998; 98ES-00002465.  
 XX  
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 XX  
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI

PI Borras Cuesta F;  
 XX WPI; 2000-411935/35.  
 XX  
 XX Peptides that antagonize binding of transforming growth factor betal.  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 XX  
 XX Disclosure; Page 31; 86pp; Spanish.  
 XX  
 XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 XX Sequence 11 AA;  
 SQ

Query Match 72.9%; Score 35; DB 3; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 6.7;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MIWTMM 9  
 DB 6 MIWTMM 11  
 |||||  
 |||||

RESULT 6  
 AAY93009  
 ID AAY93009 standard; peptide; 12 AA.  
 XX  
 XX AAY93009;  
 AC  
 XX 08-NOV-2000 (first entry)  
 DT  
 XX Transforming growth factor inhibitory peptide P55.  
 DE  
 XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX  
 XX Rattus sp.  
 OS  
 XX WO200031135-A1.  
 XX  
 XX 02-JUN-2000.  
 PD  
 XX 23-NOV-1999; 99WO-ES000375.  
 XX  
 XX 24-NOV-1998; 98ES-00002465.  
 XX  
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 XX  
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borras Cuesta F;  
 XX WPI; 2000-411935/35.  
 XX  
 XX Peptides that antagonize binding of transforming growth factor betal.  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 XX  
 XX Disclosure; Page 27; 86pp; Spanish.  
 XX  
 XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 XX Sequence 11 AA;  
 SQ

CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 12 AA;

Query Match 72.9%; Score 35; DB 3; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 7.3;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIWTMM 9  
 DB 6 MIWTMM 11  
 |||||

RESULT 7  
 AAY93010  
 ID AAY93010 standard; peptide; 12 AA.

XX AC AAY93010;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide P56.

XX KW Hepatotropic; antagonist; transforming growth factor beta1; TGF- $\beta$ 1;  
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 XX extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Rattus sp.

XX PN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 XX Borrás Cuesta F;

XX DR WPI; 2000-411935/35.

XX PT Peptides that antagonize binding of transforming growth factor beta1,  
 XX useful for treatment of liver disease, especially cirrhosis, are partial  
 XX sequences of the factor or its receptors.

XX PS Disclosure; Page 27; 86pp; Spanish.

XX CC The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor beta1 (TGF- $\beta$ 1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis

XX SQ Sequence 12 AA;

Query Match 72.9%; Score 35; DB 3; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 7.3;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MIWTMM 9  
 DB 1 MIWTMM 6  
 |||||

RESULT 8  
 AAB89123  
 ID AAB89123 standard; peptide; 18 AA.

XX AC AAB89123;

XX DT 23-MAY-2001 (first entry)

XX DE HIV gp120 protein binding peptide #216.

XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
 XX replication; CCR5; CXCR4; CD4; STRL33.

XX OS Homo sapiens.

XX PN WO200116182-A2.

XX PD 08-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US023505.

XX PR 27-AUG-1999; 99US-0151270P.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX PI Saxinger C;

XX DR WPI; 2001-244398/25.

XX PT Novel polypeptides useful for treating HIV infection, have homology to  
 XX regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,  
 XX and binds to HIV gp120 under physiological conditions.

XX PS Example 3; Page 43; 114pp; English.

XX CC The present invention describes a number of peptides which are able to  
 XX bind to HIV glycoprotein 120 (gp120). These are similar to the human  
 XX chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are  
 XX useful in the treatment of HIV, as they prevent replication of the virus.  
 XX The present sequence is an example of a peptide of the invention

XX SQ Sequence 18 AA;

Query Match 64.6%; Score 31; DB 4; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 60;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8  
 DB 3 TSLLIWVI 10  
 |||||

RESULT 9  
 AAB89121  
 ID AAB89121 standard; peptide; 18 AA.

XX AC AAB89121;

XX DT 23-MAY-2001 (first entry)

XX DE HIV gp120 protein binding peptide #214.

XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;  
 XX replication; CCR5; CXCR4; CD4; STRL33.

XX OS Homo sapiens.

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XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US023505.
XX PR 27-AUG-1999; 99US-0151270P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions.
XX PS Example 3; Page 42; 114pp; English.
XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the virus.
XX CC The present sequence is an example of a peptide of the invention
XX SQ Sequence 18 AA;
XX Query Match 64.6%; Score 31; DB 4; Length 18;
XX Best Local Similarity 62.5%; Pred. No. 60;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 11 TSLLIWVI 18

RESULT 10
AAB89122
ID AAB89122 standard; peptide; 18 AA.
AC AAB89122;
XX DT 23-MAY-2001 (first entry)
XX DE HIV gp120 protein binding peptide #215.
XX KW Human chemokine receptor; CD4; HIV; glycoprotein 120; gp120; antagonist;
XX KW replication; CCR5; CXCR4; CD4; STRL33.
XX OS Homo sapiens.
XX PN WO200116182-A2.
XX PD 08-MAR-2001.
XX PF 25-AUG-2000; 2000WO-US023505.
XX PR 27-AUG-1999; 99US-0151270P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Saxinger C;
XX DR WPI; 2001-244398/25.
XX PT Novel polypeptides useful for treating HIV infection, have homology to
XX PT regions of domains of human chemokine receptors CCR5, CXCR4 and STRL33,
XX PT and binds to HIV gp120 under physiological conditions.
XX PS Example 3; Page 42; 114pp; English.

XX CC The present invention describes a number of peptides which are able to
XX CC bind to HIV glycoprotein 120 (gp120). These are similar to the human
XX CC chemokine receptors CCR5, CXCR4 and STRL33, as well as CD4. These are
XX CC useful in the treatment of HIV, as they prevent replication of the virus.
XX CC The present sequence is an example of a peptide of the invention
XX SQ Sequence 18 AA;
XX Query Match 64.6%; Score 31; DB 4; Length 18;
XX Best Local Similarity 62.5%; Pred. No. 60;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 11 TSLLIWVI 18

RESULT 11
ADK08459
ID ADK08459 standard; peptide; 9 AA.
XX AC ADK08459;
XX DT 06-MAY-2004 (first entry)
XX DE Human papillomavirus peptide #514.
XX KW pathogenic virus; alternative reading frame; antigenic determinant;
XX KW virucide; vaccine; therapeutic agent; infection; HPV.
XX OS Human papillomavirus.
XX PN WO2004011650-A2.
XX PD 05-FEB-2004.
XX PF 24-JUL-2003; 2003WO-EP008112.
XX PR 24-JUL-2002; 2002AT-00001124.
XX PR 11-JUL-2003; 2003EP-00450171.
XX PA (INTB-) INTERCELL AG.
XX PI Mattner F, Schmidt W, Habel A;
XX DR WPI; 2004-169243/16.
XX PT New polypeptide encoded by an alternative reading frame of a pathogenic
XX PT virus comprising an antigenic determinant, useful for treating or
XX PT preventing an infection with the pathogenic virus.
XX PS Claim 18; Page 179; 220pp; English.
XX CC This invention relates to a novel polypeptide encoded by an alternative
XX CC reading frame of a pathogenic virus, where the polypeptide starts with a
XX CC methionine amino acid residue, which comprises an antigenic determinant
XX CC and more than 7 amino acid residues. The invention may be useful for the
XX CC production of compounds with a virucide activity or the development of a
XX CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
XX CC agent. It is also useful for the manufacture of a medicament for treating
XX CC or preventing an infection with the pathogenic virus. The present
XX CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
XX CC invention.
XX SQ Sequence 9 AA;
XX Query Match 58.3%; Score 28; DB 8; Length 9;
XX Best Local Similarity 37.5%; Pred. No. 1.7e+06;
XX Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIWTMM 9
DB 2 ALVLWTLI 9

```

RESULT 12  
ADK08095  
ID ADK08095 standard; peptide; 9 AA.  
XX AC ADK08095;  
XX DT 06-MAY-2004 (first entry)  
XX DE Human papillomavirus peptide #150.  
XX KW pathogenic virus; alternative reading frame; antigenic determinant;  
XX KW virucide; vaccine; therapeutic agent; infection; HPV.  
XX OS Human papillomavirus.  
XX PN WO2004011650-A2.  
XX PD 05-FEB-2004.  
XX PF 24-JUL-2003; 2003WO-EP008112.  
XX PR 24-JUL-2002; 2002AT-00001124.  
XX PR 11-JUL-2003; 2003EP-00450171.  
XX PA (INTE-) INTERCELL AG.  
XX PI Mattner F, Schmidt W, Habel A;  
XX WPI; 2004-169243/16.  
XX PT New polypeptide encoded by an alternative reading frame of a pathogenic  
XX PT virus comprising an antigenic determinant, useful for treating or  
XX PT preventing an infection with the pathogenic virus.  
XX PS Claim 18; Page 175; 220pp; English.  
XX SQ This invention relates to a novel polypeptide encoded by an alternative  
CC reading frame of a pathogenic virus, where the polypeptide starts with a  
CC methionine amino acid residue, which comprises an antigenic determinant  
CC and more than 7 amino acid residues. The invention may be useful for the  
CC production of compounds with a virucide activity or the development of a  
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic  
CC agent. It is also useful for the manufacture of a medicament for treating  
CC or preventing an infection with the pathogenic virus. The present  
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the  
CC invention.  
XX SQ Sequence 9 AA;  
Query Match 58.3%; Score 28; DB 8; Length 9;  
Best Local Similarity 37.5%; Pred. NO. 1.7e+06;  
Matches 3; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
QY 2 SLMIWTMM 9  
DB :||:|:|:  
2 ALVLWTLTLL 9  
RESULT 13  
ADG94446  
ID ADG94446 standard; peptide; 10 AA.  
XX AC ADG94446;  
XX DT 25-MAR-2004 (first entry)  
XX DE Human JAM-1 permeabilising peptide SEQ ID NO:425.  
XX KW human; permeabilising; interferon-beta; IFN-beta; mucosal delivery;  
XX KW immunosuppressive; virucide; autoimmune disease; viral disease;  
XX KW multiple sclerosis; chronic hepatitis B; condyloma acuminata;  
KW papilloma virus; childhood viral encephalitis; wart.  
XX OS Homo sapiens.  
XX PN WO2004002404-A2.  
XX PD 08-JAN-2004.  
XX PF 18-JUN-2003; 2003WO-US019261.  
XX PR 28-JUN-2002; 2002US-0393066P.  
XX PA (NAST-) NASTECH PHARM CO INC.  
XX PI Quay SC, Gupta M, De Meireles JC, Abd El- Shafy M;  
XX WPI; 2004-122360/12.  
XX PT Stable pharmaceutical composition comprising interferon compound(s)  
XX PT formulated for mucosal delivery to mammalian subjects in combination with  
XX PT mucosal delivery-enhancing agent(s).  
XX PS Disclosure; SEQ ID NO 425; 353pp; English.  
XX CC The invention relates to a novel stable pharmaceutical composition  
XX CC comprising one or more interferon (IFN) beta compound(s) formulated for  
XX CC mucosal delivery to a mammalian subject in combination with one or more  
XX CC mucosal delivery-enhancing agent(s), where the composition following  
XX CC mucosal administration to the subject yields enhanced mucosal delivery of  
XX CC the one or more IFN-beta compound(s). A composition of the invention has  
XX CC immunosuppressive and virucide activity. The composition is useful for  
XX CC treating autoimmune diseases, viral disease, for alleviating one or more  
XX CC symptom(s) of multiple sclerosis (MS), chronic hepatitis B, condyloma  
XX CC acuminata, papilloma virus warts of the larynx or skin or childhood viral  
XX CC encephalitis in the subject without unacceptable adverse side effects.  
XX CC The composition can be delivered intranasally which reduces or eliminates  
XX CC compliance problems and side effects that attend delivery by injection.  
XX CC The sequences shown in ADG94022-ADG94810 represent permeabilising  
XX CC peptides used in a composition of the invention.  
XX SQ Sequence 10 AA;  
Query Match 58.3%; Score 28; DB 8; Length 10;  
Best Local Similarity 62.5%; Pred. NO. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TSLMIWTM 8  
DB |||||:  
3 TSLKIWNV 10  
RESULT 14  
ADI46844  
ID ADI46844 standard; peptide; 10 AA.  
XX AC ADI46844;  
XX DT 06-MAY-2004 (first entry)  
XX DE Permeabilising peptide of human JAM-2 SeqID553.  
XX KW mucosal delivery; permeabilising peptide;  
XX KW mucosal epithelial paracellular transport; epithelial junction;  
XX KW epithelial membrane adhesive protein; junctional adhesion molecule; JAM;  
XX KW occludin; claudin; sexual dysfunction; male erectile sexual dysfunction;  
XX KW female sexual dysfunction; human.  
XX OS Homo sapiens.  
XX PN WO2004003145-A2.  
XX PD 08-JAN-2004.  
XX

PF 24-JUN-2003; 2003WO-US019994.  
 XX  
 PR 28-JUN-2002; 2002US-0392512P.  
 XX  
 PA (NAST-) NASTECH PHARM CO INC.  
 XX  
 PI Quay SC;  
 XX  
 DR WPI; 2004-091087/09.  
 XX  
 XX Composition comprising biologically active agent and permeabilizing  
 PT peptide that reversibly enhances mucosal epithelial paracellular  
 PT transport by modulating epithelial junctional structure and/or physiology  
 PT in mammal.  
 XX  
 PS Disclosure; SEQ ID NO 553; 426pp; English.  
 XX  
 CC This invention relates to a novel composition comprising a biologically  
 CC active agent and mucosal delivery-enhancing effective amount of  
 CC permeabilizing peptide that reversibly enhances mucosal epithelial  
 CC paracellular transport by modulating epithelial junctional structure  
 CC and/or physiology in a mammal. The agent of the invention inhibits  
 CC homotypic binding of epithelial membrane adhesive protein chosen  
 CC junctional adhesion molecule (JAM), occludin and claudin. The  
 CC biologically active agent is effective for treatment of sexual  
 CC dysfunction, for example male erectile sexual dysfunction or female  
 CC sexual dysfunction. The present sequence is that of a permeabilizing  
 CC peptide of human JAM-2 which may be used during the production of the  
 CC composition of the invention.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 58.3%; Score 28; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TSLMIWTM 8  
 ||||| :  
 DB 3 TSLKIWNV 10

RESULT 15  
 ADP87021  
 ID ADP87021 standard; peptide; 10 AA.  
 XX  
 AC ADP87021;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 XX Junctional adhesion molecule 2 (JAM-2) peptide seqid 426.  
 DE  
 DE anorectic; cytostatic; eating disorder; neuroprotective; nootropic;  
 KW cachexia; intranasal composition; peptide YY; obesity; cancer;  
 KW malnutrition; wasting; Alzheimer's disease; colon adenocarcinoma;  
 KW pancreatic adenocarcinoma; breast carcinoma; cachexia; cancer cachexia;  
 KW junctional adhesion molecule 2; JAM-2; epithelial junction; human.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2004115135-A1.  
 PN  
 XX 17-JUN-2004.  
 XX  
 PD 17-DEC-2002; 2002US-00322266.  
 XX  
 PF 17-DEC-2002; 2002US-00322266.  
 XX  
 PR 17-DEC-2002; 2002US-00322266.  
 XX  
 XX (QUAY/) QUAY S C.  
 PA  
 XX Quay SC;  
 PI  
 XX WPI; 2004-478989/45.  
 DR  
 XX

PT Intranasal compositions for treating obesity, cancer, or malnutrition or  
 PT wasting related to cancer, comprises peptide compound(s) formulated for  
 PT mucosal delivery to mammalian subject.  
 XX  
 PS Disclosure; SEQ ID NO 426; 86pp; English.  
 XX  
 CC The invention describes an intranasal composition comprising peptide YY  
 CC compound(s) formulated for mucosal delivery to a mammalian subject. Also  
 CC described is a kit for treatment of a mammalian subject comprising the  
 CC intranasal composition of peptide compound(s). The composition is used  
 CC for treating obesity, cancer, or malnutrition or wasting related to  
 CC cancer in the subject. It is used to alleviate Alzheimer's disease, colon  
 CC adenocarcinoma, pancreatic adenocarcinoma, breast carcinoma, treatment  
 CC and prevention of malnutrition resulting from iatrogenic causes or  
 CC cachexia associated with advanced disease, or cancer cachexia in the  
 CC subject. The composition alleviates the symptoms without unacceptable  
 CC adverse side effects. This is the amino acid sequence of a human  
 CC junctional adhesion molecule 2 (JAM-2) that may be used in a composition  
 CC of the invention to modulate epithelial junction structure and/or  
 CC physiology.  
 XX  
 SQ Sequence 10 AA;  
 Query Match 58.3%; Score 28; DB 8; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TSLMIWTM 8  
 ||||| :  
 DB 3 TSLKIWNV 10

Search completed: November 14, 2004, 12:02:11  
 Job time : 28.0426 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 21.2553 Seconds  
(without alignments)  
149.815 Million cell updates/sec

Title: US-09-831-253F-5  
Perfect score: 48  
Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
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- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	64.6	18	14 US-10-084-813-236	Sequence 236, App
2	31	64.6	18	14 US-10-084-813-237	Sequence 237, App
3	31	64.6	18	14 US-10-084-813-238	Sequence 238, App
4	28	58.3	10	15 US-10-462-452-425	Sequence 425, App
5	28	58.3	10	15 US-10-601-953-553	Sequence 553, App
6	28	58.3	10	16 US-10-322-266-426	Sequence 426, App
7	28	58.3	11	10 US-09-809-391-551	Sequence 551, App
8	28	58.3	11	10 US-09-882-171-551	Sequence 551, App
9	28	58.3	11	14 US-10-164-861-551	Sequence 551, App
10	28	58.3	20	10 US-09-939-769-2	Sequence 2, Appl
11	28	58.3	21	9 US-09-864-761-45075	Sequence 45075, A
12	27	56.2	20	9 US-09-864-761-33702	Sequence 33702, A
13	27	56.2	21	10 US-09-903-190-20	Sequence 20, Appl

14	27	56.2	21	14	US-10-319-763-20	Sequence 20, Appl
15	27	56.2	23	9	US-09-864-761-45706	Sequence 45706, A
16	26	54.2	9	9	US-09-796-744-10	Sequence 10, Appl
17	26	54.2	9	14	US-10-231-452-7	Sequence 7, Appl
18	26	54.2	13	10	US-09-953-354-126	Sequence 126, App
19	26	54.2	13	10	US-10-092-750-17	Sequence 17, Appl
20	26	54.2	23	9	US-09-864-761-36057	Sequence 36057, A
21	25	52.1	8	8	US-08-979-847-170	Sequence 170, App
22	25	52.1	8	14	US-10-114-104-170	Sequence 170, App
23	25	52.1	9	15	US-10-182-252A-632	Sequence 632, App
24	25	52.1	9	15	US-10-182-252A-657	Sequence 657, App
25	25	52.1	10	14	US-10-200-708-79	Sequence 79, Appl
26	25	52.1	10	14	US-10-200-708-501	Sequence 501, App
27	25	52.1	10	15	US-10-430-685-173	Sequence 173, Appl
28	25	52.1	12	9	US-09-840-277-69	Sequence 69, Appl
29	25	52.1	12	15	US-10-609-217-151	Sequence 151, App
30	25	52.1	12	15	US-10-632-388-151	Sequence 151, App
31	25	52.1	12	15	US-10-651-723-151	Sequence 151, App
32	25	52.1	12	15	US-10-645-761-151	Sequence 151, App
33	25	52.1	12	15	US-10-666-696-151	Sequence 151, App
34	25	52.1	12	15	US-10-653-048-151	Sequence 151, App
35	25	52.1	12	16	US-10-692-151-21	Sequence 21, Appl
36	25	52.1	14	9	US-09-995-494-86	Sequence 86, Appl
37	25	52.1	16	9	US-09-949-713-25	Sequence 25, Appl
38	25	52.1	16	15	US-10-449-831A-39	Sequence 39, Appl
39	25	52.1	18	14	US-10-144-929-202	Sequence 202, App
40	25	52.1	18	15	US-10-144-929-202	Sequence 202, App
41	25	52.1	20	14	US-10-280-066-332	Sequence 332, App
42	25	52.1	20	14	US-10-029-386-30555	Sequence 30555, A
43	25	52.1	22	10	US-09-974-879-593	Sequence 593, App
44	25	52.1	22	10	US-09-305-736-594	Sequence 594, App
45	25	52.1	22	10	US-09-933-767-896	Sequence 896, App

ALIGNMENTS

RESULT 1

US-10-084-813-236  
; Sequence 236, Application US/10084813  
; Publication No. US2003068615A1  
; GENERAL INFORMATION:  
; APPLICANT: SAXINGER, CARL  
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; TITLE OF INVENTION: ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE  
; FILE REFERENCE: 215875  
; CURRENT APPLICATION NUMBER: US/10/084,813  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/US00/23505  
; PRIOR FILING DATE: 2000-08-25  
; PRIOR APPLICATION NUMBER: US 60/151,270  
; PRIOR FILING DATE: 1999-08-27  
; NUMBER OF SEQ ID NOS: 1242  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 236  
; LENGTH: 18  
; TYPE: PPT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide  
US-10-084-813-236

Query Match 64.6%; Score 31; DB 14; Length 18;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 TSLMIWTM 8  
|||:  
Db 11 TSLLIWVI 18

RESULT 2  
US-10-084-813-237

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; Sequence 237, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 237
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-237

Query Match      64.6%; Score 31; DB 14; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 7 TSLLIWVI 14

RESULT 3
US-10-084-813-238
; Sequence 238, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-238

Query Match      64.6%; Score 31; DB 14; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 3 TSLLIWVI 10

RESULT 4
US-10-462-452-425
; Sequence 425, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
```

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; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-425

Query Match      58.3%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 3 TSLKIWNV 10

RESULT 5
US-10-601-953-553
; Sequence 553, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions and Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 553
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-553

Query Match      58.3%; Score 28; DB 15; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
DB 3 TSLKIWNV 10

RESULT 6
US-10-322-266-426
; Sequence 426, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions and Methods For Enhanced Mucosal Delivery Of Peptid
; FILE REFERENCE: NPCI0567
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 426
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; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-322-266-426

Query Match      58.3%; Score 28; DB 16; Length 10;
Best Local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
    ||||| :
Db 3 TSLKIMNV 10

RESULT 7
US-09-809-391-551
; Sequence 551, Application US/09809391
; Publication No. US20030049619A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 551
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; NAME/KEY: SITE
; LOCATION: (11)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-809-391-551

Query Match      58.3%; Score 28; DB 10; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.4e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWTMM 9
    |::||::
Db 1 LLLWTLL 7

RESULT 8
US-09-882-171-551
; Sequence 551, Application US/09882171
; Publication No. US20030175859A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
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; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07

; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,334
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,336
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
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; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
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; PRIOR APPLICATION NUMBER: 60/047,598
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; PRIOR APPLICATION NUMBER: 60/047,613
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,582
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,596
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,612
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,632
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
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; PRIOR APPLICATION NUMBER: 60/043,313
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,672
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; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,315  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/048,974  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/056,886  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,877  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,889  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,893  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,630  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,878  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,662  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,872  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,882  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,637  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,903  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,888  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,879  
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; PRIOR APPLICATION NUMBER: 60/056,880  
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; PRIOR APPLICATION NUMBER: 60/056,894  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,911  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,636  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,874  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,910  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,864  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,631  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,892  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,761  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/047,595  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,599  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,588  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,585  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,586  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,590  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,594  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,589  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,593  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,614  
; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/043,578  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/047,501  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,670  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/056,632  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,664  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,876  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,881  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,909  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,875  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,862  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,887  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,908  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/057,650  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/056,884  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,669  
; PRIOR FILING DATE: 1997-09-05

Query Match 58.3%; Score 28; DB 10; Length 11;  
Best Local Similarity 42.9%; Pred No. 2.4e+02;  
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWTMM 9  
Db 1 LLLWTL 7

## RESULT 9

US-10-164-861-551  
; Sequence 551, Application US/10164861  
; Publication No. US20030225248A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/10/164,861  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US/09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 757  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 551  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (9)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (11)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-164-861-551

Query Match 58.3%; Score 28; DB 14; Length 11;  
 Best Local Similarity 42.9%; Pred. No. 2.4e+02;  
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWTMM 9  
 Db 1 LLLWTL 7

## RESULT 10

US-09-939-769-2  
 ; Sequence 2, Application US/09939769  
 ; Publication No. US20030017149A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HOEFFLER, JAMES P.  
 ; APPLICANT: RUSSELL, MARIJANE  
 ; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY FUSION REAGENTS THAT REGULATE  
 ; TITLE OF INVENTION: TRANSCRIPTION IN VIVO  
 ; FILE REFERENCE: 039322/0226  
 ; CURRENT APPLICATION NUMBER: US/09/939,769  
 ; CURRENT FILING DATE: 2001-08-28  
 ; PRIOR APPLICATION NUMBER: 08/728,890  
 ; PRIOR FILING DATE: 1996-10-10  
 ; NUMBER OF SEQ ID NOS: 96  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 20  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: illustrative  
 ; OTHER INFORMATION: mitochondrial target signal  
 US-09-939-769-2

Query Match 58.3%; Score 28; DB 10; Length 20;  
 Best Local Similarity 33.3%; Pred. No. 4.3e+02;  
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTMM 9  
 Db 3 TDLWLWLL 11

## RESULT 11

US-09-864-761-45075  
 ; Sequence 45075, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 ; FILE REFERENCE: Aescmca-x-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 60/234,687  
 ; PRIOR FILING DATE: 2000-09-21  
 ; PRIOR APPLICATION NUMBER: US 09/608,408  
 ; PRIOR FILING DATE: 2000-06-30  
 ; PRIOR APPLICATION NUMBER: US 09/774,203  
 ; PRIOR FILING DATE: 2001-01-29  
 ; NUMBER OF SEQ ID NOS: 49117  
 ; SOFTWARE: Annotmax Sequence Listing Engine vers. 1.1  
 ; SEQ ID NO 45075  
 ; LENGTH: 21  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: MAP TO AC013751.3  
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.47  
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53  
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.47  
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.46  
 ; OTHER INFORMATION: EST\_HUMAN HIT: AW026680.1, EVALUATE 9.00e-06  
 US-09-864-761-45075

Query Match 58.3%; Score 28; DB 9; Length 21;  
 Best Local Similarity 75.0%; Pred. No. 4.5e+02;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMIWTMM 9  
 Db 2 SVMIMTMM 9

## RESULT 12

US-09-864-761-33702  
 ; Sequence 33702, Application US/09864761  
 ; Patent No. US20020048763A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Penn, Sharron G.  
 ; APPLICANT: Rank, David R.  
 ; APPLICANT: Hanzel, David K.  
 ; APPLICANT: Chen, Wensheng  
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
 ; FILE REFERENCE: Aescmca-x-1  
 ; CURRENT APPLICATION NUMBER: US/09/864,761  
 ; CURRENT FILING DATE: 2001-05-23  
 ; PRIOR APPLICATION NUMBER: US 60/180,312  
 ; PRIOR FILING DATE: 2000-02-04  
 ; PRIOR APPLICATION NUMBER: US 60/207,456  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/632,366  
 ; PRIOR FILING DATE: 2000-08-03  
 ; PRIOR APPLICATION NUMBER: GB 24263.6  
 ; PRIOR FILING DATE: 2000-10-04  
 ; PRIOR APPLICATION NUMBER: US 60/236,359  
 ; PRIOR FILING DATE: 2000-09-27  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667  
 ; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00664  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00669  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00665  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00668  
;; PRIOR FILING DATE: 2001-01-30  
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;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00662  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00661  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: PCT/US01/00670  
;; PRIOR FILING DATE: 2001-01-30  
;; PRIOR APPLICATION NUMBER: US 60/234,687  
;; PRIOR FILING DATE: 2000-09-21  
;; PRIOR APPLICATION NUMBER: US 09/608,408  
;; PRIOR FILING DATE: 2000-06-30  
;; PRIOR APPLICATION NUMBER: US 09/774,203  
;; PRIOR FILING DATE: 2001-01-29  
;; NUMBER OF SEQ ID NOS: 49117  
;; SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
;; SEQ ID NO 33702  
;; LENGTH: 20  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; OTHER INFORMATION: MAP TO AC007683.2  
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.77  
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.92  
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.89  
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.74  
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3  
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.89  
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2  
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7  
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2  
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1  
US-09-864-761-33702

Query Match 56.2%; Score 27; DB 9; Length 20;  
Best Local Similarity 57.1%; Pred. No. 6.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWT 7  
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Db 8 TTMWT 14

RESULT 13  
US-09-903-190-20  
;; Sequence 20, Application US/09903190  
;; Publication No. US20030162176A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
;; APPLICANT: Duclert, Aymeric  
;; APPLICANT: Bougueleret, Lydie  
;; TITLE OF INVENTION: Complementary DNAs  
;; FILE REFERENCE: GENSET 021A  
;; CURRENT APPLICATION NUMBER: US/09/903,190  
;; CURRENT FILING DATE: 2001-07-11  
;; PRIOR APPLICATION NUMBER: US/09/247,155A  
;; PRIOR FILING DATE: 1999-02-09  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10  
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273  
;; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04

;; NUMBER OF SEQ ID NOS: 182  
;; SOFTWARE: Patent.pm  
;; SEQ ID NO 20  
;; LENGTH: 21  
;; TYPE: PRT  
;; ORGANISM: Homo Sapiens  
;; FEATURE:  
;; NAME/KEY: SIGNAL  
;; LOCATION: 1..21  
;; OTHER INFORMATION: Von Heijne matrix  
;; OTHER INFORMATION: score 5.5  
;; OTHER INFORMATION: seq SFLPSALVITWSA/AF  
US-09-903-190-20

Query Match 56.2%; Score 27; DB 10; Length 21;  
Best Local Similarity 57.1%; Pred. No. 6.6e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWT 7  
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Db 13 SALVIWT 19

RESULT 14  
US-10-319-763-20  
;; Sequence 20, Application US/10319763  
;; Publication No. US2003014490A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Dumas Milne Edwards, Jean-Baptiste  
;; APPLICANT: Bougueleret, Lydie  
;; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS  
;; FILE REFERENCE: G-031.US04.DIV  
;; CURRENT APPLICATION NUMBER: US/10/319,763  
;; CURRENT FILING DATE: 2002-12-10  
;; PRIOR APPLICATION NUMBER: 60/066,677  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/069,957  
;; PRIOR FILING DATE: 1997-12-17  
;; PRIOR APPLICATION NUMBER: 60/074,121  
;; PRIOR FILING DATE: 1998-02-09  
;; PRIOR APPLICATION NUMBER: 60/081,563  
;; PRIOR FILING DATE: 1998-04-13  
;; PRIOR APPLICATION NUMBER: 60/096,116  
;; PRIOR FILING DATE: 1998-08-10  
;; PRIOR APPLICATION NUMBER: 60/099,273  
;; PRIOR FILING DATE: 1998-09-04  
;; NUMBER OF SEQ ID NOS: 229  
;; SOFTWARE: Patent.pm  
;; SEQ ID NO 20  
;; LENGTH: 21  
;; TYPE: PRT  
;; ORGANISM: Homo Sapiens  
;; FEATURE:  
;; NAME/KEY: SIGNAL  
;; LOCATION: 1..21  
;; OTHER INFORMATION: Von Heijne matrix  
;; OTHER INFORMATION: score 5.5  
;; OTHER INFORMATION: seq SFLPSALVITWSA/AF  
US-10-319-763-20

Query Match 56.2%; Score 27; DB 14; Length 21;  
Best Local Similarity 57.1%; Pred. No. 6.6e+02;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLMIWT 7  
:::|  
Db 13 SALVIWT 19

RESULT 15  
US-09-864-761-45706  
;; Sequence 45706, Application US/09864761

Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharon G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wensheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
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PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117  
SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
SEQ ID NO 45706  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO AC025539.2  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.63  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.6  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.5

Query Match 56.2%; Score 27; DB 9; Length 23;  
Best Local Similarity 55.6%; Pred. No. 7.2e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 TSLMIWTMM 9  
Db 10 TRLEIMNNI 18

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Job time : 21.2553 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 24.0319 Seconds  
(without alignments)  
215.479 Million cell updates/sec

Title: US-09-831-253F-5  
Perfect score: 48  
Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	26	54.2	21	2 Q95N72	Q95N72 equus caball
2	25	52.1	11	2 Q9UEL0	Q9uel0 homo sapien
3	25	52.1	17	2 Q6LDL9	Q6ldl9 rattus norv
4	25	52.1	17	2 AA41680	AAa41680 rattus no
5	24	50.0	17	2 Q6LEA8	Q6lea8 xenopus lae
6	24	50.0	17	2 AAA49911	AAA49911 xenopus l.
7	24	50.0	19	2 Q8W128	Q8w128 scaevola pr
8	23	47.9	15	2 Q8R5G1	Q8r5g1 spermophilu
9	23	47.9	17	2 Q81VK5	Q81vk5 homo sapien
10	21	43.8	10	2 Q9ESU5	Q9eus5 mus musculu
11	21	43.8	17	2 Q7S3Q9	Q7s3q9 neurospora
12	21	43.8	17	2 Q69074	Q69074 human herpe
13	21	43.8	19	1 DCAM ACACA	P34039 acanthamoeb
14	21	43.8	21	2 Q6LER5	Q6ler5 homo sapien
15	21	43.8	21	2 BAA00902	Baa00902 homo sapi
16	21	43.8	22	2 Q38287	Q38287 lactococcus
17	21	43.8	22	2 Q33R63	Q33r63 yersinia pe
18	21	43.8	23	2 Q9NZ61	Q9nz61 homo sapien
19	20	41.7	10	1 LABA JATMU	P13270 jatropha mu
20	20	41.7	12	2 Q8SHF6	Q8shf6 chamaeleo m
21	20	41.7	10	2 Q6WRB2	Q6wrb2 eudromia el
22	20	41.7	12	2 AAQ23391	AAq23391 eudromia
23	20	41.7	14	2 Q9NFK8	Q9nfk8 drugia paha
24	20	41.7	17	2 Q6QLL7	Q6ql17 influenza a
25	20	41.7	17	2 Q6QLL9	Q6ql19 influenza a
26	20	41.7	17	2 Q6QLM0	Q6qlm0 influenza a
27	20	41.7	17	2 Q6QLM1	Q6qlm1 influenza a
28	20	41.7	17	2 AAS57878	Aas57878 influenza
29	20	41.7	17	2 AAS57879	Aas57879 influenza
30	20	41.7	17	2 AAS57880	Aas57880 influenza
31	20	41.7	17	2 AAS57882	Aas57882 influenza

ALIGNMENTS

RESULT 1

Q95N72	PRELIMINARY;	PRT;	21 AA.
ID Q95N72			
AC Q95N72;			
DT 01-DEC-2001 (Tremblrel. 19, Created)			
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DE NRAMP1 (Fragment)			
GN Name=NRAMP1;			
OS Equus caballus (Horse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX NCBI_TaxID=9796;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Matiasovic J., Horin P.;			
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AF354453; AAK43589.1; -			
FT NON TER 1			
FT NON TER 21			
SQ SEQUENCE 21 AA; 2259 MW; A064CFFD5F9A71E4 CRC64;			

Query Match 54.2%; Score 26; DB 2; Length 21;  
Best Local Similarity 42.9%; Pred. No. 8.1e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY	1 TSLMIWT 7
Db	7 TTYLVWT 13

RESULT 2

Q9UEL0	PRELIMINARY;	PRT;	11 AA.
ID Q9UEL0			
AC Q9UEL0;			
DT 01-MAY-2000 (Tremblrel. 13, Created)			
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DE 05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE Pas antigen (CD95 antigen) (Fragment)			
GN Name=CD95;			
OS Homo sapiens (Human)			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Blood;			
RX MEDLINE=95355401; PubMed=7543095;			
RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,			
RA Nakanishi Y.;			
RT "Transcription Stimulation of the Pas-encoding gene by nuclear factor			
RT for interleukin-6 expression upon influenza virus infection.";			
RL J. Biol. Chem. 270:18007-18012(1995).			
RN [2]			

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RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
RA Kuppers R., Rajewsky K.; to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;
RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kurth J., Pernick A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kuppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; D31968; BAA20850.1; -.
DR EMBL; AJ279011; CAC35539.1; -.
DR EMBL; AJ279012; CAC35540.1; -.
DR EMBL; AJ279013; CAC35541.1; -.
DR EMBL; AJ509179; CAD48929.1; -.
DR EMBL; AJ509180; CAD48930.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 52.1%; Score 25; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 LMIWTM 9
Db 2 LGIWTLL 8

RESULT 3
Q6LDL9 PRELIMINARY; PRT; 17 AA.
ID Q6LDL9 PRELIMINARY; PRT; 17 AA.
AC Q6LDL9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM-C;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=90287121; PubMed=1694009;
RA Chen A., Reyes A., Akesson R.A.;
RT "Transcription initiation sites and structural organization of the
RT extreme 5' region of the rat neural cell adhesion molecule gene.";
RL Mol. Cell. Biol. 10:3314-3324(1990).
DR EMBL; M32612; AAA41680.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2026 MW; AEA1EB5F252E84F5 CRC64;

Query Match 52.1%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
Db 4 TKDLIWTLL 11

RESULT 5
Q6LEA8 PRELIMINARY; PRT; 17 AA.
ID Q6LEA8 PRELIMINARY; PRT; 17 AA.
AC Q6LEA8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson A.D., Ovsenek N., Tonissen K.F., Krieg P.A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L26396; AAA49911.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 50.0%; Score 24; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIWTM 8
Db 7 LIWTLL 11

RESULT 6
AAA49911 PRELIMINARY; PRT; 17 AA.
ID AAA49911 PRELIMINARY; PRT; 17 AA.
AC AAA49911;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

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DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM-C.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=90287121; PubMed=1694009;
RA Chen A., Reyes A., Akesson R.A.;
RT "Transcription initiation sites and structural organization of the
RT extreme 5' region of the rat neural cell adhesion molecule gene.";
RL Mol. Cell. Biol. 10:3314-3324(1990).
DR EMBL; M32612; AAA41680.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2026 MW; AEA1EB5F252E84F5 CRC64;

Query Match 52.1%; Score 25; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWTM 8
Db 4 TKDLIWTLL 11

RESULT 5
Q6LEA8 PRELIMINARY; PRT; 17 AA.
ID Q6LEA8 PRELIMINARY; PRT; 17 AA.
AC Q6LEA8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson A.D., Ovsenek N., Tonissen K.F., Krieg P.A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L26396; AAA49911.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 50.0%; Score 24; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIWTM 8
Db 7 LIWTLL 11

RESULT 6
AAA49911 PRELIMINARY; PRT; 17 AA.
ID AAA49911 PRELIMINARY; PRT; 17 AA.
AC AAA49911;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN NCAM.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;

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OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX PubMed=14583598;  
 RA Squire T.L., Andrews M.T.;  
 RT "The Xenopus NCM promoter: Appropriate expression in response to  
 RT neural inducing signals and identification of a conserved sequence  
 RT element.";  
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; L26396; AAA49911.1; --  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 205 MW; AEBD9B5855262107 CRC64;  
 Query Match 50.0%; Score 24; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MIWTM 8  
 Db 7 LIWTL 11  
 RESULT 7  
 ID Q8W128 PRELIMINARY; PRT; 19 AA.  
 AC Q8W128;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Nitrate reductase (Fragment).  
 GN Name=NIA;  
 OS Scaevola procera.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC campanulids; Asterales; Goodeniaceae; Scaevola.  
 OX NCBI\_TaxID=184417;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22096038; PubMed=12099803;  
 RA Howard D.G., Baum D.A.;  
 RT "Phylogenetic utility of a nuclear intron from nitrate reductase for  
 RT the study of closely related plant species.";  
 RL Mol. Phylogenet. Evol. 21:525-528 (2002).  
 DR EMBL; AF460205; AAL66737.1; --  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR InterPro; IPR005066; Mo-co dimer.  
 DR Pfam; PF03404; Mo-co\_dimer; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 19 19  
 SQ SEQUENCE 19 AA; 2357 MW; 5C0582771535B26A CRC64;  
 Query Match 50.0%; Score 24; DB 2; Length 19;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 MIWTM 9  
 Db 6 LIWNL 11  
 RESULT 8  
 ID Q8R5G1 PRELIMINARY; PRT; 15 AA.  
 AC Q8R5G1;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Pancreatic triacylglycerol lipase (Fragment).  
 GN Name=PTL;  
 OS Spermophilus tridecemlineatus (thirteen-lined ground squirrel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scuriinae;  
 OC Spermophilus.

OX NCBI\_TaxID=43179;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX PubMed=14583598;  
 RA Squire T.L., Andrews M.T.;  
 RT "Pancreatic triacylglycerol lipase in a hibernating mammal. I. Novel  
 RT genomic organization.";  
 RL Physiol. Genomics (Online) 16:119-130 (2003).  
 DR EMBL; AY071823; AAL73074.1; --  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1570 MW; C6F85151A7050414 CRC64;  
 Query Match 47.9%; Score 23; DB 2; Length 15;  
 Best Local Similarity 33.3%; Pred. No. 2.1e+03;  
 Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LMIWTM 8  
 Db 2 LLVWSL 7  
 RESULT 9  
 ID Q8IVK5 PRELIMINARY; PRT; 17 AA.  
 AC Q8IVK5;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Steerin2 protein (Fragment).  
 GN Name=STEERIN2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Peeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,  
 RA Geysen J.J.G.H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ488206; CAD32559.1; --  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 2169 MW; 1F508A5824873F9E CRC64;  
 Query Match 47.9%; Score 23; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 2.3e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 SLMIW 6  
 Db 2 SYMLW 6  
 RESULT 10  
 ID Q9ESU5 PRELIMINARY; PRT; 10 AA.  
 AC Q9ESU5;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Fas death receptor (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C3H/He;  
 RX MEDLINE=20127858; PubMed=10660538;  
 RA Munsch D., Watanabe-Fukunaga R., Bourdon J.C., Nagata S., May E.,  
 RA Yonish-Rouach E., Reisdlorff P.;  
 RT "Human and mouse Fas (APO-1/CD95) death receptor genes each contain a  
 RT p53-responsive element that is activated by p53 mutants unable to

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RT induce apoptosis.";
RL J. Biol. Chem. 275:3867-3872(2000).
DR EMBL; AF282865; AAG02410.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1242 MW; 22145E32CDC37043 CRC64;

Query Match 43.8%; Score 21; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWTM 9
DB 2 LMIWAVL 8

RESULT 11
ID Q7S3Q9 PRELIMINARY; PRT; 17 AA.
AC Q7S3Q9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name-NCU04958.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]_TaxID=5141;
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysellis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Siller S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000407; EAA30170.1; -.
SQ SEQUENCE 17 AA; 2044 MW; 33C34BDEBAF0F3A2 CRC64;

Query Match 43.8%; Score 21; DB 2; Length 17;
Best Local Similarity 40.8%; Pred. No. 5.4e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIWT 7
DB 1 LMIWT 5

RESULT 12
ID Q69074 PRELIMINARY; PRT; 17 AA.
AC Q69074;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HSV-1 glycoprotein C (Fragment).
QS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10298;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089706; PubMed=3025606;
RA Homa F.L., Otal T.M., Glorioso J.C., Levine M.;
RT "Transcriptional control signals of a herpes simplex virus type 1 late
RT (gamma-2) gene lie within bases -34 to +124 relative to the 5'
RT terminus of the mRNA.";
RL Mol. Cell. Biol. 6:3652-3666(1986).
DR EMBL; M14128; AAA45784.1; -.
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1868 MW; B4ED3CE6ABAE92 CRC64;

Query Match 43.8%; Score 21; DB 2; Length 17;
Best Local Similarity 12.5%; Pred. No. 5.4e+03;
Matches 1; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIWTM 9
DB 9 AVWLMSLL 16

RESULT 13
ID DCM ACACA STANDARD; PRT; 19 AA.
AC P34039;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE S-adenosylmethionine decarboxylase alpha subunit (EC 4.1.1.50)
DE (AdoMetDC) (SamDC) (Fragment).
OS Acanthamoeba castellanii (Amoeba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]_TaxID=5755;
RP SEQUENCE, AND CHARACTERIZATION.
RX MEDLINE=94029912; PubMed=8216217;
RA Hugo E.R., Byers T.J.;
RT "S-adenosyl-L-methionine decarboxylase of Acanthamoeba castellanii
RT (Neff): purification and properties.";
RL Biochem. J. 295:203-209(1993).
CC -!- FUNCTION: S-adenosylmethionine decarboxylase is essential for the
CC biosynthesis of spermine and spermidine. The alpha subunit
CC contains the active site.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = (5-deoxy-5-
CC adenosyl)(3-aminopropyl) methylsulfonium salt + CO(2).
CC -!- COFACTOR: Pyruvoyl group.
CC -!- PATHWAY: Decarboxylation of S-adenosylmethionine provides the
CC aminopropyl moiety required for spermidine and spermine
CC biosynthesis from putrescine.
CC -!- SUBUNIT: Heterotetramer of two alpha and two beta chains.
CC -!- DEVELOPMENTAL STAGE: Expressed only during exponential growth.
CC -!- INDUCTION: Stimulated by putrescine. Inhibited by aromatic
CC diamidines berenil, pentamidine, propamidine, hydroxyethylamine,
CC by ethidium bromide and methylglyoxal.
CC -!- SIMILARITY: Belongs to the eukaryotic AdoMetDC family.
DR PIR; S38763; S38763.
DR InterPro; IPR001985; SAM decarbox.
DR Pfam; PF01536; SAM decarbox; 1.
DR PROSITE; PS01336; ADOMETDC; PARTIAL.
KW Decarboxylase; Direct protein sequencing; Lyase; Pyruvate;
KW Spermidine biosynthesis.
FT MOD_RES 1 1 Pyruvic acid (Ser).
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2153 MW; 88B18AD9B6142AEF CRC64;

Query Match 43.8%; Score 21; DB 1; Length 19;
Best Local Similarity 33.3%; Pred. No. 6e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIW 6

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Db 1 SSMFW 6

## RESULT 14

Q6LERS PRELIMINARY; PRT; 21 AA.  
AC Q6LERS;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome P4501IE1 (Fragment).  
GN Name=CYP2E1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89166510; PubMed=3233219;  
RA Umeno M., McBride W.O., Yang C.S., Gelboin H.V., Gonzalez F.J.;  
RT "Human ethanol-ineudible P4501IE1: complete gene sequence, promoter  
characterization chromosome mapping, and cDNA-directed expression.";  
RL Biochemistry 27:9006-9013(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92138659; PubMed=1778977;  
RA Hayashi S.;  
RT "Genetic polymorphisms in the 5'-flanking region change transcriptional  
regulation of the Human cytochrome P4501IE1 gene.";  
RL J. Biochem. 110:559-565(1991).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95122459; PubMed=7529759;  
RA Watanabe J., Hayashi S., Kawajiri K.;  
RT "Different regulation and expression of the human CYP2E1 gene due to  
the Real polymorphism in the 5'-flanking region.";  
RL J. Biochem. 116:321-326(1994).  
DR EMBL; D10014; BAA00902.1; -;  
FT NON TER 21  
SQ SEQUENCE 21 AA; 2175 MW; 60A85A2B034F339B CRC64;

Query Match 43.8%; Score 21; DB 2; Length 21;  
Best Local Similarity 40.0%; Pred. No. 6.6e+03;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLMIW 6  
Db 9 ALLVW 13

## RESULT 15

BAA00902 PRELIMINARY; PRT; 21 AA.  
AC BAA00902;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome P4501IE1 (Fragment).  
GN CYP2E1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92138659; PubMed=1778977;  
RA Hayashi S.;  
RT "Genetic polymorphisms in the 5'-flanking region change transcriptional  
regulation of the Human cytochrome P4501IE1 gene.";  
RL J. Biochem. 110:559-565(1991).  
RN [2]  
RP SEQUENCE FROM N.A.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 5.55319 Seconds  
(without alignments)  
155.938 Million cell updates/sec

Title: US-09-831-253F-5

Perfect score: 48

Sequence: 1 TSLMIWTMM 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	56.2	16	2 PH1638	Ig H chain V-D-J r
2	25	52.1	7	2 PX0008	glucuronosyltransf
3	25	52.1	16	2 PH1637	Ig H chain V-D-J r
4	24	50.0	13	2 PH1636	Ig H chain V-D-J r
5	23	47.9	13	2 PH1620	Ig H chain V-D-J r
6	23	47.9	14	2 PH1625	Ig H chain V-D-J r
7	23	47.9	14	2 PH1627	Ig H chain V-D-J r
8	23	47.9	15	2 PH1613	Ig H chain V-D-J r
9	23	47.9	15	2 PH1612	Ig H chain V-D-J r
10	23	47.9	17	2 PH1630	Ig H chain V-D-J r
11	23	47.9	20	2 PH1358	Ig heavy chain DJ
12	22	45.8	14	2 A35105	hypothetical prote
13	21	43.8	14	2 PH1327	Ig heavy chain DJ
14	21	43.8	15	2 PH1590	Ig H chain V-D-J r
15	21	43.8	20	2 PLO192	Ig lambda 2 chain
16	21	43.8	20	2 S38763	S-adenosyl-L-methi
17	20	41.7	14	2 PH1626	Ig H chain V-D-J r
18	20	41.7	22	2 I58038	MHC class I transp
19	20	41.7	22	2 A64548	hypothetical prote
20	19	39.6	12	2 I58273	thyroglobulin - ra
21	19	39.6	15	2 PH0782	T-cell receptor al
22	19	39.6	17	2 PH1331	Ig heavy chain DJ
23	19	39.6	18	2 I59649	human leukocyte an
24	19	39.6	19	2 A28702	cytochrome P450-C-
25	19	39.6	19	2 I45957	protein kinase (EC
26	19	39.6	19	2 I53673	amylol protein -
27	19	39.6	19	2 PH1352	Ig heavy chain DJ
28	19	39.6	19	2 PH1315	Ig heavy chain DJ
29	19	39.6	19	2 I40063	shikimate 5-dehydr

30	19	39.6	20	2 A44927	major outer membra
31	19	39.6	20	2 S77992	cytochrome-c oxida
32	19	39.6	21	2 S62893	cold-inducible pro
33	19	39.6	22	2 PT0303	Ig heavy chain CDR
34	18	37.5	7	2 S09652	hypothetical prote
35	18	37.5	7	2 PH1602	Ig H chain V-D-J r
36	18	37.5	13	2 I51905	collecting duct wa
37	18	37.5	13	2 I54984	aeg-46.5 protein -
38	18	37.5	14	2 PH1594	Ig H chain V-D-J r
39	18	37.5	14	2 A47421	leukotriene B-4 12
40	18	37.5	17	2 H49048	T-cell receptor be
41	18	37.5	18	2 PT0239	Ig heavy chain CDR
42	18	37.5	19	2 I49422	L-lactate dehydrog
43	18	37.5	19	2 PQ0678	photosystem I 8.0K
44	18	37.5	20	2 S09735	photosystem I prot
45	18	37.5	20	2 T46626	hypothetical prote

ALIGNMENTS

RESULT 1

PH1638

Ig H chain V-D-J region (clone B-less 228) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C;Accession: PH1638

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1638

A;Molecule type: DNA

A;Residues: 1-16 <LSV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 56.2%; Score 27; DB 2; Length 16;  
Best Local Similarity 57.1%; Pred. No. 58;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIWT 7

Db 10 TTSMLWT 16

RESULT 2

PX0008

glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)

N;Alternate names: UDP-glucuronyltransferase

C;Species: Rattus norvegicus (Norway rat)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 07-Feb-1997

C;Accession: PX0008

R;Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A;Title: Purification and properties of a form of UDP-glucuronyltransferase from liver

A;Reference number: PX0008; MUID:89197852; PMID:3149280

A;Accession: PX0008

A;Molecule type: protein

A;Residues: 1-7 <YOK>

C;Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 52.1%; Score 25; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIW 6

Db 1 TKLLVW 6

RESULT 3

PH1637

RESULT 4  
 PH1636  
 Ig H chain V-D-J region (clone B-less 224) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1637  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A:Reference number: PH1580; MUID:93301609; PMID:8315387  
 A:Accession: PH1637  
 A:Molecule type: DNA  
 A:Residues: 1-16 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 52.1%; Score 25; DB 2; Length 16;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 TSLMIWT 7  
 Db 10 TLTLMLWT 16  
 |||

RESULT 4  
 PH1636  
 Ig H chain V-D-J region (clone B-less 224) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1636  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A:Reference number: PH1580; MUID:93301609; PMID:8315387  
 A:Accession: PH1636  
 A:Molecule type: DNA  
 A:Residues: 1-13 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 50.0%; Score 24; DB 2; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MIWT 7  
 Db 10 MVWT 13  
 |||

RESULT 5  
 PH1620  
 Ig H chain V-D-J region (clone B-less 40) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1620  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A:Reference number: PH1580; MUID:93301609; PMID:8315387  
 A:Accession: PH1620  
 A:Molecule type: DNA  
 A:Residues: 1-13 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 2.5e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MIWT 7  
 Db 10 MLWT 13  
 |||

RESULT 6  
 PH1625  
 Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1625  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A:Reference number: PH1580; MUID:93301609; PMID:8315387  
 A:Accession: PH1625  
 A:Molecule type: DNA  
 A:Residues: 1-14 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 2.7e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MIWT 7  
 Db 11 MLWT 14  
 |||

RESULT 7  
 PH1627  
 Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1627  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A:Reference number: PH1580; MUID:93301609; PMID:8315387  
 A:Accession: PH1627  
 A:Molecule type: DNA  
 A:Residues: 1-14 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 2.7e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MIWT 7  
 Db 11 MLWT 14  
 |||

RESULT 8  
 PH1613  
 Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1613  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A:Reference number: PH1580; MUID:93301609; PMID:8315387  
 A:Accession: PH1613  
 A:Molecule type: DNA  
 A:Residues: 1-15 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 2.9e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 MIWT 7  
 Db 12 MLWT 15  
 |||



Db

8 TTTTWT 14

## RESULT 9

PH1612  
 Ig H chain V-D-J region (wild-type clone 344) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C;Accession: PH1612  
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A;Reference number: PH1580; MUID:93301609; PMID:8315387  
 A;Accession: PH1612  
 A;Molecule type: DNA  
 A;Residues: 1-15 <LEV>  
 A;Experimental source: bone marrow pre-B lymphocyte  
 C;Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 2.9e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIWT 7  
 | : ||  
 Db 12 MLWT 15

## RESULT 10

PH1630  
 Ig H chain V-D-J region (clone B-less 156) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C;Accession: PH1630  
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A;Reference number: PH1580; MUID:93301609; PMID:8315387  
 A;Accession: PH1630  
 A;Molecule type: DNA  
 A;Residues: 1-17 <LEV>  
 A;Experimental source: bone marrow pre-B lymphocyte  
 C;Keywords: immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 3.3e+02;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 MIWT 7  
 | : ||  
 Db 14 MLWT 17

## RESULT 11

PH1358  
 Ig heavy chain DJ region (clone C178-117) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1358  
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A;Reference number: PH1302; MUID:93094761; PMID:1460419  
 A;Accession: PH1358  
 A;Molecule type: DNA  
 A;Residues: 1-20 <WAS>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 47.9%; Score 23; DB 2; Length 20;  
 Best Local Similarity 42.9%; Pred. No. 3.9e+02;  
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLMIWT 7  
 | : ||

## RESULT 12

A35105  
 hypothetical protein - Neurospora crassa mitochondrion (fragment)  
 C;Species: mitochondrion Neurospora crassa  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 07-Dec-1999  
 C;Accession: A35105  
 R;Saville, B.J.; Collins, R.A.  
 Cell 61, 685-696, 1990  
 A;Title: A site-specific self-cleavage reaction performed by a novel RNA in neurospora  
 A;Reference number: A35105; MUID:90263093; PMID:2160856  
 A;Accession: A35105  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-14 <SAV>  
 C;Genetics:

A;Genome: mitochondrion  
 A;Genetic code: SGC3  
 C;Keywords: mitochondrion

Query Match 45.8%; Score 22; DB 2; Length 14;  
 Best Local Similarity 40.0%; Pred. No. 4.1e+02;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWTMM 9  
 : || :  
 Db 4 LWTLL 8

## RESULT 13

PH1327  
 Ig heavy chain DJ region (clone C113-105) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
 C;Accession: PH1327  
 R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
 J. Exp. Med. 176, 1577-1581, 1992  
 A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
 A;Reference number: PH1302; MUID:93094761; PMID:1460419  
 A;Accession: PH1327  
 A;Molecule type: DNA  
 A;Residues: 1-14 <WAS>  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 21; DB 2; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 6.3e+02;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 WTMM 9  
 | : ||  
 Db 2 WVTMM 5

## RESULT 14

PH1590  
 Ig H chain V-D-J region (wild-type clone 141) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C;Accession: PH1590  
 R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic  
 A;Reference number: PH1580; MUID:93301609; PMID:8315387  
 A;Accession: PH1590  
 A;Molecule type: DNA  
 A;Residues: 1-15 <LEV>  
 A;Experimental source: bone marrow pre-B lymphocyte  
 C;Keywords: immunoglobulin

Query Match 43.8%; Score 21; DB 2; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 6.8e+02;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LMIWT 7  
| : ||  
Db 11 LYLWT 15

## RESULT 15

PL0192  
Ig lambda 2 chain - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 07-May-1999  
C;Accession: PL0192  
R;Alonso, A.; Chang, L.A.; Murialdo, H.  
Mol. Immunol. 27, 115-127, 1990  
A;Title: Analysis of the expression of murine lambda genes transfected into immunocompetent cells  
A;Reference number: PL0192; MUID:90205873; PMID:2108323  
A;Accession: PL0192  
A;Molecule type: DNA  
A;Residues: 1-20 <ALO>  
C;Genetics:  
A;Introns: 16/2  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin

Query Match 43.8%; Score 21; DB 2; Length 20;  
Best Local Similarity 50.0%; Pred. NO. 9e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 MIWTMM 9  
| : ||  
Db 1 MAWTSL 6

Search completed: November 14, 2004, 12:03:12  
Job time : 6.55319 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:56:07 ; Search time 100 Seconds  
(without alignments)  
86.306 Million cell updates/sec

Title: US-09-831-253F-4  
Perfect score: 75  
Sequence: 1 SNPSAFQVDIIVDI 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 7754

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	37.3	9	2 Q7RA82	Q7ra82 plasmodium
2	26	34.7	12	2 Q9S550	Q9s550 streptococ
3	25	33.3	10	2 Q76MW5	Q76mw5 eurypharynx
4	25	33.3	10	2 BAB87140	Bab87140 euryphary
5	25	33.3	11	2 Q7M154	Q7m154 bacillus th
6	25	33.3	12	2 Q7XB05	Q7xb05 zea mays (m
7	25	33.3	13	2 Q7X761	Q7x761 zea mays (m
8	25	33.3	13	2 Q79A22	Q79a22 borrelia bu
9	25	33.3	14	2 P81801	P81801 streptomyc
10	24	32.0	8	2 Q91U19	Q91u19 influenza a
11	24	32.0	8	2 Q91U21	Q91u21 influenza a
12	23	30.7	10	2 Q76MK9	Q76mk9 eurypharynx
13	23	30.7	10	2 BAB87148	Bab87148 euryphary
14	23	30.7	10	2 BAB87156	Bab87156 euryphary
15	23	30.7	10	2 BAB87164	Bab87164 euryphary
16	23	30.7	14	2 Q9RS18	Q9rs18 vibrio algi
17	23	30.7	15	2 Q9F8B2	Q9f8b2 silene aega
18	22	29.3	8	1 ALL3_CVDPO	P82154 cydia pomon
19	22	29.3	11	2 P83128	P83128 bos indicus
20	22	29.3	12	1 VESP_VESMA	Q7m3t3 vespa manda
21	22	29.3	14	2 Q7S366	Q7s366 neurospora
22	22	29.3	15	1 ALLS_MANSE	P42559 manduca sex
23	22	29.3	15	1 IRBP_CRISP	P12865 cricetidae
24	22	29.3	15	2 Q9TWE9	Q9twe9 galliera me
25	21	28.0	7	1 ALL5_CARMA	P81808 carcinus ma
26	21	28.0	13	2 Q7M014	Q7m014 bacillus ce
27	21	28.0	14	1 CATA_ACICA	P83715 acinetobact
28	21	28.0	15	1 LEC3_AXIPO	P28588 axinella po
29	21	28.0	15	2 Q7M4Y2	Q7m4y2 fusarium sp
30	21	28.0	15	2 Q9UCC4	Q9ucc4 homo sapien
31	20	26.7	9	2 Q7M2M7	Q7m2m7 bos taurus

32 20 26.7 9 2 Q6EKR5  
33 20 26.7 10 2 Q84140  
34 20 26.7 11 2 P83168  
35 20 26.7 12 2 Q89243  
36 20 26.7 14 2 Q71GT6  
37 20 26.7 14 2 Q71GW6  
38 20 26.7 14 2 Q71GZ0  
39 20 26.7 14 2 Q71H06  
40 20 26.7 14 2 Q71H14  
41 20 26.7 14 2 Q71H34  
42 20 26.7 14 2 AAQ07615  
43 20 26.7 14 2 AAQ07635  
44 20 26.7 14 2 AAQ07643  
45 20 26.7 14 2 AAQ07659

## ALIGNMENTS

RESULT 1  
Q7RA82 PRELIMINARY; PRT; 9 AA.  
AC Q7RA82;  
DT 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DE Hypothetical protein (Fragment)...  
GN Name=PY06620;  
OS Plasmodium yoelii yoelii.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=73239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=17XNL;  
RX PubMed=12368865;  
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;  
RT "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii.";  
RL Nature 419:512-519(2002).  
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.  
CC EMBL: AABL01002263; EAA18865.1; -.  
DR Hypothetical protein.  
KW NON TER  
SQ SEQUENCE 9 AA; 1001 MW; 4687A5AB476455B7 CRC64;

Query Match 37.3%; Score 28; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred.No.1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPS 5  
Db 3 SNPS 7

RESULT 2  
Q9S550 PRELIMINARY; PRT; 12 AA.  
ID Q9S550  
AC Q9S550;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
DexB (Fragment).

GN Name=dexB;  
 OS Streptococcus pneumoniae.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1313;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D39;  
 RX MEDLINE=99214122; PubMed=10198036;  
 RA Iannelli F., Pearce B.J., Pozzi G.;  
 RT "The type 2 capsule locus of Streptococcus pneumoniae.";  
 RL J. Bacteriol. 181:2652-2654(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D39;  
 RA Pearce B.J., Iannelli F., Pozzi G.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF026471; AAD10169.1; -;  
 FT NON TER 1  
 SQ SEQUENCE 12 AA; 1405 MW; 90A979D2B2B9CDDA CRC64;

Query Match 34.7%; Score 26; DB 2; Length 12;  
 Best Local Similarity 40.0%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFOVDII 12

Db ||| |||

3 PWDAPCVELL 12

## RESULT 3

Q76MMS ID Q76MMS PRELIMINARY; PRT; 10 AA.

AC Q76MMS;

DT 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE NADH dehydrogenase subunit 2 (Fragment).

GN Name=ND2;

OS Eurypharynx pelecyanoides (pelican eel).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;

OC Eurypharyngidae; Eurypharynx.

OX NCBI\_TaxID=55117;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=22967687; PubMed=12949142;  
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
 RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";  
 RL Mol. Biol. Evol. 20:1917-1924(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB046477; BAB87140.1; -;  
 DR GO; GO:0005739; Mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPVSAPQV 9

Db ||| |||

2 NPVVMFLV 9

## RESULT 4

BAB87140

ID BAB87140 PRELIMINARY; PRT; 10 AA.  
 AC BAB87140;  
 DT 02-MAR-2004 (TRENBLrel. 27, Created)  
 DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)  
 DE NADH dehydrogenase subunit 2 (Fragment).  
 GN ND2.  
 OS Eurypharynx pelecyanoides (pelican eel).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
 OC Eurypharyngidae; Eurypharynx.  
 OX NCBI\_TaxID=55117;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A;  
 RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
 RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Eels.";  
 RL Mol. Biol. Evol. 20:1917-1924(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A;  
 RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB046477; BAB87140.1; -;  
 KW Mitochondrion.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPVSAPQV 9

Db ||| |||

2 NPVVMFLV 9

## RESULT 5

Q7M154

ID Q7M154 PRELIMINARY; PRT; 11 AA.

AC Q7M154;

DT 01-MAR-2004 (TRENBLrel. 26, Created)

DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Parasporal crystal protein, wax moth-specific (fragment).

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1428;

RN [1]  
 RP SEQUENCE.

RA Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,  
 Stepanov V.M.;  
 RT "Bacillus thuringiensis ssp. galleriae simultaneously produces two  
 RT delta-endotoxins differing strongly in primary structure and  
 RT entomocidal activity.";  
 RL FEBS Lett. 232:249-251(1988).  
 DR PIR; S00616; S00616.  
 FT NON TER 1  
 FT NON TER 11  
 SQ SEQUENCE 11 AA; 1237 MW; C6FF9BD64764444D CRC64;

Query Match 33.3%; Score 25; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5

Db :|||

5 NNPYS 9

## RESULT 6

Q7XB05  
ID Q7XB05 PRELIMINARY; PRT; 12 AA.  
AC Q7XB05;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Phytoene synthase 2 (Fragment).  
GN Name=psy2;  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Y-14;  
RX MEDLINE=22779048; PubMed=12897253;  
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;  
RT "Contrasting effects of selection on sequence diversity and linkage  
RT disequilibrium at two phytoene synthase loci.";  
RL Plant Cell 15:1795-1806(2003).  
DR EMBL; AY300568; AAP55307.1; --  
FT NON\_TER 1  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1335 MW; 9B1E0AA00869C325 CRC64;  
Query Match 33.3%; Score 25; DB 2; Length 12;  
Best Local Similarity 54.5%; Pred. No. 1.e+03;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11  
| : | | | |  
DB 1 SDTVSKPPVDI 11

RESULT 7  
Q7X761  
ID Q7X761 PRELIMINARY; PRT; 13 AA.  
AC Q7X761;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Phytoene synthase 2 (Fragment).  
GN Name=psy2;  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W-17, and W-50;  
RX MEDLINE=22779048; PubMed=12897253;  
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;  
RT "Contrasting effects of selection on sequence diversity and linkage  
RT disequilibrium at two phytoene synthase loci.";  
RL Plant Cell 15:1795-1806(2003).  
DR EMBL; AY300592; AAP55331.1; --  
DR EMBL; AY300599; AAP55338.1; --  
FT NON\_TER 1  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1449 MW; 9B1E0AA05615C325 CRC64;  
Query Match 33.3%; Score 25; DB 2; Length 13;  
Best Local Similarity 54.5%; Pred. No. 2.e+03;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11  
| : | | | |  
DB 2 SDTVSKPPVDI 12

RESULT 8

Q79A22  
ID Q79A22 PRELIMINARY; PRT; 13 AA.  
AC Q79A22;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE MoxR protein (Fragment).  
GN Name=moxR;  
OS Borrelia burgdorferi (Lyme disease spirochete).  
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
OX NCBI\_TaxID=139;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=212;  
RX Old I.G.;  
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; X95668; CAA64970.1; --  
FT NON\_TER 13  
FT NON\_TER 13  
SQ SEQUENCE 13 AA; 1484 MW; C7C2DF4CFD83A046 CRC64;  
Query Match 33.3%; Score 25; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.e+03;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 SAFQVDIIVD 14  
| : | : | : | :  
DB 3 SGFQIDSEVE 12

RESULT 9  
P81801  
ID P81801 PRELIMINARY; PRT; 14 AA.  
AC P81801;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Puromycin-hydrolyzing enzyme (EC 3.-.-.-) (Fragment).  
OS Streptomyces morookaensis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1970;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=JCM4673 / KCC S-0673;  
RX PubMed=9538199;  
RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;  
RT "Purification and characterization of a puromycin-hydrolyzing enzyme  
RT from blastocidin S-producing Streptomyces morookaensis.";  
RL J. Biochem. 123:247-252(1998).  
RN [2]  
RP CHARACTERIZATION, AND FUNCTION.  
RA Nishimura M., Matsuo H., Sugiyama M.;  
RT "Blastocidin S-producing Streptomyces morookaensis possesses an enzyme  
RT activity with hydrolyzes puromycin.";  
RL FEMS Microbiol. Lett. 132:95-100(1995).  
CC -1- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF  
CC THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-  
CC TYROSINE MOIETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL  
CC TEMPERATURE IS 45 DEGREES CELSIUS.  
CC -1- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.  
CC -1- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC  
CC ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND  
CC N-ETHYLMALIMIDE. PARTIALLY INHIBITED BY COBALT ION.  
CC -1- SUBUNIT: MONOMER.  
CC -1- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.  
DR GO; GO:0004177; F:aminopeptidase activity; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
KW Amino-peptidase; Hydrolase.  
FT NON\_TER 14  
FT NON\_TER 14  
SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45BF3D8 CRC64;  
Query Match 33.3%; Score 25; DB 2; Length 14;  
Best Local Similarity 55.6%; Pred. No. 2.1e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PYSAFQVDI 11  
DB 5 PYGAWSQPI 13

## RESULT 10

Q91U19 PRELIMINARY; PRT; 8 AA.  
AC Q91U19;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Nuclear export protein NS2 (Fragment).  
OS Influenza A virus (A/Hong Kong/503/97(H5N1)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenzavirus A; H5N1 subtype.  
OX NCBI\_TaxID=155224;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/Hong Kong/503/97;  
RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Kraus S.L., Guan Y.,  
RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF256192; AAK49326.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 869 MW; D9D9D5A5A2D1A455 CRC64;

Query Match 32.0%; Score 24; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. NO. 1.8e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAFQ 8  
DB 1 SNTVSSFQ 8

## RESULT 11

Q91U21 PRELIMINARY; PRT; 8 AA.  
AC Q91U21;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Nuclear export protein NS2 (Fragment).  
OS Influenza A virus (A/Hong Kong/491/97(H5N1)).  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenzavirus A; H5N1 subtype.  
OX NCBI\_TaxID=155223;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A/Hong Kong/491/97;  
RA Shaw M.W., Cooper L.A., Xu X., Thompson W.W., Kraus S.L., Guan Y.,  
RA Zhou N.N., Klimov A., Cox N.J., Webster R.G., Lim W., Shortridge K.F.,  
RA Subbarao K.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF256191; AAK49324.1; -.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 869 MW; D9D9D5A5A2D1A455 CRC64;

Query Match 32.0%; Score 24; DB 2; Length 8;  
Best Local Similarity 62.5%; Pred. NO. 1.8e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAFQ 8  
DB 1 SNTVSSFQ 8

## RESULT 12

Q76MK9 PRELIMINARY; PRT; 10 AA.  
AC Q76MK9;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE NADH dehydrogenase subunit 2 (Fragment).  
GN Name=ND2;  
OS Eurypharynx pelecanoides (pelican eel).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
OC Eurypharyngidae; Eurypharynx.  
OX NCBI\_TaxID=55117;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22967687; PubMed=12949142;  
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels.";  
RL Mol. Biol. Evol. 20:1917-1924(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB046485; BAB87156.1; -.  
DR EMBL; AB046489; BAB87164.1; -.  
DR EMBL; AB046481; BAB87148.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

Query Match 30.7%; Score 23; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. NO. 3.5e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAF 7  
DB 2 NPYVMF 7

## RESULT 13

BAB87148 PRELIMINARY; PRT; 10 AA.  
AC BAB87148;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE NADH dehydrogenase subunit 2 (Fragment).  
GN ND2.  
OS Eurypharynx pelecanoides (pelican eel).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
OC Eurypharyngidae; Eurypharynx.  
OX NCBI\_TaxID=55117;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B;  
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-scale gene rearrangements originated within the Eels.";  
RL Mol. Biol. Evol. 20:1917-1924(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB046481; BAB87148.1; -.  
KW Mitochondrion.  
FT NON\_TER 10 10

SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

Query Match 30.7%; Score 23; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.5e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NPYSAP 7  
Db 2 NPYVMF 7

## RESULT 14

BAB87156 ID BAB87156 PRELIMINARY; PRT; 10 AA.  
AC BAB87156;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE NADH dehydrogenase subunit 2 (Fragment).  
GN ND2.  
OS Eurypharynx pelecanoides (pelican eel).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
OC Eurypharyngidae; Eurypharynx.  
OX NCBI\_TaxID=55117;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C;  
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
RT "Evolution of the Deep-Sea Gulper Bel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Bels.";  
RL Mol. Biol. Evol. 20:1917-1924(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C;  
RA Inoue J.G., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB046485; BAB87156.1;  
KW Mitochondrion.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

Query Match 30.7%; Score 23; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.5e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NPYSAP 7  
Db 2 NPYVMF 7

## RESULT 15

BAB87164 ID BAB87164 PRELIMINARY; PRT; 10 AA.  
AC BAB87164;  
DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE NADH dehydrogenase subunit 2 (Fragment).  
GN ND2.  
OS Eurypharynx pelecanoides (pelican eel).  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;  
OC Eurypharyngidae; Eurypharynx.  
OX NCBI\_TaxID=55117;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D;  
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;  
RT "Evolution of the Deep-Sea Gulper Bel Mitochondrial Genomes: Large-Scale Gene Rearrangements Originated Within the Bels.";  
RL

RL Mol. Biol. Evol. 20:1917-1924(2003).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D;  
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB046489; BAB87164.1;  
KW Mitochondrion.  
FT NON TER 10 10  
SQ SEQUENCE 10 AA; 1293 MW; 356FAE29C682DB47 CRC64;

Query Match 30.7%; Score 23; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.5e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NPYSAP 7  
Db 2 NPYVMF 7

Search completed: November 14, 2004, 13:16:22  
Job time : 101 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:03:52 ; Search time 18.3333 Seconds  
(without alignments)  
78.723 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPYSAFQVDIIIVDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	33.3	11	2 S00616	parasporal crystal
2	23	30.7	13	2 A54326	glandular kallikrein
3	23	30.7	14	2 B44854	L-2,4-diaminobutyrate
4	22	29.3	12	2 A61360	vespakinin M - hor
5	22	29.3	15	2 PS0185	27K protein A 3.4/
6	22	29.3	15	2 A61612	allatostatin - tob
7	22	29.3	15	2 G24417	interphotoreceptor
8	21	28.0	11	2 PT0229	Ig heavy chain CDR
9	21	28.0	12	2 S36899	ribosomal protein
10	21	28.0	13	2 PC2369	unidentified BSK p
11	21	28.0	15	2 PA0061	protein QF200039 -
12	21	28.0	15	2 S29174	D-galactose-binding
13	20	26.7	9	2 S10784	enamelin i - bovin
14	20	26.7	14	2 A59018	MUC1 enhancer bind
15	20	26.7	15	2 S08209	hypothetical prote
16	20	26.7	15	2 PQ0778	NADH2 dehydrogenas
17	19	25.3	9	2 S36898	ribosomal protein
18	19	25.3	11	2 A40795	glycoprotein H-a -
19	19	25.3	13	2 S65612	tubulin alpha-chain
20	19	25.3	13	2 G22565	R-phycocerythrin ga
21	19	25.3	13	2 PQ0700	unidentified 6.3/4
22	19	25.3	14	2 A28018	very late antigen-
23	19	25.3	14	2 S07768	soluble hydrogenas
24	18	24.0	8	2 D47393	neuropeptide calla
25	18	24.0	11	2 PT0250	Ig heavy chain CRD
26	18	24.0	12	2 S70344	amine oxidase (cop
27	18	24.0	13	2 B20907	Ig kappa-1 chain J
28	18	24.0	14	2 S29209	avenin alpha-2 - o
29	18	24.0	14	2 T46634	acyl carrier prote

30	18	24.0	14	2 B56884	Pax-QNR, long form
31	18	24.0	15	2 PH1365	Ig heavy chain DJ
32	18	24.0	15	2 S62641	porphobilinogen sy
33	18	24.0	15	2 PT0090	alpha-glucosidase
34	18	24.0	15	4 I38335	hypothetical TEL/M
35	17	22.7	8	2 I49404	prealbumin - weste
36	17	22.7	9	2 PQ0914	MHC class I histoc
37	17	22.7	10	2 PA0050	protein QA100052 -
38	17	22.7	10	2 C39111	Ig heavy chain C x
39	17	22.7	10	2 B33710	ornithine decarbox
40	17	22.7	12	2 S63123	proton-translocati
41	17	22.7	12	2 PH0771	T-cell receptor be
42	17	22.7	12	2 I40663	bma protein - Clos
43	17	22.7	13	2 S47361	T-cell antigen rec
44	17	22.7	14	2 S21247	H+-transporting tw
45	17	22.7	14	2 PS0371	hypothetical prote

ALIGNMENTS

RESULT 1

S00616

parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleria N; Alternate names: delta-endotoxin; parasporal crystal protein positive chain C; Species: Bacillus thuringiensis C; Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004 C; Accession: S00616 R; Chestukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M. FEBS Lett. 232, 249-251, 1988 A; Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotoxins A; Reference number: S00615 A; Accession: S00616 A; Molecule type: protein A; Residues: 1-11 <CHE> A; Cross-references: UNIPROT:Q7M154 C; Comment: This toxin is effective against the larvae of Galleria mellonella (greater wax moth); Superfamily: parasporal crystal protein C; Keywords: delta-endotoxin

Query Match 33.3%; Score 25; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	SNPYS	5
DB	5	NNPYS	9

RESULT 2

A54326

glandular kallikrein-1 - human (fragment) C; Species: Homo sapiens (man) C; Date: 29-Aug-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995 C; Accession: A54326 R; Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J. Mol. Cell. Endocrinol. 76, 181-190, 1991 A; Title: Identification and androgen-regulated expression of two major human glandular A; Reference number: A54326; MUID:92324494; PMID:1726490 A; Accession: A54326 A; Status: preliminary; not compared with conceptual translation A; Residues: 1-13 <RIE> A; Experimental source: prostate A; Note: sequence extracted from NCBI backbone (NCBI:P108060)

Query Match 30.7%; Score 23; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 6.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	SNPYS	5
DB	2	SHPYS	6

RESULT 3  
B44854  
L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-) - *Vibrio alginolyticus* (fragment)  
C:Species: *Vibrio alginolyticus*  
C:Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: B44854; B41817  
R:Tamamoto, S.; Tsunaki, Y.; Tougo, K.; Shinoda, S.  
J. Gen. Microbiol. 138, 1461-1465, 1992  
A:Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from *V. alginolyticus*  
A:Reference number: A44854; MUID:92381494; PMID:1512577  
A:Accession: B44854  
A:Molecule type: protein  
A:Residues: 1-14 <YAM>  
A:Cross-references: UNIPROT:Q9R518  
A>Note: sequence extracted from NCBI backbone (NCBIP:112332)  
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 30.7%; Score 23; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 7.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAQFVD 10  
DB 2 TAFEVD 7

RESULT 4  
A61360  
vespakinin M - hornet (*Vespa mandarinia*)  
C:Species: *Vespa mandarinia*  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
C:Accession: A61360  
R:Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.  
Chem. Pharm. Bull. 24, 2896-2897, 1976  
A:Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the venom of *Vespa mandarinia*  
A:Reference number: A61360; MUID:77114342; PMID:1017116  
A:Accession: A61360  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-12 <KIS>  
A:Cross-references: UNIPROT:Q7M3T3  
A:Superfamily: unassigned animal peptides  
C:Keywords: hydroxyproline; venom  
F:4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 29.3%; Score 22; DB 2; Length 12;  
Best Local Similarity 42.9%; Pred. No. 9.4e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10  
DB 6 FSPFRID 12

RESULT 5  
PS0185  
27K protein A 3.4/5 - rice (fragment)  
C:Species: *Oryza sativa* (rice)  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 24-Feb-1995  
C:Accession: PS0185  
R:Kamo, M.; Tsugita, A.  
submitted to JIPID, June 1991  
A:Reference number: PS0184  
A:Accession: PS0185  
A:Molecule type: protein  
A:Residues: 1-15 <KAM>

Query Match 29.3%; Score 22; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 QVDIIVDI 15  
DB 1 QXEYIVDV 8

RESULT 6  
A61612  
allatostatin - tobacco hornworm  
C:Species: *Manduca sexta* (tobacco hornworm)  
C:Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: A61612  
R:Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney, R.  
Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991  
A:Title: Identification of an allatostatin from the tobacco hornworm *Manduca sexta*.  
A:Reference number: A61612; MUID:92052112; PMID:1946359  
A:Accession: A61612  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <KRA>  
A:Cross-references: UNIPROT:P42559  
A:Keywords: neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 29.3%; Score 22; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAP 7  
DB 10 NPISCF 15

RESULT 7  
G24417  
interphotoreceptor retinoid-binding protein - hamster (fragment)  
N:Alternate names: interstitial retinol-binding protein  
C:Species: *Cricetinae* gen. sp. (hamster)  
C:Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 09-Jul-2004  
C:Accession: G24417  
R:Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B.  
FEBS Lett. 205, 309-312, 1986  
A:Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10 different species  
A:Reference number: A91365; MUID:86301171; PMID:3743780  
A:Accession: G24417  
A:Molecule type: protein  
A:Residues: 1-15 <FON>  
A:Cross-references: UNIPROT:P12665

Query Match 29.3%; Score 22; DB 2; Length 15;  
Best Local Similarity 33.3%; Pred. No. 1.2e+03;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 FQVDIIVDI 15  
DB 7 FQPSIVLDM 15

RESULT 8  
PT0229  
Ig heavy chain CDR3 region (clone 1-115) - human (fragment)  
C:Species: *Homo sapiens* (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0229  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0229  
A:Molecule type: DNA  
A:Residues: 1-11 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.0%; Score 21; DB 2; Length 11;  
Best Local Similarity 38.5%; Pred. No. 1.3e+03;  
Matches 5; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 2 NPYSAFQVDIIIVD 14  
|||  
Db 2 NPY-----YDILTE 10  
|||

## RESULT 9

S36899  
ribosomal protein S6 - Mycobacterium bovis (fragment)  
C;Species: Mycobacterium bovis  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
C;Accession: S36899  
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
FEBS Lett. 331, 9-14, 1993  
A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobacterium bovis  
A;Reference number: S36887; MUID:94009653; PMID:8405418  
A;Accession: S36899  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-12 <OHA>  
C;Keywords: protein biosynthesis; ribosome

Query Match 28.0%; Score 21; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10  
|||  
Db 3 PYEIMVVD 10  
|||

## RESULT 10

PC2369  
unidentified 85K protein [imported] - Bacillus cereus (strain ts-4) (fragment)  
C;Species: Bacillus cereus  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: PC2369  
R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatanoto, S.  
BioSci. Biotechnol. Biochem. 59, 231-235, 1995  
A;Title: Identification of DNA-binding proteins changed after induction of sporulation in Bacillus cereus  
A;Reference number: PC2369; MUID:95218265; PMID:7766022  
A;Accession: PC2369  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-13 <MAS>  
A;Cross-references: UNIPROT:Q7MOL4

Query Match 28.0%; Score 21; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAF 7  
|||  
Db 8 NPWAKF 13  
|||

## RESULT 11

PA0061  
protein OF200039 - fungus (Fusarium sporotrichioides) (fragment)  
C;Species: Fusarium sporotrichioides  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: PA0061  
R;Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Taugita, A.  
submitted to JIPID, October 1994  
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides  
A;Reference number: PA0051  
A;Accession: PA0061  
A;Molecule type: protein  
A;Residues: 1-15 <CHO>  
A;Cross-references: UNIPROT:Q7MAY2

Query Match 28.0%; Score 21; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.8e+03;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 SAFQVDIIIVD 14  
:| || |:  
Db 3 TAAQVAIVKD 12  
|||

## RESULT 12

S29174  
D-galactose-binding lectin III - Axinella polypoides (fragment)  
C;Species: Axinella polypoides  
C;Date: 19-Mar-1997 #sequence\_revision 14-Nov-1997 #text\_change 09-Jul-2004  
C;Accession: S29174  
R;Buck, F.; Luth, C.; Strupat, K.; Bretting, H.  
Biochim. Biophys. Acta 1159, 1-8, 1992  
A;Title: Comparative investigations on the amino-acid sequences of different isolectins  
A;Reference number: S29172; MUID:93003351; PMID:1390906  
A;Accession: S29174  
A;Molecule type: protein  
A;Residues: 1-15 <BUC>  
A;Cross-references: UNIPROT:P28588

Query Match 28.0%; Score 21; DB 2; Length 15;  
Best Local Similarity 20.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIIVD 15  
:| || |:  
Db 1 ASPXENYQXYVILNL 15  
|||

## RESULT 13

S10784  
enamelin i - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 19-Mar-1997 #sequence\_revision 21-Nov-1998 #text\_change 09-Jul-2004  
C;Accession: S10784  
R;Strawich, E.; Glincher, M.J.  
Eur. J. Biochem. 191, 47-56, 1990  
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is also  
A;Reference number: S10780; MUID:90336641; PMID:2379503  
A;Accession: S10784  
A;Molecule type: protein  
A;Residues: 1-9 <STR>  
A;Cross-references: UNIPROT:Q7M2M7  
C;Keywords: enamel; phosphoprotein

Query Match 26.7%; Score 20; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAF 7  
|||  
Db 2 PYDGF 6  
|||

## RESULT 14

A59018  
MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 08-May-1998  
C;Accession: A59018  
R;Abe, M.; Smith, C.J.; Larson, C.J.  
submitted to the Protein Sequence Database, May 1998  
A;Description: Involvement of "Ku-like" proteins in the transcription of MUC1/DF3, a  
A;Reference number: A59018  
A;Accession: A59018  
A;Molecule type: protein  
A;Residues: 1-14 <ABE>  
A;Experimental source: breast cancer cell line MCF-7

A>Note: 3-Val was also found  
C:Keywords: DNA binding, heterodimer

Query Match 26.7%; Score 20; DB 2; Length 14;  
Best Local Similarity 33.3%; Pred. No. 2.5e+03;  
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQV 9  
Db 2 SQIYGSYQI 10

# RESULT 15

S08209  
hypothetical protein 2 - garden pea  
N:Alternate names: phytochrome  
C:Species: Pisum sativum (garden pea)  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Sep-1997  
C:Accession: S08209  
P:Sato, N.  
Plant Mol. Biol. 11, 697-710, 1988  
A:Title: Nucleotide sequence and expression of the phytochrome gene in Pisum sativum: di  
A:Reference number: S06856  
A:Accession: S08209  
A:Molecule type: DNA  
A:Residues: 1-15 <SAT>  
A:Cross-references: EMBL:X14077; NID:g20836; PID:g20838  
C:Genetics:  
A:Gene: phy

Query Match 26.7%; Score 20; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.7e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NPY 4  
Db 12 NPY 14

Search completed: November 14, 2004, 13:17:22  
Job time : 18.3333 secs



```

XX SQ Sequence 15 AA;
Query Match 100.0%; Score 75; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIIVDI 15
|||||
Db 1 SNPYSAFQVDIIIVDI 15
|||||

RESULT 2
AAY93066
ID AAY93066 standard; peptide; 15 AA.
XX
AC AAY93066;
XX
XX 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P106.
XX
KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Rattus sp.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
PT Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
PS Disclosure; Page 28; 86pp; Spanish.
XX
CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 75; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIIVDI 15
|||||
Db 1 SNPYSAFQVDIIIVDI 15
|||||

RESULT 3
AAY93066
ID AAY93066 standard; peptide; 15 AA.
XX
AC AAY93066;
XX
XX 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P106.
XX
KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Rattus sp.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
PT Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
PS Disclosure; Page 28; 86pp; Spanish.
XX
CC The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 75; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIIVDI 15
|||||
Db 1 SNPYSAFQVDIIIVDI 15
|||||

RESULT 4
AAY93099
ID AAY93099 standard; peptide; 14 AA.
XX
AC AAY93099;
XX
XX 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P145.
XX
KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX

```

AAY92951

ID AAY92951 standard; peptide; 14 AA.

XX

AC AAY92951;

XX

DT 08-NOV-2000 (first entry)

XX

DE Transforming growth factor inhibitory peptide #7.

XX

KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX

OS Homo sapiens.

XX

PN WO200031135-A1.

XX

PD 02-JUN-2000.

XX

PF 23-NOV-1999; 99WO-ES000375.

XX

PR 24-NOV-1998; 98ES-00002465.

XX

PA (CIEN-) INST CIENTIFICO &amp; TECNOLÓGICO NAVARRA.

XX

PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

PI Borrás Cuesta F;

XX

DR WPI; 2000-411935/35.

XX

PT Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX

PS Claim 8; Page 82; 86pp; Spanish.

XX

CC The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis

XX

SQ Sequence 14 AA;

XX

Query Match 86.7%; Score 65; DB 3; Length 14;

Best Local Similarity 85.7%; Pred. No. 2.8e-05;

Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDIIIVD 14

Db 1 SNPYSAFQVDIIIVD 14

|||||

RESULT 4

AAY93099

ID AAY93099 standard; peptide; 14 AA.

XX

AC AAY93099;

XX

DT 08-NOV-2000 (first entry)

XX

DE Transforming growth factor inhibitory peptide P145.

XX

KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX

```

OS Homo sapiens.
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 31; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX Sequence 14 AA;
SQ
Query Match 86.7%; Score 65; DB 3; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.8e-05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVDIIIVD 14
Db 1 SNPYSAFQVDITID 14
|||||
|

RESULT 5
AAY93059
ID AAY93059 standard; peptide; 15 AA.
XX
XX AAY93059;
AC
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P105.
XX
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Rattus sp.
OS
XX WO200031135-A1.
PN
XX
PD 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 31; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX Sequence 14 AA;
SQ
Query Match 86.7%; Score 65; DB 3; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.8e-05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVDIIIVD 14
Db 1 SNPYSAFQVDITID 14
|||||
|

RESULT 6
AAY93067
ID AAY93067 standard; peptide; 15 AA.
XX
XX AAY93067;
AC
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P107.
XX
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Rattus sp.
OS
XX WO200031135-A1.
PN
XX
PD 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 28; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX Sequence 15 AA;
SQ
Query Match 70.7%; Score 53; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVD 10
Db 6 SNPYSAFQVD 15
|||||
|

RESULT 6
AAY93067
ID AAY93067 standard; peptide; 15 AA.
XX
XX AAY93067;
AC
XX
DT 08-NOV-2000 (first entry)
XX
DE Transforming growth factor inhibitory peptide P107.
XX
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Rattus sp.
OS
XX WO200031135-A1.
PN
XX
PD 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 28; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX Sequence 15 AA;
SQ
Query Match 70.7%; Score 53; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVD 10
Db 6 SNPYSAFQVD 15
|||||
|

```

CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 XX Sequence 15 AA;

Query Match 62.7%; Score 47; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.078; 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Gaps 0;

QY 6 AFQVDIIVDI 15  
 DB 1 AFQVDIIVDI 10  
 |||||

RESULT 7  
 ABP55430  
 ID ABP55430 standard; peptide; 15 AA.  
 XX  
 AC ABP55430;

XX 04-FEB-2003 (first entry)

XX Human breast susceptible gene protein 10.45 N-terminal peptide SEQ:7.  
 DE Human;  
 XX Human; breast susceptible gene coded protein 10.45; tumour;  
 KW embryonic development deformity.  
 XX Homo sapiens.  
 OS

XX CN1342702-A.  
 XX 03-APR-2002.  
 XX 12-SEP-2000; 2000CN-00125173.  
 XX 12-SEP-2000; 2000CN-00125173.  
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 PA Mao Y, Xie Y;  
 PI  
 XX WPI; 2002-529778/57.

XX A novel human breast susceptible gene coded protein 10.45 polypeptide,  
 PT and the polynucleotide encoding it, useful for treating several diseases  
 PT e.g. embryonic development deformity and tumors.  
 XX

PS Example 5; Page 20 (Disclosure); 34pp; Chinese.

XX The present invention describes human breast susceptible gene coded  
 CC protein 10.45 (I). Also described is a process for preparing (I) using  
 CC DNA recombination techniques. (I) can be used for treating several  
 CC diseases e.g. embryonic development deformity and tumors. The present  
 CC sequence represents the N-terminal peptide of (I), which is used in an  
 CC example from the present invention  
 XX

Sequence 15 AA;  
 Query Match 41.3%; Score 31; DB 5; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 84;  
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAFQVDII 12  
 DB 5 SPYFRVNVII 15  
 :||| |::|

RESULT 8  
 ABR75594

ID ABR75594 standard; peptide; 15 AA.

XX  
 AC ABR75594;

XX 28-AUG-2003 (first entry)

XX Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:332.  
 DE Biomarker; liver response; liver response-associated protein isoform;  
 KW LRPI; liver response-associated feature; LRF.  
 XX Synthetic.

XX WO2003038444-A2.

XX 08-MAY-2003.

XX 31-OCT-2002; 2002WO-US034847.

XX 31-OCT-2001; 2001US-0335964P.

XX (PFIZ ) PFIZER PROD INC.  
 PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.  
 XX Amacher DE, Fasulo LM, Herath HWAC, Holt GD, Stiger TR;

XX WPI; 2003-430566/40.

XX Screening, diagnosing, staging or identifying subject at risk of  
 PT developing, liver response, or monitoring effect of therapy on liver  
 PT response, by detecting Liver Response-Associated Protein Isoforms in  
 PT subject sample.

XX Claim 1; Page 66; 256pp; English.

XX The present invention describes a method (M1) for screening or diagnosing  
 CC a liver response in a subject, determining the stage or severity of a  
 CC liver response in a subject, identifying a subject at risk of developing  
 CC liver response, or monitoring the effect of therapy administered to a  
 CC subject having liver response, involving detecting liver response-  
 CC associated protein isoforms (LRPIs) (see the peptides given in ABR75395  
 CC to ABR75806) in a test biological sample from the subject. Alternatively,  
 CC screening or diagnosing a liver response in a subject, or monitoring the  
 CC effect of a drug or therapy administered to a subject, involves  
 CC contacting at least one oligonucleotide probe comprising 10 or more  
 CC consecutive nucleotides complementary to a nucleotide sequence encoding  
 CC an LRPI with RNA obtained from a biological sample from the subject or  
 CC with cDNA copied from the RNA, where the contacting occurs under  
 CC conditions that permit hybridisation of the probe to the nucleotide  
 CC sequence if present, detecting hybridisation, if any, between the probe  
 CC and the nucleotide sequence, and comparing the hybridisation, if any,  
 CC detected in the above step, with the hybridisation detected in a control  
 CC sample, or with a previously determined reference range. M1 is useful for  
 CC screening or diagnosing a liver response in a subject, determining the  
 CC stage or severity of a liver response in a subject, identifying a subject  
 CC at risk of developing liver response, and monitoring the effect of  
 CC therapy administered to a subject having liver response  
 XX

XX Sequence 15 AA;

Query Match 41.3%; Score 31; DB 6; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 84;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFOVDIIVD 14  
 DB 2 YFGSQDILID 12  
 |::|

RESULT 9  
 ADN07473



ID ADN07473 standard; peptide; 15 AA.  
XX AC ADN07473;  
XX DT 17-JUN-2004 (first entry)  
XX DE Liver response-associated feature LRF405 #3.  
XX DE Liver response; liver response-associated protein isoform; LRPI;  
KW drug monitoring; therapy monitoring; liver response-associated feature;  
KW LRF.  
XX OS Homo sapiens.  
XX PN US2003228583-A1.  
XX PD 11-DEC-2003.  
XX PF 31-OCT-2002; 2002US-00285394.  
XX PR 31-OCT-2001; 2001US-0335964P.  
XX PA (AMAC/) AMACHER D E.  
PA (FASU/) FASULO L M.  
PA (HERA/) HERATH H M A C.  
PA (HOLT/) HOLT G D.  
PA (STIG/) STIGER T R.  
XX PI Amacher DE, Fasulo LM, Herath H MAC, Holt GD, Stiger TR;  
XX WPI; 2003-430566/40.  
XX Screening, diagnosing, staging or identifying subject at risk of  
PT developing, liver response, or monitoring effect of therapy on liver  
PT response, by detecting Liver Response-Associated Protein isoforms in  
PT subject sample.  
XX Disclosure; SEQ ID NO 332; 75pp; English.  
XX The invention describes a method of screening (MI) or diagnosing a liver  
CC response in a subject, determining the stage or severity of a liver  
CC response in a subject, identifying a subject at risk of developing liver  
CC response, or monitoring the effect of therapy administered to a subject  
CC having liver response. The method involves detecting Liver Response-  
CC Associated Protein Isoforms (LRPIs) in a test biological sample from the  
CC subject, which has an activity or level indicative of a liver response.  
CC LRPIs are selected from any one of the compounds given in the  
CC specification e.g. LRPI-1.1, LRPI-2.1, LRPI-3.1 and LRPI-4.1.  
CC Alternatively, screening or diagnosing a liver response in a subject, or  
CC monitoring the effect of a drug or therapy administered to a subject,  
CC involves contacting at least one oligonucleotide probe comprising 10 or  
CC more consecutive nucleotides complementary to a nucleotide sequence  
CC encoding an LRPI with RNA obtained from a biological sample from the  
CC subject or with cDNA copied from the RNA, where the contacting occurs  
CC under conditions that permit hybridisation of the probe to the nucleotide  
CC sequence if present, detecting hybridisation, if any, between the probe  
CC and the nucleotide sequence, and comparing the hybridisation, if any,  
CC detected in the above step, with the hybridisation detected in a control  
CC sample, or with a previously determined reference range. The method is  
CC useful for screening or diagnosing a liver response in a subject,  
CC determining the stage or severity of a liver response in a subject,  
CC identifying a subject at risk of developing liver response, and  
CC monitoring the effect of therapy administered to a subject having liver  
CC response. This is the amino acid sequence of a liver response-associated  
CC feature (LRP) comprising one or more LRPI.  
XX SQ Sequence 15 AA;  
Query Match 41.3%; Score 31; DB 7; Length 15;  
Best Local Similarity 45.5%; Pred. No. 84;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
QY 4 YSAFQVDIIVD 14

Db 2 YPGSQLDILID 12  
RESULT 10  
ADL70819  
ID ADL70819 standard; peptide; 15 AA.  
XX AC ADL70819;  
XX DT 03-JUN-2004 (first entry)  
XX DE PTP1B phosphopeptide, SEQ ID 17.  
XX CYTOSTATIC; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;  
KW Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;  
KW phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;  
KW inflammation; multiple sclerosis; angiogenesis-dependent disease;  
KW infectious disease; appetite suppressor; congestive heart failure;  
KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;  
KW protein tyrosine phosphatase 1B.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Modified-site 6  
FT FT /note= "Phosphotyrosine"  
XX PN WO2004020466-A1.  
XX PD 11-MAR-2004.  
XX PF 20-AUG-2003; 2003WO-EP050385.  
XX PR 29-AUG-2002; 2002EP-00019357.  
XX PA (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.  
XX PI Hoofst Van Huijsduijn R, Walchli S, Arigoni F;  
XX WPI; 2004-269210/25.  
XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful  
PT for manufacturing a medicament for preventing or treating e.g. cancer,  
PT diabetes, obesity, inflammation, multiple sclerosis or infectious  
PT diseases.  
XX Example 1; SEQ ID NO 17; 77pp; English.  
XX The present invention relates to phosphopeptides that inhibit protein  
CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or  
CC for manufacturing a medicament for the treatment and/or prevention of  
CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,  
CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.  
CC solid cancer or metastatic cancer) or infectious disease (i.e.  
CC leishmaniasis), or as a suppressor of appetite. These may also be used  
CC for preventing or treating congestive heart failure, neurodegenerative  
CC diseases, ischaemic events of the brain or demyelinating diseases. The  
CC present sequence is one such phosphopeptide from protein tyrosine  
CC phosphatase 1B (PTP1B).  
XX SQ Sequence 15 AA;  
Query Match 40.0%; Score 30; DB 8; Length 15;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 4 YSAFQVD 10  
Db 6 YNAYQVD 12  
RESULT 11



KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;  
 KW protein tyrosine phosphatase 1B.

OS Synthetic.

FH Key Location/Qualifiers  
 FT Modified-site 9 /note= "Phosphotyrosine"  
 FT Modified-site 12 /note= "Phosphotyrosine"

XX WO2004020466-A1.

XX 11-MAR-2004.

XX 20-AUG-2003; 2003WO-EP050385.

XX 29-AUG-2002; 2002EP-00019357.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Hoofst Van Huijsduijn R, Walchli S, Arigoni F;

XX WPI; 2004-269210/25.

XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful

PT for manufacturing a medicament for preventing or treating e.g. cancer,

PT diabetes, obesity, inflammation, multiple sclerosis or infectious

PT diseases.

XX Example 1; Fig 1; 77pp; English.

XX The present invention relates to phosphopeptides that inhibit protein

CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or

CC for manufacturing a medicament for the treatment and/or prevention of

CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,

CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.

CC solid cancer or metastatic cancer) or infectious disease (i.e.

CC leishmaniasis), or as a suppressor of appetite. These may also be used

CC for preventing or treating congestive heart failure, neurodegenerative

CC diseases, ischaemic events of the brain or demyelinating diseases. The

CC present sequence is one such phosphopeptide from protein tyrosine

CC phosphatase 1B (PTP1B).

XX Sequence 15 AA;

SQ

Query Match 40.0%; Score 30; DB 8; Length 15;

Best Local Similarity 71.4%; Pred. No. 1.3e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10

Db 9 YNAYQVD 15

RESULT 14

ADL70908

ID ADL70908 standard; peptide; 15 AA.

XX ADL70908;

AC ADL70908;

XX 03-JUN-2004 (first entry)

XX PTP1B phosphopeptide #22.

XX Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;

XX Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;

XX phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;

XX inflammation; multiple sclerosis; angiogenesis-dependent disease;

XX infectious disease; appetite suppressor; congestive heart failure;

XX neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;

XX protein tyrosine phosphatase 1B.

XX Synthetic.

OS

XX

FH Key Location/Qualifiers

FT Modified-site 9 /note= "Phosphotyrosine"

FT Modified-site 12 /note= "Phosphotyrosine"

XX WO2004020466-A1.

XX 11-MAR-2004.

XX 20-AUG-2003; 2003WO-EP050385.

XX 29-AUG-2002; 2002EP-00019357.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Hoofst Van Huijsduijn R, Walchli S, Arigoni F;

XX WPI; 2004-269210/25.

XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful

PT for manufacturing a medicament for preventing or treating e.g. cancer,

PT diabetes, obesity, inflammation, multiple sclerosis or infectious

PT diseases.

XX Example 1; Fig 1; 77pp; English.

XX The present invention relates to phosphopeptides that inhibit protein

CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or

CC for manufacturing a medicament for the treatment and/or prevention of

CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,

CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.

CC solid cancer or metastatic cancer) or infectious disease (i.e.

CC leishmaniasis), or as a suppressor of appetite. These may also be used

CC for preventing or treating congestive heart failure, neurodegenerative

CC diseases, ischaemic events of the brain or demyelinating diseases. The

CC present sequence is one such phosphopeptide from protein tyrosine

CC phosphatase 1B (PTP1B).

XX Sequence 15 AA;

SQ

Query Match 40.0%; Score 30; DB 8; Length 15;

Best Local Similarity 71.4%; Pred. No. 1.3e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10

Db 9 YNAYQVD 15

RESULT 15

AAG66403

ID AAG66403 standard; peptide; 15 AA.

XX AAG66403;

AC AAG66403;

XX 16-OCT-2001 (first entry)

XX Human vascular epithelium cadherin 54 peptide fragment.

XX Human; vascular epithelium cadherin 54; cancer; HIV infection; anti-HIV;

XX cytotatic.

XX Homo sapiens.

OS CN1296963-A.

XX 30-MAY-2001.

XX 22-NOV-1999; 99CN-00124058.

XX 22-NOV-1999; 99CN-00124058.

XX

XX

PA (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.  
XX  
PI Mao Y, Xie Y;  
XX  
DR WPI; 2001-483895/53.  
XX  
PT Human vascular epithelium cadherin 54 and polynucleotide for coding said  
XX polypeptide.  
PT  
PS Example 6; Page 18 (Disclosure); 34pp; Chinese.  
XX  
CC The present invention relates to human vascular epithelium cadherin 54  
CC and coding sequence (see AAH75794 and AAG66401). Vascular epithelium  
CC cadherin 54 is useful for treating diseases e.g. cancer and HIV  
CC infection. The present sequence is a peptide of vascular epithelium  
CC cadherin 54, which was used in example from the present invention. Note:  
CC the present sequence is the SEQ ID 7 shown on page 18 of the disclosure.  
CC This sequence differs from the SEQ ID 7 shown in the sequence listing  
CC (see AAG66402)  
XX  
SQ Sequence 15 AA;  
  
Query Match 38.7%; Score 29; DB 4; Length 15;  
Best Local Similarity 30.8%; Pred. NO. 2e+02;  
Matches 4; Conservative 6; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 SNPYSAFQVDIIV 13  
| | | : : : : :  
Db 3 SVPYTEWELSVII 15  
  
Search completed: November 14, 2004, 13:11:15  
Job time : 94.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:16:33 ; Search time 79.6667 Seconds  
(without alignments)  
66.619 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPSAFQVDIIVDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 238011

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09D\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	41.3	15	14	US-10-285-394-332
2	28	37.3	10	10	US-09-880-748-3097
3	28	37.3	10	14	US-10-293-418-3097
4	28	37.3	13	11	US-09-842-776A-30
5	27	36.0	9	14	US-10-084-813-973
6	27	36.0	9	14	US-10-084-813-974
7	27	36.0	11	10	US-10-084-813-975
8	27	36.0	11	10	US-09-880-748-2839
9	27	36.0	11	14	US-10-293-418-2839
10	27	36.0	12	14	US-10-084-813-1019
11	27	36.0	12	14	US-10-084-813-1020
12	27	36.0	12	14	US-10-084-813-1021
13	27	36.0	12	14	US-10-084-813-1022

14	27	36.0	12	14	US-10-084-813-1023	Sequence 1023, Ap
15	27	36.0	12	14	US-10-084-813-1024	Sequence 1024, Ap
16	27	36.0	12	14	US-10-286-457-177	Sequence 177, Ap
17	27	36.0	12	16	US-10-128-520-34	Sequence 34, Appl
18	27	36.0	15	14	US-10-084-813-780	Sequence 780, App
19	27	36.0	15	14	US-10-084-813-781	Sequence 781, App
20	27	36.0	15	14	US-10-084-813-782	Sequence 782, App
21	27	36.0	15	14	US-10-084-813-783	Sequence 783, App
22	27	36.0	15	14	US-10-084-813-784	Sequence 784, App
23	27	36.0	15	14	US-10-084-813-785	Sequence 785, App
24	27	36.0	15	14	US-10-084-813-786	Sequence 786, App
25	27	36.0	15	14	US-10-084-813-787	Sequence 787, App
26	27	36.0	15	14	US-10-084-813-788	Sequence 788, App
27	27	36.0	15	14	US-10-354-240-95	Sequence 95, Appl
28	26.5	35.3	10	14	US-10-151-882-26	Sequence 26, Appl
29	26	34.7	7	9	US-09-927-180-3	Sequence 3, Appli
30	26	34.7	9	14	US-10-334-726-118	Sequence 118, App
31	26	34.7	9	14	US-10-334-726-220	Sequence 220, App
32	26	34.7	13	16	US-10-408-765A-3056	Sequence 3056, Ap
33	26	34.7	13	16	US-10-468-496-1532	Sequence 1532, Ap
34	26	34.7	14	15	US-10-403-847-59	Sequence 59, Appl
35	26	34.7	14	15	US-10-403-847-83	Sequence 83, Appl
36	25	33.3	7	14	US-10-400-991-50	Sequence 50, Appl
37	25	33.3	9	10	US-09-995-529-83	Sequence 83, Appl
38	25	33.3	9	11	US-09-995-529-83	Sequence 83, Appl
39	25	33.3	10	10	US-09-572-404B-2428	Sequence 2428, Ap
40	25	33.3	10	16	US-10-327-598-519	Sequence 519, App
41	25	33.3	10	16	US-10-327-598-705	Sequence 705, App
42	25	33.3	11	9	US-09-966-871-70	Sequence 70, Appl
43	25	33.3	11	13	US-10-039-645-70	Sequence 70, Appl
44	25	33.3	11	14	US-10-139-084-70	Sequence 70, Appl
45	25	33.3	11	14	US-10-239-313A-238	Sequence 238, App

ALIGNMENTS

RESULT 1

US-10-285-394-332  
; Sequence 332, Application US/10285394  
; Publication No. US20030228593A1  
; GENERAL INFORMATION:  
; APPLICANT: AMACHER, DAVID E.  
; APPLICANT: FASULO, LISA M.  
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI  
; APPLICANT: HOLT, GORDON DUANE  
; APPLICANT: STIGER, THOMAS R.  
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE  
; FILE REFERENCE: POA-003.01  
; CURRENT APPLICATION NUMBER: US/10/285,394  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/335,964  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 412  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 332  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-285-394-332

Query Match 41.3%; Score 31; DB 14; Length 15;  
Best Local Similarity 45.5%; Pred. No. 11e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDIIVD 14  
| | | | | | | | | | | | | | | |  
Db 2 YPGSQLDILID 12

RESULT 2

US-09-880-748-3097  
; Sequence 3097, Application US/09880748

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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3097
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-3097

Query Match      37.3%; Score 28; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
      :|||:
Db      3 SPYDAFDI 10

RESULT 3
US-10-293-418-3097
; Sequence 3097, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3097
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-293-418-3097

Query Match      37.3%; Score 28; DB 14; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 NPYSAFQV 9
      :|||:
Db      3 SPYDAFDI 10

US-09-842-776A-30
; Sequence 30, Application US/09842776A
; Publication No. US20040023316A1
; GENERAL INFORMATION:
; APPLICANT: CONNEX GMBH
; TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS
; FILE REFERENCE: 41735
; CURRENT APPLICATION NUMBER: US/09/842,776A
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/EP99/08212
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Complementarity determining region (CDR3) of an
; OTHER INFORMATION: antibody heavy chain directed to a beta-urease
; OTHER INFORMATION: epitope (alternative sequence)
; US-09-842-776A-30

Query Match      37.3%; Score 28; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNPYS 5
      :|||:
Db      6 SNPYS 10

RESULT 5
US-10-084-813-973
; Sequence 973, Application US/10084813
; Publication No. US2003006815A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 973
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
; US-10-084-813-973

Query Match      36.0%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FOVDIIV 13
      :::|||:
Db      3 FKIDIV 9

RESULT 6
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US-10-084-813-974
; Sequence 974, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 974
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-974

Query Match          36.0%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 FOVDIV 13
|::|||
Db 2 FKDIV 8

RESULT 7
US-10-084-813-975
; Sequence 975, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 975
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-975

Query Match          36.0%; Score 27; DB 14; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 FOVDIV 13
|::|||
Db 1 FKDIV 7

RESULT 8
US-09-880-748-2839
; Sequence 2839, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2839

Query Match          36.0%; Score 27; DB 10; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQV 9
|::|||
Db 5 PYDAFDI 11

RESULT 9
US-10-293-418-2839
; Sequence 2839, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2839
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2839

Query Match          36.0%; Score 27; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQV 9
|::|||
Db 5 PYDAFDI 11
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RESULT 10
US-10-084-813-1019
; Sequence 1019, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1019
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1019

Query Match          36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FOVDIIV 13
        |::||:|
Db      6 FKIDIVV 12

RESULT 11
US-10-084-813-1020
; Sequence 1020, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1020
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1020

Query Match          36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FOVDIIV 13
        |::||:|
Db      6 FKIDIVV 12

RESULT 12
US-10-084-813-1021
; Sequence 1021, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1021
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1021

Query Match          36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FOVDIIV 13
        |::||:|
Db      5 FKIDIVV 11

RESULT 13
US-10-084-813-1022
; Sequence 1022, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1022
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1022

Query Match          36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      7 FOVDIIV 13
        |::||:|
Db      4 FKIDIVV 10

RESULT 14
US-10-084-813-1023
; Sequence 1023, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; ACIDS, ANTIBODIES, COMPOSITIONS, AND METHODS OF USE
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813

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; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1023
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1023
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Query Match      36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      7 FQVDIIV 13
      |::|||
Db      2 FKIDIV 8
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RESULT 15
US-10-084-813-1024
; Sequence 1024, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1024
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-1024
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Query Match      36.0%; Score 27; DB 14; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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QY      7 FQVDIIV 13
      |::|||
Db      1 FKIDIV 7
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Search completed: November 14, 2004, 13:36:58  
Job time : 79.6667 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 13:04:13 ; Search time 23.3333 Seconds  
(without alignments)  
42.633 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPVSFAQVDIIVDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 157298

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	27	36.0	14	2	US-08-934-222-110
2	27	36.0	14	2	US-08-933-402-110
3	27	36.0	14	2	US-09-207-621-110
4	27	36.0	14	2	US-08-532-818-110
5	27	36.0	14	2	US-09-231-797-110
6	27	36.0	14	3	US-08-934-224-110
7	27	36.0	14	3	US-08-933-843-110
8	27	36.0	14	3	US-08-934-223-110
9	27	36.0	14	3	US-09-413-492-110
10	27	36.0	15	4	US-09-142-524D-95
11	26	34.7	7	1	US-08-281-193-3
12	26	34.7	7	1	US-08-422-106-3
13	26	34.7	7	2	US-08-735-716-3
14	26	34.7	7	2	US-08-555-568B-3
15	26	34.7	7	3	US-09-519-223-3
16	26	34.7	7	4	US-09-927-180-3
17	26	34.7	7	5	PCT-US95-08069-3
18	25	33.3	8	3	US-08-444-818-304
19	25	33.3	8	3	US-08-444-818-305
20	25	33.3	12	3	US-08-819-286-22
21	24	32.0	14	2	US-08-811-949-25
22	24	32.0	15	5	PCT-US91-09422-27
23	23	30.7	7	1	US-07-698-352C-57
24	23	30.7	7	2	US-08-474-379C-57
25	23	30.7	7	3	US-09-146-249A-57
26	23	30.7	7	3	US-08-206-188B-57
27	23	30.7	7	5	PCT-US91-02714-55

28	23	30.7	9	3	US-09-187-859-2837	Sequence 2837, Ap
29	23	30.7	9	4	US-09-839-542B-2837	Sequence 2837, Ap
30	23	30.7	10	3	US-09-187-859-2840	Sequence 2840, Ap
31	23	30.7	10	4	US-09-839-542B-2840	Sequence 2840, Ap
32	23	30.7	10	6	5166058-8	Patent No. 5166058
33	23	30.7	11	2	US-08-621-803-99	Sequence 99, Appl
34	23	30.7	11	2	US-08-598-873-39	Sequence 99, Appl
35	23	30.7	11	3	US-08-605-430-39	Sequence 39, Appl
36	23	30.7	11	3	US-09-217-352-99	Sequence 99, Appl
37	23	30.7	11	4	US-09-717-054-39	Sequence 39, Appl
38	23	30.7	12	1	US-08-212-433A-10	Sequence 10, Appl
39	23	30.7	12	3	US-08-716-256-10	Sequence 10, Appl
40	23	30.7	12	3	US-08-329-799-21	Sequence 21, Appl
41	23	30.7	12	5	PCT-US95-03239-10	Sequence 10, Appl
42	23	30.7	14	2	US-08-348-353-36	Sequence 36, Appl
43	23	30.7	14	2	US-08-465-965-36	Sequence 36, Appl
44	23	30.7	14	3	US-08-465-966-36	Sequence 36, Appl
45	23	30.7	15	1	US-08-213-452-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1

US-08-934-222-110  
; Sequence 110, Application US/08934222  
; Patent No. 5928896  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Plank A Protein-Protein Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,222  
; FILING DATE: 19-SEPT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-934-222-110

Query Match 36.0%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||: ||  
Db 1 NPWTVFQ 7

## RESULT 2

US-08-933-402-110  
; Sequence 110, Application US/08933402  
; Patent No. 5948887  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/933,402  
; FILING DATE: 19-SEPT-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-933-402-110

Query Match 36.0%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||: ||  
Db 1 NPWTVFQ 7

## RESULT 3

US-09-207-621-110  
; Sequence 110, Application US/09207621  
; Patent No. 5952465  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW

; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/207,621  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/051,741  
; FILING DATE: 23-APR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-207-621-110

Query Match 36.0%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||: ||  
Db 1 NPWTVFQ 7

## RESULT 4

US-08-532-818-110  
; Sequence 110, Application US/08532818  
; Patent No. 5965698  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; TITLE OF INVENTION: Site  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/532,818  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-532-818-110

Query Match 36.0%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
DB 1 NPWTVFQ 7

RESULT 5  
US-09-231-797-110  
Sequence 110, Application US/09231797  
Patent No. 6084066  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/231.797  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-231-797-110

Query Match 36.0%; Score 27; DB 3; Length 14;

Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 2 NPYSAFQ 8  
DB 1 NPWTVFQ 7

RESULT 6  
US-08-934-224-110  
Sequence 110, Application US/08934224  
Patent No. 6100044  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,224  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-224-110

Query Match 36.0%; Score 27; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
DB 1 NPWTVFQ 7

RESULT 7  
US-08-933-843-110  
Sequence 110, Application US/08933843  
Patent No. 6111069  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
CONSTRAINING GROUPS WHICH FLANK A PROTEIN-PROTEIN INTERACTION  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,843  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-843-110

Query Match 36.0%; Score 27; DB 3; Length 14;

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; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction
;
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,843
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; US-08-933-843-110
;
; Query Match 36.0%; Score 27; DB 3; Length 14;
; Best Local Similarity 57.1%; Pred. No. 1.3e+02;
; Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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; QY 2 NPYSAFQ 8
; DB 1 NPTVTFQ 7
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; RESULT 8
; US-08-934-223-110
; Sequence 110, Application US/08934223
; Patent No. 6147189
;
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:
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; US-08-934-223-110
; Sequence 110, Application US/08934223
; Patent No. 6147189
;
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,223
; FILING DATE:
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; US-08-933-843-110
; Sequence 110, Application US/09413492
; Patent No. 6258550
;
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
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; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; US-08-934-223-110
;
; Query Match 36.0%; Score 27; DB 3; Length 14;
; Best Local Similarity 57.1%; Pred. No. 1.3e+02;
; Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
;
; QY 2 NPYSAFQ 8
; DB 1 NPTVTFQ 7
;
; RESULT 9
; US-09-413-492-110
; Sequence 110, Application US/09413492
; Patent No. 6258550
;
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; constraining Groups Which Flank A Protein-Protein Interaction
; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/413,492
; FILING DATE:
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
;
; APPLICATION NUMBER: PCT/US94/04294
; FILING DATE: 21-APR-1994
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Isaacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 110:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; US-08-934-223-110
```

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-413-492-110

Query Match 36.0%; Score 27; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
DB 1 NPWTVFQ 7

## RESULT 10

US-09-142-524D-95  
; Sequence 95, Application US/09142524D  
; Patent No. 6719976  
; GENERAL INFORMATION:  
; APPLICANT: Sone, Toshio  
; APPLICANT: Kume, Akino  
; APPLICANT: Dairiki, Kazuo  
; APPLICANT: Iwama, Akiko  
; APPLICANT: Kino, Kohsuke  
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease  
; FILE REFERENCE: SPO-103  
; CURRENT APPLICATION NUMBER: US/09/142,524D  
; CURRENT FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: PCT/JP97/00740  
; PRIOR FILING DATE: 1997-03-10  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 95  
; LENGTH: 15  
; TYPE: PPT  
; ORGANISM: Cryptomeria japonica  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)...(15)  
; OTHER INFORMATION: Cryj2 peptide, Figure 2, Row 12  
US-09-142-524D-95

Query Match 36.0%; Score 27; DB 4; Length 15;  
Best Local Similarity 45.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PYSAPQVDIIIV 13  
DB 5 PHFTFKVDGII 15

## RESULT 11

US-08-281-193-3  
; Sequence 3, Application US/08281193  
; Patent No. 5466595  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 15  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/281,193  
; FILING DATE:  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-281-193-3

Query Match 34.7%; Score 26; DB 1; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
DB 1 NPHSGFR 7

## RESULT 12

US-08-422-106-3  
; Sequence 3, Application US/08422106  
; Patent No. 5589170  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 15  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,106  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/281,193  
; FILING DATE: 27-JUL-1994  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
US-08-422-106-3

Query Match 34.7%; Score 26; DB 1; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
DB 1 NPHSGFR 7

## RESULT 13

US-08-735-716-3  
; Sequence 3, Application US/08735716  
; Patent No. 5840511  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Simon  
; APPLICANT: Tang, Jim  
; TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
; NUMBER OF SEQUENCES: 15  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/735,716  
; FILING DATE: 23-OCT-1996

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
US-08-519-223-3  
Sequence 3, Application US/09519223  
Patent No. 6274140  
FILING DATE: 27-JUL-1994  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-735-716-3

Query Match 34.7%; Score 26; DB 2; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
Db 1 NPHSGFR 7

RESULT 14  
US-08-555-568B-3  
Sequence 3, Application US/08555568B  
Patent No. 5976854  
GENERAL INFORMATION:  
APPLICANT: Jones, Simon  
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/555,568B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-08-555-568B-3

Query Match 34.7%; Score 26; DB 2; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
Db 1 NPHSGFR 7

RESULT 15  
US-09-519-223-3  
Sequence 3, Application US/09519223  
Patent No. 6274140  
GENERAL INFORMATION:  
APPLICANT: Jones, Simon  
TITLE OF INVENTION: Calcium Independent Phospholipase A2/B  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/519,223  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/555,568  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Scott A.  
REGISTRATION NUMBER: 32,724  
TELEPHONE: (617) 498-8224  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
US-09-519-223-3

Query Match 34.7%; Score 26; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
Db 1 NPHSGFR 7

Search completed: November 14, 2004, 13:18:38  
Job time : 24.3333 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 13:57:40 ; Search time 37 Seconds  
(without alignments)  
23.404 Million cell updates/sec

Title: US-09-831-253F-5  
Perfect score: 48  
Sequence: 1 TSLMIWTWM 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 791

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	52.1	7	2 PX0008	glucuronosyltransf
2	18	37.5	7	2 S09652	hypothetical prote
3	18	37.5	7	2 PH1602	Ig H chain V-D-J r
4	16	33.3	4	2 PT0661	T-cell receptor be
5	16	33.3	6	2 B34835	dnaA protein - bee
6	16	33.3	7	4 I55382	hypothetical pepti
7	16	33.3	9	2 A43848	cell surface adhes
8	16	33.3	9	2 G85802	hypothetical prote
9	15	31.2	7	2 PT0586	T-cell receptor be
10	15	31.2	7	2 S32244	neuromodulatory pe
11	15	31.2	7	2 S32245	neuromodulatory pe
12	15	31.2	7	2 S32246	neuromodulatory pe
13	15	31.2	9	2 I52974	seminal vesicle pr
14	14	29.2	6	2 I49808	D-SP2.5 region - m
15	14	29.2	6	2 F41946	T-cell receptor ga
16	14	29.2	7	2 PN0649	pullulanase (EC 3.
17	14	29.2	8	2 A39308	glycine reductase
18	13	27.1	6	2 PT0519	T-cell receptor be
19	13	27.1	8	2 T10952	hypothetical prote
20	13	27.1	8	2 S19288	acylase - Kluyvera
21	13	27.1	9	2 S07241	litorin - Rohde's
22	13	27.1	9	2 I58350	gene c-mpl protein
23	12	25.0	5	2 PT0281	Ig heavy chain CRD
24	12	25.0	6	2 A60986	N-formyl oligopept
25	12	25.0	6	2 I59142	platelet-derived g
26	12	25.0	8	2 PQ0012	cholecystokinin -
27	12	25.0	8	2 A43001	cholecystokinin -
28	12	25.0	8	2 A59495	Vesicle associated
29	12	25.0	8	2 JS0316	leucokinin VI - Ma

30	12	25.0	8	2 A41117	acetylcholinestera
31	12	25.0	9	2 S07205	litorin 2-Glu - Au
32	12	25.0	9	2 S07204	litorin 1 - Austr
33	12	25.0	9	2 A44873	caldesmon - rabbit
34	12	25.0	9	2 JS0302	xenopsin-related p
35	12	25.0	9	2 A60320	xenopsin-related p
36	11	22.9	3	3 P37196	bradykinin-potenti
37	11	22.9	4	2 A34626	RPCH-related neuro
38	11	22.9	4	2 B53284	T-cell receptor be
39	11	22.9	5	2 A32516	cholecystokinin-5
40	11	22.9	5	2 T10954	hypothetical prote
41	11	22.9	5	2 A60803	neuropeptide - sea
42	11	22.9	5	2 JH0253	gut pentapeptide -
43	11	22.9	5	2 PT0308	Ig heavy chain CRD
44	11	22.9	5	2 PT0729	T-cell receptor be
45	11	22.9	5	2 PT0580	T-cell receptor be

ALIGNMENTS

RESULT 1

PX0008  
glucuronosyltransferase (EC 2.4.1.17), hepatic - rat (fragment)  
N:Alternate names: UDP-glucuronyltransferase  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 07-Feb-1997  
C:Accession: PX0008

R:Yokota, H.; Yuasa, A.; Sato, R.

J. Biochem. 104, 531-536, 1988

A:Title: Purification and properties of a form of UDP-glucuronyltransferase from liver mi

A:Reference number: PX0008; MUID:89197852; PMID:3149280

A:Accession: PX0008

A:Molecule type: protein

A:Residues: 1-7 <YOK>

C:Keywords: glycosyltransferase; hexosyltransferase; liver

Query Match 52.1%; Score 25; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLMIW 6

DB 1 TKLLWM 6

RESULT 2

S09652  
hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)

C:Species: Enterobacter cloacae

C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 08-Oct-1999

C:Accession: S09652

R:Vliegenthart, J. S.; Ketelaar-van Gaalen, P. A. G.; van de Klundert, J. A. M.

Antimicrob. Agents Chemother. 33, 1153-1159, 1989

A:Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant invo

A:Reference number: S09651; MUID:90024972; PMID:2552900

A:Accession: S09652

A:Molecule type: DNA

A:Residues: 1-7 <VLI>

A:Cross-references: EMBL:X51534; NID:g40878; PIDN:CAA35914.1; PID:g581034

Query Match 37.5%; Score 18; DB 2; Length 7;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LMIW 6

DB 1 MIW 4

RESULT 3

PH1602  
Ig H chain V-D-J region (wild-type clone 313) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
 C:Accession: PH1602  
 R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
 J. Exp. Med. 178, 317-329, 1993  
 A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
 A:Reference number: PH1580; MUID:93301609; PMID:8315387  
 A:Accession: PH1602  
 A:Molecule type: DNA  
 A:Residues: 1-7 <LEV>  
 A:Status: 1-7 <LEV>  
 A:Experimental source: bone marrow pre-B lymphocyte  
 C:Keywords: immunoglobulin

Query Match 37.5%; Score 18; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IWT 7  
 :||  
 Db 5 LWT 7

RESULT 4  
 PT0661  
 T-cell receptor beta chain V-D-J region (121-18V) - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004  
 C:Accession: PT0661  
 R:Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A:Reference number: PT0509; MUID:91277601; PMID:1711558  
 A:Accession: PT0661  
 A:Status: translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-4 <FEE>  
 A:Cross-references: UNIPROT:Q8BZQ7; UNIPROT:Q8CCN5  
 A:Experimental source: day 4 postnatal thymus, strain BALB/c  
 C:Keywords: T-cell receptor

Query Match 33.3%; Score 16; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WT 7  
 ||  
 Db 3 WT 4

RESULT 5  
 B34835  
 dnaA protein - Pseudomonas aeruginosa (fragment)  
 C:Species: Pseudomonas aeruginosa  
 C:Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 08-Oct-1999  
 C:Accession: B34835  
 R:Yee, T.W.; Smith, D.W.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990  
 A:Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es  
 A:Reference number: A34835; MUID:90160310; PMID:2106132  
 A:Accession: B34835  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-6 <YEE>  
 A:Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421  
 C:Keywords: DNA binding

Query Match 33.3%; Score 16; DB 2; Length 6;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLMW 6  
 ||:  
 Db 2 SVELW 6

## RESULT 6

15382  
 Hypothetical peptide PAII promoter region - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 20-Apr-2000  
 C:Accession: I55382  
 R:Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.  
 J. Biol. Chem. 268, 10739-10745, 1993  
 A:Title: The two allele sequences of a common polymorphism in the promoter of the plasmi  
 A:Reference number: I55382; MUID:93266509; PMID:8388372  
 A:Accession: I55382  
 A:Status: translation not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-7 <DAW>  
 A:Cross-references: GB:M91557; NID:g190020; PIDN:AAA60110.1; PID:g190021  
 C:Comment: This is the hypothetical translation of a sequence from the PAII gene promoter  
 C:Genetics:  
 A:Gene: GDB:PAII  
 A:Cross-references: GDB:120297; OMIM:173360  
 A:Map position: 7q21.3-7q22

Query Match 33.3%; Score 16; DB 4; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WT 7

Db 1 WT 2

## RESULT 7

A43848  
 cell surface adhesin for heparan sulfate, 66K - Staphylococcus aureus (fragment)  
 C:Species: Staphylococcus aureus  
 C:Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 C:Accession: A43848  
 R:Liang, O.D.; Ascencio, F.; Franssen, L.A.; Wadstrom, T.  
 Infect. Immun. 60, 899-906, 1992  
 A:Title: Binding of heparan sulfate to Staphylococcus aureus.  
 A:Reference number: A43848; MUID:92176005; PMID:1541563  
 A:Accession: A43848  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-9 <LIA>  
 A:Cross-references: UNIPROT:Q9RSM1  
 A>Note: sequence extracted from NCBI backbone (NCBIP:85442)

Query Match 33.3%; Score 16; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WT 7

Db 2 WT 3

## RESULT 8

G85802  
 hypothetical protein Z2947 [imported] - Escherichia coli (strain O157:H7, substrain EDL9;  
 C:Species: Escherichia coli  
 C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C:Accession: G85802  
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,  
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: G85802  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-9 <STO>

A;Cross-references: UNIPROT:Q8X4G1; GB:AE005174; NID:gl2515957; PIDN:AAG56883.1; GSPDB:D  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: Z2947

Query Match 33.3%; Score 16; DB 2; Length 9;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 MIWTMM 9  
| : |  
Db 1 MTYTFM 6

## RESULT 9

PT0586

T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0586; PT0592

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0586

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <PEE>

A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)

C;Keywords: T-cell receptor

Query Match 31.2%; Score 15; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IW 6  
| : |  
Db 4 IW 5

## RESULT 10

S33244

neuromodulatory peptide Wwamide-1 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S33244

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33244

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

A;Cross-references: UNIPROT:P35921

Query Match 31.2%; Score 15; DB 2; Length 7;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LMIW 6  
| : |  
Db 4 MSVW 7

## RESULT 11

S33245

neuromodulatory peptide Wwamide-2 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S33245

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of tl

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33245

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

A;Cross-references: UNIPROT:P35919

Query Match 31.2%; Score 15; DB 2; Length 7;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LMIW 6  
| : |  
Db 4 MSVW 7

## RESULT 12

S33246

neuromodulatory peptide Wwamide-3 - giant African snail

C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S33246

R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.

FEBS Lett. 323, 104-108, 1993

A;Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of tl

A;Reference number: S33244; MUID:93265912; PMID:8495720

A;Accession: S33246

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <MIN>

A;Cross-references: UNIPROT:P35920

Query Match 31.2%; Score 15; DB 2; Length 7;  
Best Local Similarity 25.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LMIW 6  
| : |  
Db 4 MSVW 7

## RESULT 13

152974

seminal vesicle protein IV - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

C;Accession: 152974

R;Teng, C.T.; Harris, S.E.

DNA 2, 105-111, 1983

A;Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sites

A;Reference number: 152974; MUID:83261204; PMID:6307619

A;Accession: 152974

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-9 <RES>

A;Cross-references: GB:M27324; NID:g207124; PIDN:AAA63501.1; PID:g207125

C;Genetics:

A;Gene: SVSIV

Query Match 31.2%; Score 15; DB 2; Length 9;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSLMI 5  
| : |  
Db 4 TSLFL 8

## RESULT 14

I49808

D-SP2.5 region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999

C:Accession: I49808

R:Kurosawa, Y.; Tonegawa, S.

J. Exp. Med. 155, 201-218, 1982

A:Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity

A:Reference number: I49808; PMID:82099938; PMID:6798155

A:Accession: I49808

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: GB:J00432; NID:gl94370; PIDN:AAA7904.1; PID:G450452

C:Genetics:

A:Gene: Igh

Query Match

Best Local Similarity 29.2%; Score 14; DB 2; Length 6;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SLMWT 7

Db 1 STMVTT 6

RESULT 15

F41946

T-cell receptor gamma chain (1a.27) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C:Accession: F41946

R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge

A:Reference number: A41946; PMID:92049316; PMID:1658619

A:Accession: F41946

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-6 <WHE>

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 29.2%; Score 14; DB 2; Length 6;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IW 6

Db 4 VW 5

Search completed: November 14, 2004, 14:07:59

Job time : 49 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 11.8085 Seconds  
(without alignments)  
84.242 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75  
Sequence: 1 SNFYSAFQVDIIVDI 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	48.0	17	3	US-09-177-249-173
2	32	42.7	22	1	US-08-116-733-5
3	29	38.7	16	3	US-08-819-286-20
4	29	38.7	20	3	US-08-819-286-21
5	29	38.7	20	3	US-08-630-052-25
6	27.5	36.7	17	3	US-08-652-877-1
7	27.5	36.7	17	3	US-08-476-515A-1
8	27	36.0	14	2	US-08-934-222-110
9	27	36.0	14	2	US-08-933-402-110
10	27	36.0	14	2	US-09-207-621-110
11	27	36.0	14	2	US-08-532-818-110
12	27	36.0	14	3	US-09-231-797-110
13	27	36.0	14	3	US-08-934-224-110
14	27	36.0	14	3	US-08-933-843-110
15	27	36.0	14	3	US-08-934-223-110
16	27	36.0	14	3	US-09-413-492-110
17	27	36.0	15	4	US-09-142-524D-95
18	27	36.0	17	1	US-08-435-925C-7
19	27	36.0	17	1	US-08-435-925C-8
20	27	36.0	17	1	US-08-173-510B-63
21	27	36.0	17	1	US-08-458-218-61
22	27	36.0	17	2	US-08-450-497-63
23	27	36.0	17	4	US-08-060-433C-13
24	27	36.0	19	1	US-08-520-977A-9
25	27	36.0	21	1	US-08-290-373B-7
26	27	36.0	21	1	US-08-127-499A-18
27	27	36.0	21	1	US-08-482-847-18

28	26.5	35.3	20	5	PCT-US93-03076-11	Sequence 11, Appl
29	26	34.7	7	1	US-08-281-193-3	Sequence 3, Appl
30	26	34.7	7	1	US-08-422-106-3	Sequence 3, Appl
31	26	34.7	7	2	US-08-735-716-3	Sequence 3, Appl
32	26	34.7	7	2	US-08-555-568B-3	Sequence 3, Appl
33	26	34.7	7	3	US-09-519-223-3	Sequence 3, Appl
34	26	34.7	7	4	US-09-927-180-3	Sequence 3, Appl
35	26	34.7	7	5	PCT-US95-08069-3	Sequence 3, Appl
36	26	34.7	16	3	US-09-323-433A-18	Sequence 18, Appl
37	26	34.7	16	4	US-09-826-752-18	Sequence 18, Appl
38	26	34.7	21	4	US-09-270-767-56843	Sequence 56843, A
39	25	33.3	8	3	US-08-444-818-304	Sequence 304, App
40	25	33.3	8	3	US-08-444-818-305	Sequence 305, App
41	25	33.3	12	3	US-08-819-286-22	Sequence 22, Appl
42	25	33.3	16	3	US-08-819-286-23	Sequence 23, Appl
43	25	33.3	20	3	US-08-612-973-56	Sequence 56, Appl
44	25	33.3	20	3	US-08-819-286-24	Sequence 24, Appl
45	25	33.3	20	3	US-08-927-597-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1  
US-09-177-249-173  
; Sequence 173, Application US/09177249  
; Patent No. 6229064  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit  
; TITLE OF INVENTION: Development in Plants  
; FILE REFERENCE: 023070-086120US  
; CURRENT APPLICATION NUMBER: US/09/177,249  
; CURRENT FILING DATE: 1998-10-22  
; EARLIER APPLICATION NUMBER: US 09/071,838  
; EARLIER FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 173  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-09-177-249-173

Query Match 48.0%; Score 36; DB 3; Length 17;  
Best Local Similarity 46.7%; Pred. No. 3.7;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SNFYSAFQVDIIVDI 15  
||||| : :  
Db 3 SNFYRKTNTYKDI 17

RESULT 2  
US-08-116-733-5  
; Sequence 5, Application US/08116733  
; Patent No. 5516632  
; GENERAL INFORMATION:  
; APPLICANT: PALKER, Thomas J.  
; APPLICANT: HAYNES, Barton F.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHYE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON

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; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,733
; FILING DATE: 07-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-33
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-116-733-5

Query Match 42.7%; Score 32; DB 1; Length 22;
Best Local Similarity 54.5%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
DB 1 SSPYKWFQHDV 11

RESULT 3
US-08-819-286-20
; Sequence 20, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-21

Query Match 38.7%; Score 29; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 QVDIIVDI 15
DB 7 QVDEVVDI 14

RESULT 5
US-08-630-052-25
; Sequence 25, Application US/08630052
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-20

Query Match 38.7%; Score 29; DB 3; Length 16;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 QVDIIVDI 15
DB 3 QVDEVVDI 10

RESULT 4
US-08-819-286-21
; Sequence 21, Application US/08819286
; Patent No. 6169074
; GENERAL INFORMATION:
; APPLICANT: Montal, Mauricio
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF
; TITLE OF INVENTION: NEUROTRANSMITTER SECRETION BY NEURONAL CELLS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,599
; FILING DATE: 18-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Taylor, Stacy L.
; REGISTRATION NUMBER: 34,842
; REFERENCE/DOCKET NUMBER: 07349/005001
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-819-286-21

Query Match 38.7%; Score 29; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 QVDIIVDI 15
DB 7 QVDEVVDI 14

RESULT 5
US-08-630-052-25
; Sequence 25, Application US/08630052
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Patent No. 639296  
GENERAL INFORMATION:  
APPLICANT: Brent, Roger  
APPLICANT: McCoy, John M.  
APPLICANT: Jensen, Timm H.  
APPLICANT: Xu, Chanxing Wilson  
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN  
TITLE OF INVENTION: INTERACTIONS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,052  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/504,538  
FILING DATE: July 20, 1995  
APPLICATION NUMBER: 08/278,082  
FILING DATE: July 20, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Karen F. Lech  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/311001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-052-25  
Query Match 38.7%; Score 29; DB 3; Length 20;  
Best Local Similarity 62.5%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 PYSAFQVD 10  
Db 13 PHSVFQVD 20  
RESULT 6  
US-08-652-877-1  
Sequence 1, Application US/08652877  
Patent No. 6187548  
GENERAL INFORMATION:  
APPLICANT: Akerstrom, Goran  
APPLICANT: Juhlin, Claes  
APPLICANT: Raak, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjalms, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
TITLE OF INVENTION: Thereof and DNA Encoding Same  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.

Patent No. 639296  
GENERAL INFORMATION:  
APPLICANT: Brent, Roger  
APPLICANT: McCoy, John M.  
APPLICANT: Jensen, Timm H.  
APPLICANT: Xu, Chanxing Wilson  
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING PROTEIN  
TITLE OF INVENTION: INTERACTIONS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,052  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/504,538  
FILING DATE: July 20, 1995  
APPLICATION NUMBER: 08/278,082  
FILING DATE: July 20, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Karen F. Lech  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/311001  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-052-25  
Query Match 38.7%; Score 29; DB 3; Length 20;  
Best Local Similarity 62.5%; Pred. No. 86;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 3 PYSAFQVD 10  
Db 13 PHSVFQVD 20  
RESULT 6  
US-08-652-877-1  
Sequence 1, Application US/08652877  
Patent No. 6187548  
GENERAL INFORMATION:  
APPLICANT: Akerstrom, Goran  
APPLICANT: Juhlin, Claes  
APPLICANT: Raak, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjalms, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
TITLE OF INVENTION: Thereof and DNA Encoding Same  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rhone-Poulenc Rorer Inc.

STREET: 500 Arcola Rd., 3C43  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: System 7.5.1  
SOFTWARE: Word 6.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/652,877  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/15203  
FILING DATE: 22-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/487,314  
FILING DATE: 07-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355E-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-652-877-1  
Query Match 36.7%; Score 27.5; DB 3; Length 17;  
Best Local Similarity 53.8%; Pred. No. 1.3e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;  
QY 2 NPYSAFQVDIIVD 14  
Db 4 NPYS---LDIFED 13  
RESULT 7  
US-08-476-515A-1  
Sequence 1, Application US/08476515A  
Patent No. 6239270  
GENERAL INFORMATION:  
APPLICANT: Akerstrom, Goran  
APPLICANT: Juhlin, Claes  
APPLICANT: Raak, Lars  
APPLICANT: Crumley, Gregg R.  
APPLICANT: Morse, Clarence C.  
APPLICANT: Murray, Edward M.  
APPLICANT: Hjalms, Goran  
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments  
TITLE OF INVENTION: Thereof and DNA Encoding Same  
NUMBER OF SEQUENCES: 84  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Martin Savitzky  
STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.,  
STREET: 3C43,  
CITY: Collegeville  
STATE: PA  
COUNTRY: USA  
ZIP: 19426-0107  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Compaq PC  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Word 7.0 (Patentin)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/476,515A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/344,836  
FILING DATE: 23-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/SE94/00483  
FILING DATE: 24-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SE 9301764-8  
FILING DATE: 24-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Savitzky, Martin  
REGISTRATION NUMBER: 29,699  
REFERENCE/DOCKET NUMBER: A1355D  
TELEPHONE: 610-454-3816  
TELEFAX: 610-454-3808  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal  
US-08-476-515A-1

Query Match 36.7%; Score 27.5; DB 3; Length 17;  
Best Local Similarity 53.8%; Pred. No. 1.3e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;  
QY 2 NPYSAFQDIIIVD 14  
DB 4 NPYS---LDIFED 13

RESULT 8  
US-08-934-222-110  
Sequence 110, Application US/08934222  
Patent No. 5928896  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,222  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-402-110

APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-222-110

Query Match 36.0%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
DB 1 NPWTVFQ 7

RESULT 9  
US-08-933-402-110  
Sequence 110, Application US/08933402  
Patent No. 5948887  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,402  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-402-110

Query Match 36.0%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;



Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
|:|:|  
Db 1 NPWTVFQ 7

RESULT 10  
US-09-207-621-110  
; Sequence 110, Application US/09207621  
; Patent No. 5952465  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/207,621  
; FILING DATE: 29-OCT-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 03-MAY-1996  
; APPLICATION NUMBER: PCT/US94/04294  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-207-621-110

Query Match 36.0%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
|:|:|  
Db 1 NPWTVFQ 7

RESULT 11  
US-09-207-621-110  
; Sequence 110, Application US/08532818  
; Patent No. 5965698  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,797  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-09-207-621-110

Query Match 36.0%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
|:|:|  
Db 1 NPWTVFQ 7

RESULT 12  
US-09-231-797-110  
; Sequence 110, Application US/09231797  
; Patent No. 6084066  
; GENERAL INFORMATION:  
; APPLICANT: EVANS, Herbert J.  
; APPLICANT: KINI, R. Manjunatha  
; TITLE OF INVENTION: Polypeptides That Include Conformation-  
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
; NUMBER OF SEQUENCES: 153  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: Suite 500, 3000 K Street NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20007  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/231,797  
; FILING DATE: 03-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/532,818  
; FILING DATE: 21-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: U.S. 08/143,364  
; FILING DATE: 29-OCT-1993  
; NAME: Isaacson, John P.  
; REGISTRATION NUMBER: 33,751  
; REFERENCE/DOCKET NUMBER: 040433/0148  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 14 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-532-818-110

Query Match 36.0%; Score 27; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAPQ 8  
|:|:|  
Db 1 NPWTVFQ 7

APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-09-231-797-110

Query Match 36.0%; Score 27; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||:|  
Db 1 NPWTVFQ 7

RESULT 13  
US-08-934-224-110  
Sequence 110, Application US/08934224  
Patent No. 610044  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
SOFTWARE: Patent In Release #1.0, Version #1.25  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/934,224  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
US-08-934-224-110

Query Match 36.0%; Score 27; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||:|  
Db 1 NPWTVFQ 7

RESULT 14  
US-08-933-843-110  
Sequence 110, Application US/08933843  
Patent No. 611069  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.  
APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
SOFTWARE: Patent In Release #1.0, Version #1.25  
TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein Interaction  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,843  
FILING DATE: 19-SEPT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/532,818  
FILING DATE: 03-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-933-843-110

Query Match 36.0%; Score 27; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPYSAFQ 8  
||:|  
Db 1 NPWTVFQ 7

RESULT 15  
US-08-934-223-110  
Sequence 110, Application US/08934223  
Patent No. 6147189  
GENERAL INFORMATION:  
APPLICANT: EVANS, Herbert J.

APPLICANT: KINI, R. Manjunatha  
TITLE OF INVENTION: Polypeptides That Include Conformation-  
Constraining Groups Which Flank A Protein-Protein Interaction  
TITLE OF INVENTION: Site  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: Suite 500, 3000 K Street NW  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20007  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: /08/934,223  
APPLICATION NUMBER: US/08/934,223  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/532,818  
FILING DATE: 03-MAY-1996  
APPLICATION NUMBER: PCT/US94/04294  
FILING DATE: 21-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/143,364  
FILING DATE: 29-OCT-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/051,741  
FILING DATE: 23-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Isaacson, John P.  
REGISTRATION NUMBER: 33,751  
REFERENCE/DOCKET NUMBER: 040433/0148  
INFORMATION FOR SEQ ID NO: 110:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 14 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-934-223-110

Query Match 36.0%; Score 27; DB 3; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NPYSAPQ 8  
|::||  
Db 1 NPWTVFQ 7

Search completed: November 14, 2004, 12:08:47  
Job time : 11.8085 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 43.4043 Seconds  
(without alignments)  
123.973 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNFYSAFQVDIIVIDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	100.0	15	3 AAY92948	Aay92948 Transform
2	75	100.0	15	3 AAY93066	Aay93066 Transform
3	65	86.7	14	3 AAY92951	Aay92951 Transform
4	65	86.7	14	3 AAY93099	Aay93099 Transform
5	53	70.7	15	3 AAY93059	Aay93059 Transform
6	47	62.7	15	3 AAY93067	Aay93067 Transform
7	32	42.7	19	2 AAW94737	Aaw94737 Anti-Stap
8	32	42.7	19	2 ADL35119	Adl35119 CDR2 of m
9	32	42.7	21	2 AAR34228	Aar34228 HTLV-I gp
10	32	42.7	22	2 AAY17925	Aay17925 Synthetic
11	31	41.3	15	5 ABP55430	Abp55430 Human bre
12	31	41.3	15	6 ABR75594	Abr75594 Liver res
13	31	41.3	15	7 ADN07473	Adn07473 Liver res
14	30	40.0	15	8 ADL70819	Adl70819 PTP1B pho
15	30	40.0	15	8 ADL70905	Adl70905 PTP1B pho
16	30	40.0	15	8 ADL70907	Adl70907 PTP1B pho
17	30	40.0	15	8 ADL70906	Adl70906 PTP1B pho
18	30	40.0	15	8 ADL70908	Adl70908 PTP1B pho
19	30	40.0	17	2 AAR31182	Aar31182 N-termina
20	30	40.0	18	6 ABR91851	Abr91851 P. papata
21	30	40.0	19	6 ABR91858	Abr91858 P. papata
22	30	40.0	20	7 ADC60750	Adc60750 Termitomy
23	30	40.0	22	4 AAG76637	Aag76637 Human col
24	30	40.0	23	6 ABR91880	Abr91880 P. papata
25	29	38.7	15	4 AAG66403	Aag66403 Human vas

26 29 38.7 20 2 AAW32131 Interacti  
27 29 38.7 21 7 ABM74026 DNA clone  
28 29 38.7 22 4 AAM32954 Peptide #  
29 29 38.7 22 4 AAM72723 Human bon  
30 29 38.7 22 4 AAM60111 Human bra  
31 29 38.7 22 4 ABG54421 Human liv  
32 29 38.7 22 5 ABG42547 Human pep  
33 29 38.7 23 2 AAW60840 Peptide c  
34 28 37.3 10 5 ABP47086 Human Bly  
35 28 37.3 10 7 ADG97913 scFV VHCD  
36 28 37.3 13 3 AAB10012 H. pylori  
37 28 37.3 13 4 AAB86092 H. pylori  
38 28 37.3 13 4 AAB86060 H. pylori  
39 28 37.3 15 3 AAY93058 Transform  
40 28 37.3 20 3 AAY56754 Smooth mu  
41 28 37.3 23 6 ABU03500 Angiogene  
42 27.5 36.7 17 2 AAE64137 Lys-C pap  
43 27.5 36.7 17 2 AAR95282 Calcium s  
44 27.5 36.7 17 2 AAW43315 Human cal  
45 27 36.0 9 4 AAB89867 HIV gp120

## ALIGNMENTS

## RESULT 1

AAY92948  
ID AAY92948 standard; peptide; 15 AA.

XX AC AAY92948;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide #4.

XX KW Hepatotropic; antagonist; transforming growth factor betaf; TGF-b1;  
XX KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
XX KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Homo sapiens.

XX PN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
Borras Cuesta F;

WPI; 2000-411935/35.

PT Peptides that antagonize binding of transforming growth factor betaf,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.

PS Claim 5; Page 81; 86pp; Spanish.

CC The invention relates to synthetic peptides that antagonise the binding  
CC of transforming growth (TGF) factor betaf (TGF-b1) to its receptor in  
CC vivo which have partial amino acid sequences identical, or similar, with  
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
CC examples of the peptides of the invention. The peptides act by  
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
CC they are inhibitors of stimulation of collagen synthesis in liver cells  
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
CC expression systems) encoding the peptides are used for treatment of liver  
CC disease, specifically cirrhosis

```

XX      SQ      Sequence 15 AA;
Query Match      100.0%; Score 75; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNPYSAFQVDIIVDI 15
Db      1 SNPYSAFQVDIIVDI 15

RESULT 2
AAY93066
ID      AAY93066 standard; peptide; 15 AA.
XX
AC      AAY93066;
XX
XX      08-NOV-2000 (first entry)
XX
DE      Transforming growth factor inhibitory peptide P106.
XX
KW      Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS      Rattus sp.
XX
PN      WO200031135-A1.
XX
PD      02-JUN-2000.
XX
PF      23-NOV-1999; 99WO-ES000375.
XX
PR      24-NOV-1998; 98ES-00002465.
XX
XX      (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI      Borrás Cuesta F;
XX
XX      WPI; 2000-411935/35.
XX
PT      Peptides that antagonize binding of transforming growth factor betal,
PT      useful for treatment of liver disease, especially cirrhosis, are partial
PT      sequences of the factor or its receptors.
XX
PS      Claim 8; Page 82; 86pp; Spanish.
XX
CC      The invention relates to synthetic peptides that antagonise the binding
CC      of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC      vivo which have partial amino acid sequences identical, or similar, with
CC      those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC      examples of the peptides of the invention. The peptides act by
CC      competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC      they are inhibitors of stimulation of collagen synthesis in liver cells
CC      and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC      extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC      expression systems) encoding the peptides are used for treatment of liver
CC      disease, specifically cirrhosis
XX
SQ      Sequence 15 AA;

Query Match      100.0%; Score 75; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNPYSAFQVDIIVDI 15
Db      1 SNPYSAFQVDIIVDI 15

RESULT 3
AAY93066
ID      AAY93066 standard; peptide; 15 AA.
XX
AC      AAY93066;
XX
XX      08-NOV-2000 (first entry)
XX
DE      Transforming growth factor inhibitory peptide P106.
XX
KW      Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS      Rattus sp.
XX
PN      WO200031135-A1.
XX
PD      02-JUN-2000.
XX
PF      23-NOV-1999; 99WO-ES000375.
XX
PR      24-NOV-1998; 98ES-00002465.
XX
XX      (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI      Borrás Cuesta F;
XX
XX      WPI; 2000-411935/35.
XX
PT      Peptides that antagonize binding of transforming growth factor betal,
PT      useful for treatment of liver disease, especially cirrhosis, are partial
PT      sequences of the factor or its receptors.
XX
PS      Disclosure; Page 28; 86pp; Spanish.
XX
CC      The invention relates to synthetic peptides that antagonise the binding
CC      of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC      vivo which have partial amino acid sequences identical, or similar, with
CC      those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC      examples of the peptides of the invention. The peptides act by
CC      competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC      they are inhibitors of stimulation of collagen synthesis in liver cells
CC      and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC      extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC      expression systems) encoding the peptides are used for treatment of liver
CC      disease, specifically cirrhosis
XX
SQ      Sequence 15 AA;

Query Match      100.0%; Score 75; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SNPYSAFQVDIIVDI 15
Db      1 SNPYSAFQVDIIVDI 15

RESULT 4
AAY93099
ID      AAY93099 standard; peptide; 14 AA.
XX
AC      AAY93099;
XX
XX      08-NOV-2000 (first entry)
XX
DE      Transforming growth factor inhibitory peptide P145.
XX
KW      Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX

```

```

AAY92951
ID      AAY92951 standard; peptide; 14 AA.
XX
AC      AAY92951;
XX
XX      08-NOV-2000 (first entry)
XX
DE      Transforming growth factor inhibitory peptide #7.
XX
KW      Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS      Homo sapiens.
XX
PN      WO200031135-A1.
XX
PD      02-JUN-2000.
XX
PF      23-NOV-1999; 99WO-ES000375.
XX
PR      24-NOV-1998; 98ES-00002465.
XX
XX      (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI      Borrás Cuesta F;
XX
XX      WPI; 2000-411935/35.
XX
PT      Peptides that antagonize binding of transforming growth factor betal,
PT      useful for treatment of liver disease, especially cirrhosis, are partial
PT      sequences of the factor or its receptors.
XX
PS      Claim 8; Page 82; 86pp; Spanish.
XX
CC      The invention relates to synthetic peptides that antagonise the binding
CC      of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC      vivo which have partial amino acid sequences identical, or similar, with
CC      those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC      examples of the peptides of the invention. The peptides act by
CC      competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC      they are inhibitors of stimulation of collagen synthesis in liver cells
CC      and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC      extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC      expression systems) encoding the peptides are used for treatment of liver
CC      disease, specifically cirrhosis
XX
SQ      Sequence 14 AA;

Query Match      86.7%; Score 65; DB 3; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.8e-05;
Matches 12; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 SNPYSAFQVDIIVD 14
Db      1 SNPYSAFQVDITID 14

RESULT 4
AAY93099
ID      AAY93099 standard; peptide; 14 AA.
XX
AC      AAY93099;
XX
XX      08-NOV-2000 (first entry)
XX
DE      Transforming growth factor inhibitory peptide P145.
XX
KW      Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX

```



CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 15 AA;

Query Match 62.7%; Score 47; DB 3; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.078; 0; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 AFQVDIIVDI 15  
 DB 1 AFQVDIIVDI 10

RESULT 7  
 AAW94737  
 ID AAW94737 standard; protein; 19 AA.  
 AC AAW94737;  
 XX  
 XX 22-APR-1999 (first entry)  
 DT  
 XX  
 DE Anti-Staph (HAY) 96-110 heavy chain variable region.  
 XX  
 KW Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;  
 KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;  
 KW MAB 96-110.

XX Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..19  
 FT Region /notes="complementarity determining region (CDR)"  
 FT

XX WO9857994-A2.

XX 23-DEC-1998.

XX 16-JUN-1998; 98WO-US012402.

XX 16-JUN-1997; 97US-0049871P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX Fischer GW, Schuman RF, Wong H, Stinson JL;

XX WPI; 1999-095329/08.

XX N-PSDB; AAX05581.

XX New antibodies to lipoteichoic acid of gram positive bacteria - used to  
 PT develop products for the diagnosis, prevention and treatment of  
 PT infections caused by gram positive bacteria.

XX Claim 21; Fig 12; 150pp; English.

XX The invention relates to a monoclonal antibody (MAB) to lipoteichoic acid  
 CC of gram positive bacteria, where the MAB is a chimeric immunoglobulin  
 CC comprising at least part of a human immunoglobulin constant region and at  
 CC least part of a non-human immunoglobulin variable region having  
 CC specificity to lipoteichoic acid of gram positive bacteria. The  
 CC antibodies bind to whole bacteria and enhance phagocytosis and killing of  
 CC the bacteria and enhance protection from lethal infection. The antibodies  
 CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic  
 CC acid antibody or characterised by amino acids corresponding to one or  
 CC more of the complementarity determining regions (CDRs) of the variable  
 CC region of the antibody) can be used for treating or preventing infections  
 CC caused by gram positive bacteria. They can also be used for the diagnosis

CC of gram positive bacterial infections. Sequences AAW94735-39 represent  
 CC heavy chain variable regions of the anti-lipoteichoic antibody 96-100  
 XX  
 SQ Sequence 19 AA;  
 Query Match 42.7%; Score 32; DB 2; Length 19;  
 Best Local Similarity 42.9%; Pred. No. 72;  
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 SNPYSAFQVDIIVD 14  
 DB 6 SNNYATFYADSVKD 19

RESULT 8  
 ADL35119  
 ID ADL35119 standard; peptide; 19 AA.

XX ADL35119;

XX 03-JUN-2004 (first entry)

XX CDR2 of murine anti-LTA (A110) heavy chain antibody SeqID 125.

XX antibody; variable domain; framework region; FR; huFR;  
 KW immune system molecule; lipoteichoic acid; LTA; A110; mouse; murine.

XX Mus sp.

XX WO2004020579-A2.

XX 11-MAR-2004.

XX 06-AUG-2003; 2003WO-US024637.

XX 29-AUG-2002; 2002US-00230880.

XX (SUNO-) SUNOL MOLECULAR CORP.

XX Wong HC, Stinson JR, Mosquera LA;

XX WPI; 2004-239169/22.

XX Producing humanized antibodies for diagnostic and therapeutic purposes  
 PT comprises optimizing similarity between individual antibody framework  
 PT regions to help identify human framework regions suitable for making the  
 PT antibodies.

XX Disclosure; SEQ ID NO 125; 137pp; English.

XX This invention relates to a novel method for producing a humanised  
 CC antibody variable (V) domain or its fragment by optimising sequence  
 CC similarity between individual antibody framework regions (FRs) in order  
 CC to identify suitable human FRs (huFRs). Specifically, it refers to novel  
 CC immune system molecules i.e. humanised monoclonal antibodies that exhibit  
 CC suitable binding affinity with reduced immunogenicity in humans. The  
 CC present invention describes a method of mutagenising DNA of non-human FRs  
 CC to encode humanised FRs having an amino acid sequence that is  
 CC substantially identical to the selected human FR previously identified  
 CC through sequence similarity searching. As such, this method provides  
 CC humanised light or heavy chain V domains of the sequence huFR1-huFR2  
 CC -CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic  
 CC products to treat and/or diagnose diseases in humans and animals.  
 CC Furthermore, the method expands the number of best fit possibilities that  
 CC can be generated and provides a rational basis for assembling nearly all  
 CC humanised immune system molecules of interest. This peptide sequence  
 CC represents a hypervariable region (CDR) of the murine anti-LTA (A110)  
 CC heavy chain antibody protein of the invention.

XX Sequence 19 AA;

Query Match 42.7%; Score 32; DB 8; Length 19;  
 Best Local Similarity 42.9%; Pred. No. 72;



Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVDIIVD 14  
| | | | | | | | | |  
Db 6 SNNVATYADSVKD 19

## RESULT 9

AAR34228  
ID AAR34228 standard; peptide; 21 AA.

XX AAR34228;

XX 25-MAR-2003 (revised)

DT 04-AUG-1993 (first entry)

XX HTLV-I gp46 external envelope glycoprotein fragment 4.

XX Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;

KW diagnosis; antibodies.

XX Synthetic.

XX WO9306843-A1.

XX 15-APR-1993.

XX 08-OCT-1992; 92WO-US008405.

XX 08-OCT-1991; 91US-00771553.

XX (UYDU-) UNIV DUKE.

XX Palker TJ, Haynes BF;

XX WPI; 1993-134125/16.

XX Antigenic determinant peptide(s) of HTLV envelope glycoprotein - useful  
PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.  
PT

XX Claim 4; Page 11; 50pp; English.

XX The sequence of peptide 4 corresponds to residues 129-149 from the HTLV-I  
CC gp46 external envelope glycoprotein. When covalently linked to a carrier  
CC mol. the hydrophilic peptide can induce in a mammal the prodn. of high  
CC titres of antibodies to gp46 envelope glycoprotein from HTLV-I or -II.  
CC The peptide and carrier may be used in vaccines against HTLV-I or -II  
CC infection. The peptide may be used in a diagnostic assay to detect the  
CC presence and titre of anti-HTLV antibodies. See also AAR34225-57.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 21 AA;

Query Match 42.7%; Score 32; DB 2; Length 21;

Best Local Similarity 54.5%; Pred. No. 82;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVDI 11

Db 1 SSPYWKFGHDV 11

## RESULT 10

AAV17925  
ID AAV17925 standard; peptide; 22 AA.

XX AAV17925;

XX 30-JUL-1999 (first entry)

XX Synthetic peptide derived from HTLV envelope sugar protein.

XX Hydrophilic peptide; antigen determinant; envelope sugar protein; HTLV-I;

KW HTLV-II; B lymphatic corpuscle; gp46; gp63; tetanus toxoid.

XX Synthetic.

OS Human lymphotropic virus type i.

XX JF02209889-A.

XX 21-AUG-1990.

XX 08-FEB-1989; 89JP-00029551.

XX 08-FEB-1988; 88US-00153420.

PR 30-JAN-1989; 89US-00303436.

XX (UYDU-) UNIV DUKE.

XX WPI; 1990-344000/39.

XX Synthetic hydrophilic peptide - comprises 25 unit aminoacid that  
PT corresponds to at least one antigen determinant of envelope sugar  
PT protein(s) of HTLV-I and HTLV-II.

XX Claim 4; Page 1; 15pp; Japanese.

XX The invention relates to new synthetic hydrophilic peptides (AAV17922-  
CC 934) that correspond to at least one of antigen determinants of envelope  
CC sugar proteins of HTLV-I and HTLV-II identified in the B lymphatic  
CC corpuscle. When bonded covalently to a carrier molecule, the peptides can  
CC induce the production of an antibody having a high titre to the gp46 and  
CC gp63 envelope sugar proteins of HTLV-I and HTLV-II in mammals. The  
CC carrier molecule is preferably a tetanus toxoid and selected from the  
CC group of sequences shown in AAV17935-39. The carrier molecule is  
CC preferably a dipeptide bonded to the peptide through at least one spacer molecule  
CC (preferably a dipeptide-glycine-glycine). The peptides form effectively  
CC immunological response to factors causing virus HTLV-I and HTLV-II. The  
CC method also provides an effective conjugate having the peptide  
XX

SQ Sequence 22 AA;

Query Match 42.7%; Score 32; DB 2; Length 22;

Best Local Similarity 54.5%; Pred. No. 87;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVDI 11

Db 1 SSPYWKFGHDV 11

## RESULT 11

ABP55430

ID ABP55430 standard; peptide; 15 AA.

XX ABP55430;

XX 04-FEB-2003 (first entry)

XX Human breast susceptible gene protein 10.45 N-terminal peptide SEQ.7.

XX Human; breast susceptible gene coded protein 10.45; tumour;  
KW embryotic development deformity.

XX Homo sapiens.

XX CN1342702-A.

XX 03-APR-2002.

XX 12-SEP-2000; 2000CN-00125173.

XX 12-SEP-2000; 2000CN-00125173.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX

PI Mao Y, Xie Y;  
 XX WPI; 2002-529778/57.  
 XX A novel human breast susceptible gene coded protein 10.45 polypeptide,  
 PT and the polynucleotide encoding it, useful for treating several diseases  
 PT e.g. embryonic development deformity and tumors.  
 XX  
 XX Example 5; Page 20 (Disclosure); 34pp; Chinese.  
 XX  
 CC The present invention describes human breast susceptible gene coded  
 CC protein 10.45 (I). Also described is a process for preparing (I) using  
 CC DNA recombination techniques. (I) can be used for treating several  
 CC diseases e.g. embryonic development deformity and tumors. The present  
 CC sequence represents the N-terminal peptide of (I), which is used in an  
 CC example from the present invention  
 XX  
 SQ Sequence 15 AA;  
 Query Match 41.3%; Score 31; DB 5; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 84;  
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 NPYSAFQVDII 12  
 Db ||| |:::  
 5 SPYKFRVNV 15  
 RESULT 12  
 ABR75594  
 ID ABR75594 standard; peptide; 15 AA.  
 XX  
 AC ABR75594;  
 XX  
 DT 28-AUG-2003 (first entry)  
 XX  
 DE Liver response-associated protein isoform (LRPI) peptide SEQ ID NO:332.  
 XX  
 KW Biomarker; liver response; liver response-associated protein isoform;  
 KW LRPI; liver response-associated feature; LRF.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003038444-A2.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 31-OCT-2002; 2002WO-US034847.  
 XX  
 PR 31-OCT-2001; 2001US-0335964P.  
 XX  
 PA (PFIZ) PFIZER PROD INC.  
 PA (OXFO-) OXFORD GLYSCSCIENCES UK LTD.  
 XX  
 PI Amacher DE, Fasulo LM, Herath HM, Holt GD, Stiger TR;  
 XX  
 DR WPI; 2003-430566/40.  
 XX  
 PT Screening, diagnosing, staging or identifying subject at risk of  
 PT developing, liver response, or monitoring effect of therapy on liver  
 PT response, by detecting Liver Response-Associated Protein Isoforms in  
 PT subject sample.  
 XX  
 PS Claim 1; Page 66; 256pp; English.  
 XX  
 CC The present invention describes a method (M1) for screening or diagnosing  
 CC a liver response in a subject, determining the stage or severity of a  
 CC liver response in a subject, identifying a subject at risk of developing  
 CC liver response, or monitoring the effect of therapy administered to a  
 CC subject having liver response, involving detecting liver response-  
 CC associated protein isoforms (LRPIs) (see the peptides given in ABR75395  
 CC to ABR75806) in a test biological sample from the subject. Alternatively,  
 CC screening or diagnosing a liver response in a subject, or monitoring the

CC effect of a drug or therapy administered to a subject, involves  
 CC contacting at least one oligonucleotide probe comprising 10 or more  
 CC consecutive nucleotides complementary to a nucleotide sequence encoding  
 CC an LRPI with RNA obtained from a biological sample from the subject or  
 CC with cDNA copied from the RNA, where the contacting occurs under  
 CC conditions that permit hybridisation of the probe to the nucleotide  
 CC sequence if present, detecting hybridisation, if any, between the probe  
 CC and the nucleotide sequence, and comparing the hybridisation, if any,  
 CC detected in the above step, with the hybridisation detected in a control  
 CC sample, or with a previously determined reference range. M1 is useful for  
 CC screening or diagnosing a liver response in a subject, determining the  
 CC stage or severity of a liver response in a subject, identifying a subject  
 CC at risk of developing liver response, and monitoring the effect of  
 CC therapy administered to a subject having liver response  
 XX  
 SQ Sequence 15 AA;  
 Query Match 41.3%; Score 31; DB 6; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 84;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 YSAFQVDIIVD 14  
 Db ||| |:::  
 2 YPGSQLDILID 12  
 RESULT 13  
 ADN07473  
 ID ADN07473 standard; peptide; 15 AA.  
 XX  
 AC ADN07473;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Liver response-associated feature LRF405 #3.  
 XX  
 KW liver response; liver response-associated protein isoform; LRPI;  
 KW drug monitoring; therapy monitoring; liver response-associated feature;  
 KW LRF.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003228583-A1.  
 XX  
 PD 11-DEC-2003.  
 XX  
 PF 31-OCT-2002; 2002US-00285394.  
 XX  
 PR 31-OCT-2001; 2001US-0335964P.  
 XX  
 PA (AMAC/) AMACHER D E.  
 PA (FASU/) FASULO L M.  
 PA (HERA/) HERATH H M A C.  
 PA (HOLT/) HOLT G D.  
 PA (STIG/) STIGER T R.  
 XX  
 PI Amacher DE, Fasulo LM, Herath HM, Holt GD, Stiger TR;  
 XX  
 DR WPI; 2003-430566/40.  
 XX  
 PT Screening, diagnosing, staging or identifying subject at risk of  
 PT developing, liver response, or monitoring effect of therapy on liver  
 PT response, by detecting Liver Response-Associated Protein Isoforms in  
 PT subject sample.  
 XX  
 PS Disclosure; SEQ ID NO 332; 75pp; English.  
 XX  
 CC The invention describes a method of screening (M1) or diagnosing a liver  
 CC response in a subject, determining the stage or severity of a liver  
 CC response in a subject, identifying a subject at risk of developing liver  
 CC response, or monitoring the effect of therapy administered to a subject  
 CC having liver response. The method involves detecting liver response-  
 CC associated protein isoforms (LRPIs) in a test biological sample from the

CC subject, which has an activity or level indicative of a liver response.  
 CC LRP1s are selected from any one of the compounds given in the  
 CC specification e.g. LRPI-1.1, LRPI-2.1, LRPI-3.1 and LRPI-4.1.  
 CC Alternatively, screening or diagnosing a liver response in a subject, or  
 CC monitoring the effect of a drug or therapy administered to a subject, or  
 CC involves contacting at least one oligonucleotide probe comprising 10 or  
 CC more consecutive nucleotides complementary to a nucleotide sequence  
 CC encoding an LRPI with RNA obtained from a biological sample from the  
 CC subject or with cDNA copied from the RNA, where the contacting occurs  
 CC under conditions that permit hybridisation of the probe to the nucleotide  
 CC sequence if present, detecting hybridisation, if any, between the probe  
 CC and the nucleotide sequence, and comparing the hybridisation, if any,  
 CC detected in the above step, with the hybridisation detected in a control  
 CC sample, or with a previously determined reference range. The method is  
 CC useful for screening or diagnosing a liver response in a subject,  
 CC determining the stage or severity of a liver response in a subject,  
 CC identifying a subject at risk of developing liver response, and  
 CC monitoring the effect of therapy administered to a subject having liver  
 CC response. This is the amino acid sequence of a liver response-associated  
 CC feature (LRF) comprising one or more LRPI.  
 XX  
 SQ Sequence 15 AA;

Query Match 41.3%; Score 31; DB 7; Length 15;  
 Best Local Similarity 45.5%; Pred. No. 84;  
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDIIVD 14  
 | :|:|:|  
 Db 2 YPGSQLDILID 12

RESULT 14  
 ADL70819  
 ID ADL70819 standard; peptide; 15 AA.

XX AC ADL70819;  
 XX DT 03-JUN-2004 (first entry)  
 XX DE PTP1B phosphopeptide, SEQ ID 17.  
 XX KW Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;  
 KW Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;  
 KW phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;  
 KW inflammation; multiple sclerosis; angiogenesis-dependent disease;  
 KW infectious disease; appetite suppressor; congestive heart failure;  
 KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;  
 KW protein tyrosine phosphatase 1B.  
 XX OS Synthetic.

PH Key Location/Qualifiers  
 FT Modified-site 6 /note= "Phosphotyrosine"  
 FT

XX WO2004020466-A1.

XX 11-MAR-2004.

XX 20-AUG-2003; 2003WO-EP050385.

XX 29-AUG-2002; 2002EP-00019357.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Hoofst Van Huijsduijn R, Walchli S, Arigoni F;

XX WPI; 2004-269210/25.

XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful  
 PT for manufacturing a medicament for preventing or treating e.g. cancer,  
 PT diabetes, obesity, inflammation, multiple sclerosis or infectious

PT diseases.

XX Example 1; SEQ ID NO 17; 77pp; English.

XX The present invention relates to phosphopeptides that inhibit protein  
 CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or  
 CC for manufacturing a medicament for the treatment and/or prevention of  
 CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,  
 CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.  
 CC solid cancer or metastatic cancer) or infectious disease (i.e.  
 CC leishmaniasis), or as a suppressor of appetite. These may also be used  
 CC for preventing or treating congestive heart failure, neurodegenerative  
 CC diseases, ischaemic events of the brain or demyelinating diseases. The  
 CC present sequence is one such phosphopeptide from protein tyrosine  
 CC phosphatase 1B (PTP1B).

XX Sequence 15 AA;

Query Match 40.0%; Score 30; DB 8; Length 15;  
 Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10  
 | :|:|:|  
 Db 6 YNAYQVD 12

RESULT 15  
 ADL70905  
 ID ADL70905 standard; peptide; 15 AA.

XX AC ADL70905;

XX DT 03-JUN-2004 (first entry)

XX DE PTP1B phosphopeptide #19.

XX KW Cytostatic; Antidiabetic; Anorectic; Antiinflammatory; Antimicrobial;  
 KW Cardiant; Neuroprotective; Protein tyrosine phosphatase inhibitor;  
 KW phosphopeptide; protein tyrosine phosphatase; cancer; diabetes; obesity;  
 KW inflammation; multiple sclerosis; angiogenesis-dependent disease;  
 KW infectious disease; appetite suppressor; congestive heart failure;  
 KW neurodegenerative disease; ischaemia; demyelinating disease; PTP1B;  
 KW protein tyrosine phosphatase 1B.

XX OS Synthetic.

XX WO2004020466-A1.

XX 11-MAR-2004.

XX 20-AUG-2003; 2003WO-EP050385.

XX 29-AUG-2002; 2002EP-00019357.

XX (ISTF ) ARS APPLIED RES SYSTEMS HOLDING NV.

XX Hoofst Van Huijsduijn R, Walchli S, Arigoni F;

XX WPI; 2004-269210/25.

XX New phosphopeptides that inhibit protein tyrosine phosphatases, useful  
 PT for manufacturing a medicament for preventing or treating e.g. cancer,  
 PT diabetes, obesity, inflammation, multiple sclerosis or infectious  
 PT diseases.

XX Example 1; Fig 1; 77pp; English.

XX The present invention relates to phosphopeptides that inhibit protein  
 CC tyrosine phosphatase. The phosphopeptides are useful as a medicament or  
 CC for manufacturing a medicament for the treatment and/or prevention of  
 CC cancer (i.e. stomach or intestinal cancer), diabetes and/or obesity,  
 CC inflammation, multiple sclerosis, angiogenesis-dependent disease (e.g.  
 CC solid cancer or metastatic cancer) or infectious disease (i.e.  
 CC leishmaniasis), or as a suppressor of appetite. These may also be used  
 CC for preventing or treating congestive heart failure, neurodegenerative  
 CC diseases, ischaemic events of the brain or demyelinating diseases. The  
 CC present sequence is one such phosphopeptide from protein tyrosine  
 CC phosphatase 1B (PTP1B).

CC solid cancer or metastatic cancer) or infectious disease (i.e.  
CC leishmaniasis), or as a suppressor of appetite. These may also be used  
CC for preventing or treating congestive heart failure, neurodegenerative  
CC diseases, ischaemic events of the brain or demyelinating diseases. The  
CC present sequence is one such phosphopeptide from protein tyrosine  
CC phosphatase 1B (PTP1B).  
XX

SQ Sequence 15 AA;

Query Match 40.0%; Score 30; DB 8; Length 15;  
Best Local Similarity 71.4%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFQVD 10  
|.:|||  
Db 9 YNAYQVD 15

Search completed: November 14, 2004, 12:02:09  
Job time : 46.4043 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 35.4255 Seconds  
(without alignments)  
149.815 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPYSAFQVDIIVDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	48.0	17	9	US-09-071-838-173
2	36	48.0	17	14	US-10-213-512-173
3	32	42.7	19	14	US-10-230-880-125
4	31	41.3	15	14	US-10-285-394-332
5	31	41.3	19	15	US-10-424-599-201443
6	30	40.0	18	16	US-10-481-180-685
7	30	40.0	19	16	US-10-481-180-692
8	30	40.0	22	14	US-10-106-698-7411
9	30	40.0	23	16	US-10-481-180-714
10	29	38.7	20	14	US-10-162-538-25
11	29	38.7	22	9	US-09-864-761-43921
12	28	37.3	10	10	US-09-880-748-3097
13	28	37.3	10	14	US-10-293-418-3097

14	28	37.3	13	11	US-09-842-776A-30	Sequence 30, Appl
15	28	37.3	23	15	US-10-211-462-91	Sequence 91, Appl
16	27	36.0	9	14	US-10-084-813-973	Sequence 973, Appl
17	27	36.0	9	14	US-10-084-813-974	Sequence 974, Appl
18	27	36.0	9	14	US-10-084-813-975	Sequence 975, Appl
19	27	36.0	11	10	US-09-880-748-2839	Sequence 2839, Ap
20	27	36.0	11	14	US-10-293-418-2839	Sequence 2839, Ap
21	27	36.0	12	14	US-10-084-813-1019	Sequence 1019, Ap
22	27	36.0	12	14	US-10-084-813-1020	Sequence 1020, Ap
23	27	36.0	12	14	US-10-084-813-1021	Sequence 1021, Ap
24	27	36.0	12	14	US-10-084-813-1022	Sequence 1022, Ap
25	27	36.0	12	14	US-10-084-813-1023	Sequence 1023, Ap
26	27	36.0	12	14	US-10-084-813-1024	Sequence 1024, Ap
27	27	36.0	12	14	US-10-286-457-177	Sequence 177, Appl
28	27	36.0	12	16	US-10-128-520-34	Sequence 34, Appl
29	27	36.0	15	14	US-10-084-813-780	Sequence 780, Appl
30	27	36.0	15	14	US-10-084-813-781	Sequence 781, Appl
31	27	36.0	15	14	US-10-084-813-782	Sequence 782, Appl
32	27	36.0	15	14	US-10-084-813-783	Sequence 783, Appl
33	27	36.0	15	14	US-10-084-813-784	Sequence 784, Appl
34	27	36.0	15	14	US-10-084-813-785	Sequence 785, Appl
35	27	36.0	15	14	US-10-084-813-786	Sequence 786, Appl
36	27	36.0	15	14	US-10-084-813-787	Sequence 787, Appl
37	27	36.0	15	14	US-10-084-813-788	Sequence 788, Appl
38	27	36.0	15	14	US-10-354-240-95	Sequence 95, Appl
39	27	36.0	18	10	US-09-880-748-2736	Sequence 2736, Ap
40	27	36.0	18	14	US-10-084-813-826	Sequence 826, Appl
41	27	36.0	18	14	US-10-084-813-827	Sequence 827, Appl
42	27	36.0	18	14	US-10-084-813-828	Sequence 828, Appl
43	27	36.0	18	14	US-10-084-813-829	Sequence 829, Appl
44	27	36.0	18	14	US-10-084-813-830	Sequence 830, Appl
45	27	36.0	18	14	US-10-084-813-831	Sequence 831, Appl

ALIGNMENTS

RESULT 1

US-09-071-838-173  
; Sequence 173, Application US/09071838  
; Patent No. US20020152501A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; TITLE OF INVENTION: Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; NUMBER OF SEQUENCES: 324  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,838  
; FILING DATE: 01-MAY-1998  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bastian, Kevin L.  
; REGISTRATION NUMBER: 34,774  
; REFERENCE/DOCKET NUMBER: 023070-086100US  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 173:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 17 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-071-838-173

Query Match 48.0%; Score 36; DB 9; Length 17;  
Best Local Similarity 46.7%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SNPSAFQVDIIIVDI 15  
||| | : : ||  
Db 3 SNPYRKFTNYTKDI 17  
||| | : : ||

## RESULT 2

US-10-213-512-173  
; Sequence 173, Application US/10213512  
; Publication No. US20030110536A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Robert L.  
; APPLICANT: Ohad, Nir  
; APPLICANT: Kiyosue, Tomohiro  
; APPLICANT: Yadegari, Ramin  
; APPLICANT: Margossian, Linda  
; APPLICANT: Harada, John  
; APPLICANT: Goldberg, Robert B.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and  
; TITLE OF INVENTION: Fruit Development in Plants  
; FILE REFERENCE: 023070-086110US  
; CURRENT APPLICATION NUMBER: US/10/213,512  
; CURRENT FILING DATE: 2002-08-06  
; PRIOR APPLICATION NUMBER: US/09/177,206  
; PRIOR FILING DATE: 1998-10-22  
; PRIOR APPLICATION NUMBER: US 09/071,838  
; PRIOR FILING DATE: 1998-05-01  
; NUMBER OF SEQ ID NOS: 324  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 173  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Arabidopsis sp.  
US-10-213-512-173

Query Match 48.0%; Score 36; DB 14; Length 17;  
Best Local Similarity 46.7%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SNPSAFQVDIIIVDI 15  
||| | : : ||  
Db 3 SNPYRKFTNYTKDI 17  
||| | : : ||

## RESULT 3

US-10-230-880-125  
; Sequence 125, Application US/10230880  
; Publication No. US20030190705A1  
; GENERAL INFORMATION:  
; APPLICANT: WONG, HING C.  
; APPLICANT: STINSON, JEFFREY L.  
; APPLICANT: MOSQUERA, LUIS A.  
; TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES  
; FILE REFERENCE: 71758/58066  
; CURRENT APPLICATION NUMBER: US/10/230,880  
; CURRENT FILING DATE: 2002-12-23  
; PRIOR APPLICATION NUMBER: 09/990,586  
; PRIOR FILING DATE: 2001-11-21  
; PRIOR APPLICATION NUMBER: 60/343,306

; PRIOR FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/293,854  
; PRIOR FILING DATE: 1999-04-16  
; NUMBER OF SEQ ID NOS: 174  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 125  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-230-880-125

Query Match 42.7%; Score 32; DB 14; Length 19;  
Best Local Similarity 42.9%; Pred. No. 96;  
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 SNPSAFQVDIIIVD 14  
||| | : : ||  
Db 6 SNNYATFYADSVKD 19  
||| | : : ||

## RESULT 4

US-10-285-394-332  
; Sequence 332, Application US/10285394  
; Publication No. US20030228583A1  
; GENERAL INFORMATION:  
; APPLICANT: AMACHER, DAVID E.  
; APPLICANT: PASULO, LISA M.  
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI  
; APPLICANT: HOLT, GORDON DUANE  
; APPLICANT: STIGER, THOMAS R.  
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE  
; FILE REFERENCE: POA-003.01  
; CURRENT APPLICATION NUMBER: US/10/285,394  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: 60/335,964  
; PRIOR FILING DATE: 2001-10-31  
; NUMBER OF SEQ ID NOS: 412  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 332  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-285-394-332

Query Match 41.3%; Score 31; DB 14; Length 15;  
Best Local Similarity 45.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFQVDIIIVD 14  
||| | : : ||  
Db 2 YPGSQLDILID 12  
||| | : : ||

## RESULT 5

US-10-424-599-201443  
; Sequence 201443, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 201443  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_23928C.1.pep  
US-10-424-599-201443

Query Match 41.3%; Score 31; DB 15; Length 19;  
Best Local Similarity 30.8%; Pred. No. 1.5e+02;  
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 PYSAFQVDIIIVDI 15  
||:|:|:|:  
Db 2 PYATFPMTILISL 14

## RESULT 6

US-10-481-180-685  
; Sequence 685, Application US/10481180  
; Publication No. US20040171821A1  
; GENERAL INFORMATION:  
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
; APPLICANT: HUMAN SERVICES  
; APPLICANT: Valenzuela, Jesus G.  
; APPLICANT: Belkaid, Yasmine  
; APPLICANT: Kamhawi, Shaden  
; APPLICANT: Sacks, David  
; APPLICANT: Ribeiro, Jose M. C.  
; TITLE OF INVENTION: ANTI-ARTHOPOD VECTOR VACCINES, METHODS  
; TITLE OF INVENTION: OF SELECTING AND USES THEREOF  
; FILE REFERENCE: 4239-67347  
; CURRENT APPLICATION NUMBER: US/10/481,180  
; CURRENT FILING DATE: 2003-12-17  
; PRIOR APPLICATION NUMBER: PCT/US02/19663  
; PRIOR FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/299,391  
; PRIOR FILING DATE: 2001-06-19  
; NUMBER OF SEQ ID NOS: 884  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 685  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =  
; OTHER INFORMATION: Synthetic Construct  
US-10-481-180-685

Query Match 40.0%; Score 30; DB 16; Length 18;  
Best Local Similarity 46.2%; Pred. No. 2.1e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 2 NP--YSAFQVDII 12  
||:|:|:|:  
Db 2 NPLGYGGFAVDVV 14

## RESULT 7

US-10-481-180-692  
; Sequence 692, Application US/10481180  
; Publication No. US20040171821A1  
; GENERAL INFORMATION:  
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
; APPLICANT: HUMAN SERVICES  
; APPLICANT: Valenzuela, Jesus G.  
; APPLICANT: Belkaid, Yasmine  
; APPLICANT: Kamhawi, Shaden  
; APPLICANT: Sacks, David  
; APPLICANT: Ribeiro, Jose M. C.  
; TITLE OF INVENTION: ANTI-ARTHOPOD VECTOR VACCINES, METHODS  
; TITLE OF INVENTION: OF SELECTING AND USES THEREOF  
; FILE REFERENCE: 4239-67347  
; CURRENT APPLICATION NUMBER: US/10/481,180  
; CURRENT FILING DATE: 2003-12-17  
; PRIOR APPLICATION NUMBER: PCT/US02/19663

; PRIOR FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: US 60/299,391  
; PRIOR FILING DATE: 2001-06-19  
; NUMBER OF SEQ ID NOS: 884  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 692  
; LENGTH: 19  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence; NOTE =  
; OTHER INFORMATION: Synthetic Construct  
US-10-481-180-692

Query Match 40.0%; Score 30; DB 16; Length 19;  
Best Local Similarity 46.2%; Pred. No. 2.2e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 2 NP--YSAFQVDII 12  
||:|:|:|:  
Db 2 NPLGYGGFAVDVV 14

## RESULT 8

US-10-106-698-7411  
; Sequence 7411, Application US/10106698  
; Publication No. US20030109690A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptid  
; FILE REFERENCE: PA005PI  
; CURRENT APPLICATION NUMBER: US/10/106,698  
; CURRENT FILING DATE: 2002-03-27  
; PRIOR APPLICATION NUMBER: PCT/US00/26524  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US 60/157,137  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: US 60/163,280  
; PRIOR FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 8564  
; SOFTWARE: PatentIn Ver. 3.0  
; SEQ ID NO 7411  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (20)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (22)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-106-698-7411

Query Match 40.0%; Score 30; DB 14; Length 22;  
Best Local Similarity 40.0%; Pred. No. 2.6e+02;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 YSAFQVDIIIV 13  
:|:|:|:  
Db 3 FGCFKIDIVV 12

## RESULT 9

US-10-481-180-714  
; Sequence 714, Application US/10481180  
; Publication No. US20040171821A1  
; GENERAL INFORMATION:  
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS  
; APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
; APPLICANT: HUMAN SERVICES  
; APPLICANT: Valenzuela, Jesus G.  
; APPLICANT: Belkaid, Yasmine

APPLICANT: Kamhawi, Shaden  
APPLICANT: Sacks, David  
APPLICANT: Ribeiro, Jose M. C.  
TITLE OF INVENTION: ANTI-ARTHOPOD VECTOR VACCINES, METHODS  
FILE REFERENCE: 4239-67347  
CURRENT FILING DATE: 2003-12-17  
PRIORITY FILING DATE: 2002-06-18  
PRIORITY FILING DATE: 2001-06-19  
NUMBER OF SEQ ID NOS: 884  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 714  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence; NOTE =  
OTHER INFORMATION: Synthetic Construct  
US-10-481-180-714

Query Match 40.0%; Score 30; DB 16; Length 23;  
Best Local Similarity 46.2%; Pred. No. 2.7e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 2 NP--YSAFQVDII 12  
||| |||  
Db 2 NPLGYGGFAVDVV 14

RESULT 10  
US-10-162-538-25  
Sequence 25, Application US/10162538  
Publication No. US20030113749A1  
GENERAL INFORMATION:  
APPLICANT: Brent, Roger  
McCoy, John M.  
Jessen, Timm H.  
Xu, Chanzing Wilson  
TITLE OF INVENTION: INTERACTION TRAP SYSTEMS FOR DETECTING  
PROTEIN INTERACTIONS  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/162,538  
FILING DATE: 04-Jun-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,052  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/504,538  
FILING DATE: July 20, 1995  
APPLICATION NUMBER: 08/278,082  
FILING DATE: July 20, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Karen F. Lech  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/311001  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 amino acids  
TYPE: amino acid  
STRANDEDNESS: No. US20030113749A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-10-162-538-25

Query Match 38.7%; Score 29; DB 14; Length 20;  
Best Local Similarity 62.5%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFQVD 10  
|:|:|  
Db 13 PHSVENVD 20

RESULT 11  
US-09-864-761-43921  
Sequence 43921, Application US/09864761  
Patent No. US20020048763A1  
GENERAL INFORMATION:  
APPLICANT: Penn, Sharron G.  
APPLICANT: Rank, David R.  
APPLICANT: Hanzel, David K.  
APPLICANT: Chen, Wenheng  
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
FILE REFERENCE: Aeomica-X-1  
CURRENT APPLICATION NUMBER: US/09/864,761  
CURRENT FILING DATE: 2001-05-23  
PRIOR APPLICATION NUMBER: US 60/180,312  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: US 60/207,456  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: US 09/632,366  
PRIOR FILING DATE: 2000-08-03  
PRIOR APPLICATION NUMBER: GB 24263.6  
PRIOR FILING DATE: 2000-10-04  
PRIOR APPLICATION NUMBER: US 60/236,359  
PRIOR FILING DATE: 2000-09-27  
PRIOR APPLICATION NUMBER: PCT/US01/00666  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00667  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00664  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00669  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00665  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00668  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00663  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00662  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00661  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: PCT/US01/00670  
PRIOR FILING DATE: 2001-01-30  
PRIOR APPLICATION NUMBER: US 60/234,687  
PRIOR FILING DATE: 2000-09-21  
PRIOR APPLICATION NUMBER: US 09/608,408  
PRIOR FILING DATE: 2000-06-30  
PRIOR APPLICATION NUMBER: US 09/774,203  
PRIOR FILING DATE: 2001-01-29  
NUMBER OF SEQ ID NOS: 49117



SOFTWARE: Annonax Sequence Listing Engine vers. 1.1  
SEQ ID NO 43921  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: MAP TO: AC006227.1  
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.72  
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71  
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.86  
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77  
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.61  
US-09-864-761-43921

Query Match 38.7%; Score 29; DB 9; Length 22;  
Best Local Similarity 54.5%; Pred. No. 4e+02;  
Matches 6; Conservative 1; Mismatches 0; Indels 4; Gaps 0;

Qy 1 SNPSAFQVDI 11  
Db 1 STPSSAFSVSL 11

RESULT 12  
US-09-880-748-3097  
Sequence 3097, Application US/09880748  
Publication No. US2003005937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3097  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-3097

Query Match 37.3%; Score 28; DB 10; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NPYSAFQV 9  
Db 3 SPYDAFDI 10

RESULT 13  
US-10-293-418-3097  
Sequence 3097, Application US/10293418  
Publication No. US20030223996A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PF523P2  
CURRENT APPLICATION NUMBER: US/10/293,418  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 3097  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-293-418-3097

Query Match 37.3%; Score 28; DB 14; Length 10;  
Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NPYSAFQV 9  
Db 3 SPYDAFDI 10

RESULT 14  
US-09-842-776A-30  
Sequence 30, Application US/09842776A  
Publication No. US20040023316A1  
GENERAL INFORMATION:  
APPLICANT: CONNEX GMBH  
TITLE OF INVENTION: NEW METHOD FOR DETECTING ACID-RESISTANT MICROORGANISMS  
FILE REFERENCE: 41735  
CURRENT APPLICATION NUMBER: US/09/842,776A  
CURRENT FILING DATE: 2002-08-15  
PRIOR APPLICATION NUMBER: PCT/EP99/08212  
PRIOR FILING DATE: 1999-10-29  
NUMBER OF SEQ ID NOS: 64  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 30  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
OTHER INFORMATION: Complementarity determining region (CDR3) of an  
OTHER INFORMATION: antibody heavy chain directed to a beta-urease  
OTHER INFORMATION: epitope (alternative sequence)  
US-09-842-776A-30

Query Match 37.3%; Score 28; DB 11; Length 13;  
Best Local Similarity 100.0%; Pred. No. 3.3e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNPYS 5  
Db 6 SNEYS 10

RESULT 15  
US-10-211-462-91  
Sequence 91, Application US/10211462  
Publication No. US20040033495A1  
GENERAL INFORMATION:  
APPLICANT: Murray, Richard  
APPLICANT: Glynn, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Aziz, Natasha

; APPLICANT: Eos Biotechnology, Inc.  
; TITLE OF INVENTION: Methods of Diagnosis of Angiogenesis, Compositions and  
; TITLE OF INVENTION: Methods of Screening for Angiogenesis Modulators  
; FILE REFERENCE: 018501-006200US  
; CURRENT APPLICATION NUMBER: US/10/211,462  
; CURRENT FILING DATE: 2003-02-13  
; PRIOR APPLICATION NUMBER: US 09/784,356  
; PRIOR FILING DATE: 2001-02-14  
; PRIOR APPLICATION NUMBER: US 09/791,390  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: US 60/310,025  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/334,244  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 230  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 91  
; LENGTH: 23  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-211-462-91

Query Match 37.3%; Score 28; DB 15; Length 23;  
Best Local Similarity 50.0%; Pred. NO. 6.3e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPSAFQVD 10  
Db 3 SIPYTVFQTN 12

Search completed: November 14, 2004, 12:26:59  
Job time : 35.4255 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 40.0532 Seconds  
(without alignments)  
215.479 Million cell updates/sec

Title: US-09-831-253F-4  
Perfect score: 75  
Sequence: 1 SNPYSAFQVDIIVIDI 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	38.7	18	2 Q9QV11	Q9qv11 rattus sp.
2	28	37.3	9	2 Q7RA82	Q7ra82 plasmodium
3	27	36.0	20	2 Q9QVB2	Q9qv2 mus sp. . s
4	26	34.7	12	2 Q9S550	Q9s550 streptococ
5	26	34.7	16	2 Q7R3P0	Q7rsp0 plasmodium
6	26	34.7	19	2 Q9QV10	Q9qv10 rattus sp.
7	26	34.7	22	2 Q7M0L1	Q7m0l1 clostridium
8	25	33.3	10	2 Q76WM5	Q76wm5 eurypharynx
9	25	33.3	10	2 BAB87140	Bab87140 euryphary
10	25	33.3	11	2 Q7M154	Q7m154 bacillus th
11	25	33.3	12	2 Q7XB05	Q7xb05 zea mays (m
12	25	33.3	13	2 Q7X761	Q7x761 zea mays (m
13	25	33.3	13	2 Q79A22	Q79a22 borrelia bu
14	25	33.3	14	2 P81801	P81801 streptomyc
15	25	33.3	17	2 Q7XB06	Q7xb06 zea mays (m
16	25	33.3	18	2 Q7XB07	Q7xb07 zea mays (m
17	25	33.3	20	2 Q69381	Q69381 human herpe
18	25	33.3	22	2 Q68988	Q68988 human herpe
19	24.5	32.7	20	2 Q8RIQ1	Q8riq1 mus musculu
20	24.5	32.7	21	2 Q9JK03	Q9jk03 mus musculu
21	24	32.0	8	2 Q91U19	Q91u19 influenza a
22	24	32.0	8	2 Q91U21	Q91u21 influenza a
23	24	32.0	16	2 Q7RGW0	Q7rgw0 plasmodium
24	24	32.0	16	2 Q9TQV6	Q9tqv6 oryctolagus
25	24	32.0	16	2 Q33429	Q33429 anas platyr
26	24	32.0	17	2 Q9UC43	Q9uc43 homo sapien
27	24	32.0	18	2 Q9R5G0	Q9r5g0 alcaligenes
28	24	32.0	21	2 Q7RRF7	Q7rrf7 plasmodium
29	24	32.0	22	2 Q7R7E7	Q7r7e7 plasmodium
30	24	32.0	22	2 Q7RLB6	Q7rlb6 plasmodium
31	24	32.0	22	2 Q9QV59	Q9qv59 cavia (guin

32 23.5 31.3 19 2 Q8SEP2 Q8sep2 genista tyr  
33 23.5 31.3 19 2 Q8SKW8 Q8skw8 genista val  
34 23.5 31.3 19 2 Q8SKX1 Q8skx1 genista gas  
35 23.5 31.3 19 2 Q8SKX3 Q8skx3 genista eph  
36 23.5 31.3 19 2 Q8SKX5 Q8skx5 genista dor  
37 23.5 31.3 19 2 Q8SKX7 Q8skx7 genista dem  
38 23.5 31.3 19 2 Q8SKX9 Q8skx9 genista cil  
39 23.5 31.3 21 2 Q7SHB6 Q7shb6 neurospora  
40 23 30.7 10 2 Q76WK9 Q76wk9 eurypharynx  
41 23 30.7 10 2 BAB87148 Bab87148 euryphary  
42 23 30.7 10 2 BAB87156 Bab87156 euryphary  
43 23 30.7 10 2 BAB87164 Bab87164 euryphary  
44 23 30.7 14 2 Q9R518 Q9r518 vibrio algi  
45 23 30.7 15 2 Q9F5B2 Q9fab2 silene aega

ALIGNMENTS

RESULT 1

Q9QV11 PRELIMINARY; PRT; 18 AA.  
AC Q9QV11;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Sucrase-alpha-dextrinase subunit beta, S-D subunit beta  
DE (Fragment).  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP MEDLINE=92031479; PubMed=1931964;  
RX Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;  
RT "Structural and functional correlates of sucrase-alpha-dextrinase in  
RT intact brush border membranes.";  
RL Biochemistry 30:10399-10408(1991).  
FT NON\_TER 1  
FT NON\_TER 18  
SQ SEQUENCE 18 AA; 2122 MW; 68FFIABA87B24E49 CRC64;

Query Match 38.7%; Score 29; DB 2; Length 18;  
Best Local Similarity 45.5%; Pred. No. 5.1e+02;  
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11  
||| |:::  
DB 5 SNPISELRVEV 15

RESULT 2

Q7RA82 PRELIMINARY; PRT; 9 AA.  
AC Q7RA82;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein (Fragment).  
GN Names=PY06620;  
OS Plasmodium yoelii Yoelii.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=73239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=17XNL;  
RX PubMed=12368865;  
RA Carlson J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,  
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,  
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,

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RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., White O.R.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.B., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW EMBL; AABL01002263; EAA18865.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1001 MW; 4687ASAB476455B7 CRC64;

Query Match 37.3%; Score 28; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5
DB 3 SNPYS 7

RESULT 3
Q9QVB2 ID Q9QVB2 PRELIMINARY; PRT; 20 AA.
AC Q9QVB2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Serine protease (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=93020730; PubMed=1404084;
RA Damjanov A., Damjanov I.;
RT "Isolation of serine protease from granulated metrial gland cells of
RT mice and rats with lectin from Dolichos biflorus.";
RL J. Reprod. Fertil. 95:679-684(1992).
SQ SEQUENCE 20 AA; 2290 MW; 0A304F61A22C50D CRC64;

Query Match 36.0%; Score 27; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAF 7
DB 11 SRPYNAF 17

RESULT 4
Q9S550 ID Q9S550 PRELIMINARY; PRT; 12 AA.
AC Q9S550;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE DexB (Fragment).
GN Name=dexB;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D39;
RX MEDLINE=99214122; PubMed=10198036;
RA Iannelli F., Pearce B.J., Pozzi G.,

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RT "The type 2 capsule locus of Streptococcus pneumoniae.";
RL J. Bacteriol. 181:2652-2654(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D39;
RA Pearce B.J., Iannelli F., Pozzi G.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026471; AAD10169.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1405 MW; 90A979D2B2B9CDDA CRC64;

Query Match 34.7%; Score 26; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYSAFOVDII 12
DB 3 PWDAPCVELL 12

RESULT 5
Q7RSP0 ID Q7RSP0 PRELIMINARY; PRT; 16 AA.
AC Q7RSP0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY00315;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteau M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwyl S.B.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.B., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW EMBL; AABL01000088; EAA22680.1; -.
SQ SEQUENCE 16 AA; 1979 MW; A87BC2C996760379 CRC64;

Query Match 34.7%; Score 26; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 YSAFOVDII 12
DB 3 YCRFSIDIL 11

RESULT 6
Q9QV10 ID Q9QV10 PRELIMINARY; PRT; 19 AA.
AC Q9QV10;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Sucrase-alpha-dextrinase subunit alpha, S-D subunit alpha

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DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92031479; PubMed=1931964;
RA Zhu J.S., Conklin K.A., Scheving L.A., Smith A.J., Gray G.M.;
RT "Structural and functional correlates of sucrose-alpha-dextrinase in
RT intact brush border membranes.";
RL Biochemistry 30:10399-10408(1991).
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2119 MW; C84537919B7149D1 CRC64;

Query Match 34.7%; Score 26; DB 2; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 YSAFQVDIIV 13
   ||| : : ||
Db 5 FSALEISLIV 14

RESULT 7
Q7MOL1 PRELIMINARY; PRT; 22 AA.
AC Q7MOL1
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Exoenzyme C3 (Fragment).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE.
RX MEDLINE=89338716; PubMed=2474453;
RA Toratani S., Yokosawa N., Yokosawa H., Ishii S.I., Oguma K.;
RT "Immuno-crossreactivity between botulinum neurotoxin type C1 or D and
RT exoenzyme C3.";
RL FEBS Lett. 252:83-87(1989).
DR PIR; S05236; S05236.
FT NON_TER 1
FT NON_TER 22
SQ SEQUENCE 22 AA; 2449 MW; C3A42F8BE7FF41E3 CRC64;

Query Match 34.7%; Score 26; DB 2; Length 22;
Best Local Similarity 45.5%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 SNPYSAFQVDI 11
   ||| : : ||
Db 3 SNTYQBFNTNI 13

RESULT 8
Q76MM5 PRELIMINARY; PRT; 10 AA.
AC Q76MM5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN Name=ND2;
OS Eurypharynx pelecyanoides (pelican eel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22967687; PubMed=12949142;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-
RT scale gene rearrangements originated within the eels.";
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046477; BAB87140.1; -.
DR GO; GO:0005739; Mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9
   ||| : ||
Db 2 NPYVMFLV 9

RESULT 9
BAB87140 PRELIMINARY; PRT; 10 AA.
AC BAB87140
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 2 (Fragment).
GN ND2.
OS Eurypharynx pelecyanoides (pelican eel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
OX NCBI_TaxID=55117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the Deep-Sea Gulper Eel Mitochondrial Genomes: Large-
RT Scale Gene Rearrangements Originated Within the Eels.";
RL Mol. Biol. Evol. 20:1917-1924(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046477; BAB87140.1; -.
KW Mitochondrion.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1261 MW; 357BFE29C682DB47 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NPYSAFQV 9
   ||| : ||
Db 2 NPYVMFLV 9

RESULT 10
Q7M154 PRELIMINARY; PRT; 11 AA.
AC Q7M154
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Paraportal crystal protein, wax moth-specific (Fragment).  
 OS Bacillus thuringiensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 ON NCBI\_TaxID=1428;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Chestukhina G.G., Kostina L.I., Zalunin I.A., Khodova O.M.,  
 RA Stepanov V.M.;  
 RT "Bacillus thuringiensis esp. galleriae simultaneously produces two  
 RT delta-endotoxins differing strongly in primary structure and  
 RT entomocidal activity";  
 RL FEBS Lett. 232:249-251(1988).  
 DR EMBL; S00616; S00616.1  
 FT NON\_TER 1  
 FT NON\_TER 11  
 SQ SEQUENCE 11 AA; 1237 MW; C6FF9BD6476444D CRC64;  
 Query Match 33.3%; Score 25; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 SNPYS 5  
 Db :|||  
 5 NNPYS 9  
 RESULT 11  
 Q7XB05 PRELIMINARY; PRT; 12 AA.  
 AC Q7XB05;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Phytoene synthase 2 (Fragment).  
 GN Name=psy2;  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 ON NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;  
 RX MEDLINE=22779048; PubMed=12897253;  
 RT "Contrasting effects of selection on sequence diversity and linkage  
 RT disequilibrium at two phytoene synthase loci";  
 RL Plant Cell 15:1795-1806(2003).  
 DR EMBL; AY300568; AAP5307.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 12  
 SQ SEQUENCE 12 AA; 1335 MW; 9B1E0AA00869C325 CRC64;  
 Query Match 33.3%; Score 25; DB 2; Length 12;  
 Best Local Similarity 54.5%; Pred. No. 1.8e+03;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SNPYSFAQVDI 11  
 Db :|||  
 1 SDTVSKFPVDI 11  
 RESULT 12  
 Q7X761 PRELIMINARY; PRT; 13 AA.  
 AC Q7X761;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Phytoene synthase 2 (Fragment).  
 GN Name=psy2;  
 OS Zea mays (Maize).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 ON NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;  
 RX MEDLINE=22779048; PubMed=12897253;  
 RT "Contrasting effects of selection on sequence diversity and linkage  
 RT disequilibrium at two phytoene synthase loci";  
 RL Plant Cell 15:1795-1806(2003).  
 DR EMBL; AY300568; AAP5331.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1449 MW; 9B1E0AA05615C325 CRC64;  
 Query Match 33.3%; Score 25; DB 2; Length 13;  
 Best Local Similarity 54.5%; Pred. No. 2e+03;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 SNPYSFAQVDI 11  
 Db :|||  
 2 SDTVSKFPVDI 12  
 RESULT 13  
 Q79A22 PRELIMINARY; PRT; 13 AA.  
 AC Q79A22;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE MoxR protein (Fragment).  
 GN Name=moxR;  
 OS Borrelia burgdorferi (Lyme disease spirochete).  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 ON NCBI\_TaxID=139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Old I.G.;  
 RC STRAIN=212;  
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X95868; CAA64970.1; -.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1484 MW; C7C2DF4CFD83A046 CRC64;  
 Query Match 33.3%; Score 25; DB 2; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 2e+03;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 5 SAFQVDIIVD 14  
 Db :|||  
 3 SGFQIDSEVE 12  
 RESULT 14  
 P81801 PRELIMINARY; PRT; 14 AA.  
 AC P81801;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Purpocycin-hydrolyzing enzyme (EC 3.-.-) (Fragment).  
 OS Streptomyces morookaensis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 ON NCBI\_TaxID=1970;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=JCM4673 / KCC S-0673;  
 RX PubMed=9538199;

RA Nishimura M., Matsuo H., Nakamura A., Sugiyama M.;  
 RT "Purification and Characterization of a puromycin-hydrolyzing enzyme  
 from blastoidin S-producing *Streptomyces morookaensis*.";  
 RL J. Biochem. 123:247-252(1998).  
 RN [2]  
 RP CHARACTERIZATION, AND FUNCTION.  
 RA Nishimura M., Matsuo H., Sugiyama M.;  
 RT "Blasticidin S-producing *Streptomyces morookaensis* possesses an enzyme  
 activity with hydrolyzes puromycin.";  
 RL FEMS Microbiol. Lett. 132:95-100(1995).  
 CC -|- FUNCTION: INACTIVATES PUROMYCIN BY CATALYZING THE HYDROLYSIS OF  
 CC THE AMIDE LINKAGE BETWEEN ITS AMINONUCLEOSIDE AND O-METHYL-L-  
 CC TYROSINE MOETIES. THE OPTIMUM PH IS 8.0 AND THE OPTIMAL  
 CC TEMPERATURE IS 45 DEGREES CELSIUS.  
 CC -|- FUNCTION: MAY HAVE AMINOPEPTIDASE ACTIVITY.  
 CC -|- ENZYME REGULATION: STIMULATED BY DTT. STRONGLY INHIBITED BY ZINC  
 CC ION, FERROUS ION, CUPRIC ION, MERCURY ION, N-BROMOSUCCINIMIDE AND  
 CC N-ETHYLMALEIMIDE. PARTIALLY INHIBITED BY COBALT ION.  
 CC -|- SUBUNIT: MONOMER.  
 CC -|- MISCELLANEOUS: HAS AN ISOELECTRIC POINT OF 6.4.  
 DR GO; GO:0004177; F:aminopeptidase activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 KW Aminopeptidase; Hydrolase.  
 FT NON\_TER 14 14  
 SQ SEQUENCE 14 AA; 1492 MW; 3F980730E45EF3D8 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 2.1e+03;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 PYSAFQVDI 11  
 Db 5 PYGAWQSPI 13

RESULT 15  
 Q7XB06 PRELIMINARY; PRT; 17 AA.  
 AC Q7XB06;  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Phytoene synthase 2 (Fragment).  
 GN Name=psy2;  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PI587132;  
 RX MEDLINE=22779048; PubMed=12897253;  
 RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;  
 RT "Contrasting effects of selection on sequence diversity and linkage  
 RT disequilibrium at two phytoene synthase loci.";  
 RL Plant Cell 15:1795-1806(2003).  
 DR EMBL; AY300558; AAF55297.1; -.  
 FT NON\_TER 1 1  
 FT NON\_TER 17 17  
 SQ SEQUENCE 17 AA; 1869 MW; 8EB5FAA056459674 CRC64;

Query Match 33.3%; Score 25; DB 2; Length 17;  
 Best Local Similarity 54.5%; Pred. No. 2.6e+03;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNPYSAFQVDI 11  
 Db 6 SDTVSKFPVDI 16

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 9.25532 Seconds  
(without alignments)  
155.938 Million cell updates/sec

Title: US-09-831-253F-4

Perfect score: 75

Sequence: 1 SNPYSAFQVDIIVIDI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0

Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	41.3	22	C39800	calcium-activated
2	31	41.3	23	PS0446	potassium channel
3	27	36.0	16	S16376	L-serine dehydrata
4	27	36.0	21	S69371	duodenase - bovine
5	26	34.7	22	S05236	exoenzyme C3 - Clo
6	25	33.3	11	S00616	paraagoral crystal
7	25	33.3	17	A58946	formylmethanofuran
8	25	33.3	23	A48968	exo-poly-alpha-gal
9	24	32.0	18	A45138	arsenite oxidase I
10	23	30.7	13	A54326	glandular kallikre
11	23	30.7	14	B44854	L-2,4-diaminobuty
12	22	29.3	12	A61360	vespakinin M - hor
13	22	29.3	15	PS0185	27K protein A 3.4/
14	22	29.3	15	A61612	allatostatin - tob
15	22	29.3	15	G24417	interphotoreceptor
16	22	29.3	16	A48301	glutamate-1-semial
17	22	29.3	17	A61334	trypsin (EC 3.4.21
18	22	29.3	18	S43834	brain-associated s
19	22	29.3	18	A61392	interphotoreceptor
20	22	29.3	19	D24417	hypothetical prote
21	22	29.3	20	A85659	interphotoreceptor
22	22	29.3	23	C24417	ig heavy chain CDR
23	21	28.0	11	P70229	ribosomal protein
24	21	28.0	12	S36899	unidentified 85K p
25	21	28.0	13	PC2369	protein QF200039 -
26	21	28.0	15	PA0061	D-galactose-bindin
27	21	28.0	15	S29174	ermG leader peptid
28	21	28.0	19	B26930	ig heavy chain DJ
29	21	28.0	19	PH1313	

interphotoreceptor  
lysophospholipase  
mast cell proteina  
probable transcrip  
ig heavy chain DJ  
ig heavy chain V r  
enamelin i - bovin  
MUC1 enhancer bind  
hypothetical prote  
NADH2 dehydrogenas  
methane monooxygen  
MHC class II histo  
pregnancy-specific  
glycosomal protein  
glycoprotein H-a -  
tubulin alpha-chai

ALIGNMENTS

RESULT 1

C39800

calcium-activated potassium channel, alternate exon B - fruit fly (Drosophila melanogaster)

C;Species: Drosophila melanogaster

C;Date: 27-Mar-1992 #sequence\_revision 27-Mar-1992 #text\_change 09-Jul-2004

C;Accession: C39800

R;Atkinson, N.S.; Robertson, G.A.; Ganetzky, B.

Science 253, 551-555, 1991

A;Title: A component of calcium-activated potassium channels encoded by the Drosophila

A;Reference number: A39800; MUID:91313401; PMID:1857984

A;Accession: C39800

A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A;Molecule type: mRNA

A;Residues: 1-22 <ATK>

A;Cross-references: UNIPROT:Q03720

C;Genetics:

A;Gene: FlyBase:slo

A;Cross-references: FlyBase:FBgn0003429

Query Match 41.3%; Score 31; DB 2; Length 22;

Best Local Similarity 44.4%; Pred. No. 46;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFQV 9

DB 6 ANPYAGYQL 14

RESULT 2

PS0446

potassium channel protein slo II - fruit fly (Drosophila melanogaster) (fragment)

C;Species: Drosophila melanogaster

C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 09-Jul-2004

C;Accession: PS0446

R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bon

Neuron 9, 209-216, 1992

A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs

A;Reference number: JH0697; MUID:92360298; PMID:1497890

A;Accession: PS0446

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-23 <ADB>

A;Cross-references: UNIPROT:Q03720

C;Genetics:

A;Gene: FlyBase:slo

A;Cross-references: FlyBase:FBgn0003429

C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match 41.3%; Score 31; DB 2; Length 23;

Best Local Similarity 44.4%; Pred. No. 48;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPYSAFOV 9  
Db 7 ANPYAGYQL 15

## RESULT 3

S16376  
L-serine dehydratase beta chain - Peptostreptococcus asaccharolyticus  
C:Species: Peptostreptococcus asaccharolyticus  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S16376  
R:Grabowski, R.; Buckel, W.  
Eur. J. Biochem. 199, 89-94, 1991  
A:Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat  
A:Reference number: S16224; MUID:91293139; PMID:2065681  
A:Accession: S16376  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-16 <EUR>  
A:Cross-references: UNIPROT:P33074

Query Match 36.0%; Score 27; DB 2; Length 16;  
Best Local Similarity 83.3%; Pred. No. 1.7e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YSAFOV 9  
Db 1 YSAFEV 6

## RESULT 4

S69371  
duodenase - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 09-Jul-2004.  
C:Accession: S69371  
R:Zamolodchikova, T.S.; Vorotyntseva, T.I.; Antonov, V.K.  
Eur. J. Biochem. 227, 866-872, 1995  
A:Title: Duodenase, a new serine protease of unusual specificity from bovine duodenal mu  
A:Reference number: S69371; MUID:95172075; PMID:7867648  
A:Accession: S69371  
A:Molecule type: protein  
A:Residues: 1-21 <ZAM>  
A:Cross-references: UNIPROT:Q9GLN2  
C:Superfamily: trypsin; trypsin homology

Query Match 36.0%; Score 27; DB 2; Length 21;  
Best Local Similarity 71.4%; Pred. No. 2.3e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPYSAF 7  
Db 11 SRPYMAF 17

## RESULT 5

S05236.  
exoenzyme C3 - Clostridium botulinum (fragment)  
C:Species: Clostridium botulinum  
C>Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S05236  
R:Toratani, S.; Yokosawa, N.; Yokosawa, H.; Ishii, S.I.; Oguma, K.  
FEBS Lett. 252, 83-87, 1989  
A:Title: Immuno-crossreactivity between botulinum neurotoxin type C1 or D and exoenzyme  
A:Reference number: S05236; MUID:89338716; PMID:2474453  
A:Accession: S05236  
A:Molecule type: protein  
A:Residues: 1-22 <TOR>  
A:Cross-references: UNIPROT:Q7M0U1

Query Match 34.7%; Score 26; DB 2; Length 22;  
Best Local Similarity 45.5%; Pred. No. 3.6e+02;

Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
QY 1 SNPYSAFOVDI 11  
Db 3 SNTYQEFNTNI 13

## RESULT 6

S00616  
parasporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain galleria:  
N:Alternate names: delta-endotoxin; parasporal crystal protein positive chain  
C:Species: Bacillus thuringiensis  
C>Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C:Accession: S00616  
R:Chetukhina, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.  
FEBS Lett. 232, 249-251, 1988  
A:Title: Bacillus thuringiensis ssp. galleriae simultaneously produces two delta-endotox  
A:Reference number: S00615  
A:Accession: S00616  
A:Molecule type: protein  
A:Residues: 1-11 <CHE>  
A:Cross-references: UNIPROT:Q7MI54  
C:Comment: This toxin is effective against the larvae of Galleria mellonella (greater wax  
C:Superfamily: parasporal crystal protein  
C:Keywords: delta-endotoxin

Query Match 33.3%; Score 25; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 2.5e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5  
Db 5 NNPS 9

## RESULT 7

AS8946  
formylmethanofuran dehydrogenase (EC 1.2.99.5) (molybdenum) chain C - Methanobacterium t  
N:Alternate names: formylmethanofuran dehydrogenase (molybdenum) chain B [misidentifica  
C:Species: Methanobacterium thermoautotrophicum  
C>Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 04-Feb-2000  
C:Accession: AS8946  
R:Hochheimer, A.; Schmitz, R.A.; Thauer, R.K.; Hedderich, R.  
Eur. J. Biochem. 234, 910-920, 1995  
A:Title: The tungsten formylmethanofuran dehydrogenase from Methanobacterium thermoaut  
A:Reference number: S63519; MUID:96163477; PMID:8575452  
A:Accession: AS8946  
A:Molecule type: protein  
A:Residues: 1-17 <HOC>  
A>Note: the authors identify this peptide as the amino terminus of chain B, but it appe  
C:Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin; oxidoreducta

Query Match 33.3%; Score 25; DB 2; Length 17;  
Best Local Similarity 41.7%; Pred. No. 4e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;.

QY 3 PYSAPQVDIIVD 14  
Db 6 PTSDPQIGLEAD 17

## RESULT 8

AS8968  
exo-poly-alpha-galacturonosidase (EC 3.2.1.82) - Clostridium thermosaccharolyticum (fra  
N:Alternate names: exo-poly-alpha-galacturonate hydrolase  
C:Species: Clostridium thermosaccharolyticum, Clostridium tartarivorum  
C>Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 06-Dec-1996  
C:Accession: A48968  
R:van Rijssel, M.; Gerwig, G.J.; Hansen, T.A.  
FEBS Lett. 252, 83-87, 1989  
A:Title: Isolation and characterization of an extracellular glycosylated protein comple  
A:Reference number: A48968; MUID:93243739; PMID:8481009  
A:Accession: A48968

A;Status: preliminary  
A;Molecule type: protein

A;Residues: 1-23 <VAM>

A;Note: sequence extracted from NCBI backbone (NCBIP:130462)

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 33.3%; Score 25; DB 2; Length 23;  
Best Local Similarity 57.1%; Pred. No. 5.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10  
|:|:|:  
Db 3 YAAPEYD 9

## RESULT 9

A45138  
arsenite oxidase II - Alcaligenes faecalis (fragment)

C;Species: Alcaligenes faecalis

C;Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: A45138

R;Anderson, G.L.; Williams, J.; Hille, R.

J. Biol. Chem. 267, 23674-23682, 1992

A;Title: The purification and characterization of arsenite oxidase from *Alcaligenes faecalis*

A;Reference number: A45138; MUID:93054722; PMID:1331097

A;Accession: A45138

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <AND>

A;Cross-references: UNIPROT:Q7SIF3; UNIPROT:Q9R5G0

A;Note: sequence extracted from NCBI backbone (NCBIP:118544)

Query Match 32.0%; Score 24; DB 2; Length 18;  
Best Local Similarity 33.3%; Pred. No. 6.5e+02;  
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 YSAFQVDIIVDI 15  
|:|:|:|:  
Db 5 YPACQVSVKNL 16

## RESULT 10

A54326  
glandular kallikrein-1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-Aug-1994 #sequence\_revision 18-Nov-1994 #text\_change 23-Mar-1995

C;Accession: A54326

R;Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.

Mol. Cell. Endocrinol. 76, 181-190, 1991

A;Title: Identification and androgen-regulated expression of two major human glandular kallikreins

A;Reference number: A54326; MUID:92324494; PMID:1726490

A;Accession: A54326

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-13 <RIE>

A;Experimental source: prostate

A;Note: sequence extracted from NCBI backbone (NCBIP:108060)

Query Match 30.7%; Score 23; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 6.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNPYS 5  
|:|:|:  
Db 2 SHPYS 6

## RESULT 11

B44854

L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.1) - *Vibrio alginolyticus* (fragment)

C;Species: *Vibrio alginolyticus*

C;Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: B44854; B41817

R;Yamamoto, S.; Tsuzaki, Y.; Tougou, K.; Shinoda, S.

J. Gen. Microbiol. 138, 1461-1465, 1992

A;Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from *Vibrio alginolyticus*

A;Reference number: A44854; MUID:92381494; PMID:1512577

A;Accession: B44854

A;Molecule type: protein

A;Residues: 1-14 <YAM>

A;Cross-references: UNIPROT:Q9R5I8

A;Note: sequence extracted from NCBI backbone (NCBIP:112332)

C;Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 30.7%; Score 23; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 7.4e+02;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SAFOVD 10  
|:|:|:  
Db 2 TAPEVD 7

## RESULT 12

A61360

vespakinin M - hornet (*Vespa mandarinia*)

C;Species: *Vespa mandarinia*

C;Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004

C;Accession: A61360

R;Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.

Chem. Pharm. Bull. 24, 2896-2897, 1976

A;Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the venom of the hornet (*Vespa mandarinia*)

A;Reference number: A61360; MUID:77114342; PMID:1017116

A;Accession: A61360

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <KIS>

A;Cross-references: UNIPROT:Q7M3T3

C;Superfamily: unassigned animal peptides

C;Keywords: hydroxyproline; venom

F;4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 29.3%; Score 22; DB 2; Length 12;  
Best Local Similarity 42.9%; Pred. No. 9.4e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 YSAFQVD 10  
|:|:|:  
Db 6 FSPFRID 12

## RESULT 13

PS0185

27K protein A 3.4/5 - rice (fragment)

C;Species: *Oryza sativa* (rice)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 24-Feb-1995

C;Accession: PS0185

R;Kamo, M.; Tsugita, A.

submitted to JIPID, June 1991

A;Reference number: PS0184

A;Accession: PS0185

A;Molecule type: protein

A;Residues: 1-15 <KAM>

Query Match 29.3%; Score 22; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 QVDIIIVDI 15  
|:|:|:  
Db 1 QXEYIIVDV 8

## RESULT 14

A61612

allatostatin - tobacco hornworm

C/Species: Manduca sexta (tobacco hornworm)  
C/Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C/Accession: A61612  
R/Kramer, S.J.; Toschi, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney, Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991  
A/Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta.  
A/Reference number: A61612; MUID:92052112; PMID:1946359

A/Accession: A61612  
A/Status: Preliminary  
A/Molecule type: protein  
A/Residues: 1-15 <KRA>  
A/Cross-references: UNIPROT:P42559  
C/Keywords: neuropeptide; pyrrolidone carboxylic acid  
F;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 29.3%; Score 22; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. NO. 1.2e+03;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYSAF 7  
|||  
Db 10 NPISCF 15

RESULT 15  
G24417  
interphotoreceptor retinoid-binding protein - hamster (fragment)  
N/Alternate names: interstitial retinol-binding protein  
C/Species: Cricetinae gen. sp. (hamster)  
C/Date: 21-May-1988 #sequence\_revision 21-May-1988 #text\_change 09-Jul-2004  
C/Accession: G24417  
R/Fong, S.L.; Cook, R.G.; Alvarez, R.A.; Liou, G.I.; Landers, R.A.; Bridges, C.D.B. FENS Lett. 205, 309-312, 1986  
A/Title: N-terminal sequence homologies in interstitial retinol-binding proteins from 10  
A/Reference number: A91365; MUID:86301171; PMID:3743780  
A/Accession: G24417  
A/Molecule type: protein  
A/Residues: 1-15 <FON>  
A/Cross-references: UNIPROT:P12655

Query Match 29.3%; Score 22; DB 2; Length 15;  
Best Local Similarity 33.3%; Pred. NO. 1.2e+03;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 FQVDIIVDI 15  
|||  
Db 7 FQPSLVLDI 15

Search completed: November 14, 2004, 12:03:11  
Job time : 10.2553 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 12:37:20 ; Search time 155 Seconds  
(without alignments)  
27.773 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 497672

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_23Sep04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63	100.0	12	3 AAY92947	Aay92947 Transform
2	63	100.0	12	3 AAY93008	Aay93008 Transform
3	58	92.1	12	3 AAY93009	Aay93009 Transform
4	50	79.4	11	3 AAY93094	Aay93094 Transform
5	48	76.2	12	3 AAY93093	Aay93093 Transform
6	37	58.7	12	3 AAY93007	Aay93007 Transform
7	36.5	57.9	9	3 AAY93096	Aay93096 Transform
8	36.5	57.9	9	3 AAY92949	Aay92949 Transform
9	35	55.6	7	3 AAY93095	Aay93095 Transform
10	35	55.6	12	3 AAY93010	Aay93010 Transform
11	31.5	50.0	9	3 AAY93097	Aay93097 Transform
12	29	46.0	7	2 AAW46010	Aaw46010 Peptide #
13	28	44.4	12	2 AAR86068	Aar86068 Anti-ELAM
14	28	44.4	12	2 AAR86065	Aar86065 Anti-ELAM
15	28	44.4	12	2 AAW26904	Aaw26904 ELAM-1 bi
16	28	44.4	12	2 AAW26900	Aaw26900 ELAM-1 bi
17	28	44.4	12	2 AAW26865	Aaw26865 ELAM-1 bi
18	28	44.4	12	2 AAW63875	Aaw63875 ELAM-1 pe
19	28	44.4	12	2 AAW63886	Aaw63886 ELAM-1 pe
20	28	44.4	12	2 AAW63878	Aaw63878 ELAM-1 pe
21	27	42.9	9	7 ADE67540	Ade67540 Human 161
22	27	42.9	10	7 ADE66432	Ade66432 Human 161
23	27	42.9	10	7 ADE67609	Ade67609 Human 161
24	27	42.9	10	7 ADE70007	Ade70007 Human 161
25	27	42.9	10	7 ADE67387	Ade67387 Human 161

26	27	42.9	10	7	AD569708	Ad569708 Human 161
27	26	41.3	9	4	AAM22800	Aam22800 HIV pepti
28	26	41.3	9	8	ADK08459	Adk08459 Human pap
29	26	41.3	9	8	ADK08095	Adk08095 Human pap
30	26	41.3	10	5	ABG34100	Abg34100 Antigenic
31	26	41.3	10	5	ABG34094	Abg34094 Antigenic
32	26	41.3	11	2	AAW13936	Aaw13936 CDR-3 fra
33	25	39.7	8	4	ABP14228	Abp14228 HIV A02 s
34	25	39.7	8	4	ABP19690	Abp19690 HIV B62 s
35	25	39.7	8	7	ADL17639	Adl17639 ERBIN PDZ
36	25	39.7	9	4	AAM22772	Aam22772 HIV pepti
37	25	39.7	9	4	AAM22747	Aam22747 HIV pepti
38	25	39.7	9	4	ABP16598	Abp16598 HIV A24 s
39	25	39.7	9	4	ABP14239	Abp14239 HIV A02 s
40	25	39.7	9	4	ABP18424	Abp18424 HIV B58 s
41	25	39.7	9	4	ABP22273	Abp22273 HIV A03 m
42	25	39.7	9	4	ABP11937	Abp11937 HIV A01 s
43	25	39.7	9	4	ABP19680	Abp19680 HIV B62 s
44	25	39.7	10	4	ABP19688	Abp19688 HIV B62 s
45	25	39.7	10	4	ABP14253	Abp14253 HIV A02 s

ALIGNMENTS

RESULT 1  
AAY92947  
ID AAY92947 standard; peptide; 12 AA.  
XX AAY92947;  
XX  
XX 08-NOV-2000 (first entry)  
XX  
XX Transforming growth factor inhibitory peptide #3.  
XX  
XX Hepatotropic; antagonist; transforming growth factor betai; TGF-b1;  
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
XX  
XX Homo sapiens.  
XX  
XX WO200031135-A1.  
XX  
XX 02-JUN-2000.  
XX  
XX 23-NOV-1999; 99WO-ES000375.  
XX  
XX 24-NOV-1998; 98ES-00002465.  
XX  
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
XX  
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
PI Borrás Cuesta F;  
XX  
XX WPI; 2000-411935/35.  
XX  
XX Peptides that antagonize binding of transforming growth factor betai,  
PT useful for treatment of liver disease, especially cirrhosis, are partial  
PT sequences of the factor or its receptors.  
XX  
XX Claim 4; Page 80; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
XX of transforming growth (TGF) factor betai (TGF-b1) to its receptor in  
XX vivo which have partial amino acid sequences identical, or similar, with  
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
XX examples of the peptides of the invention. The peptides act by  
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
XX they are inhibitors of stimulation of collagen synthesis in liver cells  
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the  
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or  
XX disease, specifically cirrhosis

```

XX
SQ      Sequence 12 AA;
      Query Match      100.0%; Score 63; DB 3; Length 12;
      Best Local Similarity 100.0%; Pred. No. 0.00011;
      Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TSLDATMIWTMM 12
      1 TSLDATMIWTMM 12
      |||||
Db      1 TSLDATMIWTMM 12
      1 TSLDATMIWTMM 12
      |||||

RESULT 2
AAY93008
ID      AAY93008 standard; peptide; 12 AA.
XX
AC      AAY93008;
XX
DT      08-NOV-2000 (first entry)
XX
XX      Transforming growth factor inhibitory peptide P54.
DE
KW      Hepatotrophic; antagonist; transforming growth factor beta1; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS      Rattus sp.
XX
PN      WO200031135-A1.
XX
PD      02-JUN-2000.
XX
PP      23-NOV-1999; 99WO-ES000375.
XX
PR      24-NOV-1998; 98ES-00002465.
XX
PA      (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI      Borras Cuesta F;
XX
PN      WPI; 2000-411935/35.
XX
PD      02-JUN-2000.
XX
PP      23-NOV-1999; 99WO-ES000375.
XX
PR      24-NOV-1998; 98ES-00002465.
XX
PA      (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI      Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI      Borras Cuesta F;
XX
PN      WPI; 2000-411935/35.
XX
PT      Peptides that antagonize binding of transforming growth factor beta1;
PT      useful for treatment of liver disease, especially cirrhosis, are partial
PT      sequences of the factor or its receptors.
XX
PS      Disclosure; Page 27; 86pp; Spanish.
XX
CC      The invention relates to synthetic peptides that antagonise the binding
CC      of transforming growth (TGF) factor beta1 (TGF-b1) to its receptor in
CC      vivo which have partial amino acid sequences identical, or similar, with
CC      those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC      examples of the peptides of the invention. The peptides act by
CC      competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC      they are inhibitors of stimulation of collagen synthesis in liver cells
CC      and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC      extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC      expression systems) encoding the peptides are used for treatment of liver
CC      disease, specifically cirrhosis
XX
SQ      Sequence 12 AA;
      Query Match      92.1%; Score 58; DB 3; Length 12;
      Best Local Similarity 100.0%; Pred. No. 0.00091;
      Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SLDATMIWTMM 12
      1 SLDATMIWTMM 11
      |||||
Db      1 SLDATMIWTMM 11
      1 SLDATMIWTMM 11
      |||||

RESULT 4
AAY93094
ID      AAY93094 standard; peptide; 11 AA.
XX
AC      AAY93094;
XX
DT      08-NOV-2000 (first entry)
XX
XX      Transforming growth factor inhibitory peptide P140.
DE
KW      Hepatotrophic; antagonist; transforming growth factor beta1; TGF-b1;
KW      competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW      extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX

```

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OS Homo sapiens.
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borras Cuesta F;
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Disclosure; Page 31; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis
XX
XX Sequence 11 AA;
XX
XX Query Match 79.4%; Score 50; DB 3; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.023;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 4 DATMIWTMM 12
XX Db 3 DATMIWTMM 11
XX
XX RESULT 5
XX AAY93093
XX AC AAY93093 standard; peptide; 12 AA.
XX
XX 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide P139.
XX
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Homo sapiens.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borras Cuesta F;
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Disclosure; Page 31; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with
XX those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
XX examples of the peptides of the invention. The peptides act by
XX competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
XX they are inhibitors of stimulation of collagen synthesis in liver cells
XX and inhibitors of synthesis of proteolytic enzymes able to degrade the
XX extracellular matrix. The peptides, their mimetopes and/or DNA (or
XX expression systems) encoding the peptides are used for treatment of liver
XX disease, specifically cirrhosis
XX
XX Sequence 12 AA.
XX
XX Query Match 76.2%; Score 48; DB 3; Length 12;
XX Best Local Similarity 100.0%; Pred. No. 0.058;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 TSLDAMTW 9
XX Db 1 TSLDAMTW 9
XX
XX RESULT 6
XX AAY93007
XX ID AAY93007 standard; peptide; 12 AA.
XX
XX AC AAY93007;
XX
XX 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide P53.
XX
XX Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;
XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;
XX extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Rattus sp.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
XX Borras Cuesta F;
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
XX useful for treatment of liver disease, especially cirrhosis, are partial
XX sequences of the factor or its receptors.
XX
XX Disclosure; Page 27; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
XX of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
XX vivo which have partial amino acid sequences identical, or similar, with

```

CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 12 AA;

Query Match 58.7%; Score 37; DB 3; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5,6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLDATMI 8  
 DB 5 TSLDATMI 12  
 |||||

RESULT 7  
 AAY93096  
 ID AAY93096 standard; peptide; 9 AA.  
 XX  
 AC AAY93096;  
 XX  
 DT 08-NOV-2000 (first entry)  
 XX  
 DE Transforming growth factor inhibitory peptide P142.  
 XX  
 KW Hepatotropic; antagonist; transforming growth factor betal; TGF- $\beta$ 1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200031135-A1.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 23-NOV-1999; 99WO-ES000375.  
 XX  
 PR 24-NOV-1998; 98ES-00002465.  
 XX  
 PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;  
 XX  
 XX WPI; 2000-411935/35.  
 XX  
 XX Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 XX  
 PS Disclosure; Page 31; 86pp; Spanish.  
 XX  
 XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF- $\beta$ 1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 9 AA;

Query Match 57.9%; Score 36.5; DB 3; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 TSLDATMIWTMM 12  
 DB 1 TSL---MIWTMM 9  
 |||||

RESULT 9  
 AAY93095  
 ID AAY93095 standard; peptide; 7 AA.  
 XX  
 AC AAY93095;  
 XX

Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 OY 1 TSLDATMIWTMM 12  
 DB 1 TSL---MIWTMM 9  
 |||||

RESULT 8  
 AAY92949  
 ID AAY92949 standard; peptide; 9 AA.  
 XX  
 AC AAY92949;  
 XX  
 DT 08-NOV-2000 (first entry)  
 XX  
 DE Transforming growth factor inhibitory peptide #5.  
 XX  
 KW Hepatotropic; antagonist; transforming growth factor betal; TGF- $\beta$ 1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200031135-A1.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 23-NOV-1999; 99WO-ES000375.  
 XX  
 PR 24-NOV-1998; 98ES-00002465.  
 XX  
 PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;  
 XX  
 XX WPI; 2000-411935/35.  
 XX  
 XX Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.  
 XX  
 PS Claim 6; Page 81; 86pp; Spanish.  
 XX  
 XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF- $\beta$ 1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 9 AA;

Query Match 57.9%; Score 36.5; DB 3; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 OY 1 TSLDATMIWTMM 12  
 DB 1 TSL---MIWTMM 9  
 |||||

RESULT 9  
 AAY93095  
 ID AAY93095 standard; peptide; 7 AA.  
 XX  
 AC AAY93095;  
 XX



```

DT 08-NOV-2000 (first entry)
XX Transforming growth factor inhibitory peptide P141.
DE
XX Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Homo sapiens.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 31; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX Sequence 7 AA;
SQ
XX
XX Query Match 55.6%; Score 35; DB 3; Length 7;
XX Best Local Similarity 100.0%; Pred. NO. 1.7e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 DATMIW 9
XX 1 DATMIW 6
XX
XX RESULT 10
XX AAY93010
XX ID AAY93010 standard; peptide; 12 AA.
XX
XX AC AAY93010;
XX
XX 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide P56.
XX
XX Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Rattus sp.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 31; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX Sequence 12 AA;
SQ
XX
XX Query Match 55.6%; Score 35; DB 3; Length 12;
XX Best Local Similarity 100.0%; Pred. NO. 13;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 7 MIWTMM 12
XX 1 MIWTMM 6
XX
XX RESULT 11
XX AAY93097
XX ID AAY93097 standard; peptide; 9 AA.
XX
XX AC AAY93097;
XX
XX 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide P143.
XX
XX Hepatotrophic; antagonist; transforming growth factor betal; TGF-b1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX Homo sapiens.
XX
XX WO200031135-A1.
XX
XX 02-JUN-2000.
XX
XX 23-NOV-1999; 99WO-ES000375.
XX
XX 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor betal,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 27; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX Sequence 12 AA;
SQ

```

PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

PS Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor beta1 (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their minetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis

XX Sequence 9 AA;

Query Match 50.0%; Score 31.5; DB 3; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 TSLDATMIWTMM 12  
 ||||| |||  
 Db 1 TSLDAT---TMM 9

RESULT 12

AAW46010  
 ID AAW46010 standard; peptide; 7 AA.

AC AAW46010;

XX 03-JUL-1998 (first entry)

XX Peptide #41 based on human SSTR 4 (residues 282-290).

XX Hormone; receptor; antibody; vaccine; immunogen; somatostatin; IGF;  
 KW insulin-like growth factor binding protein; IIGFBP; SSTR; diabetes;  
 KW somatostatin receptor; insulin-like growth factor.

XX Synthetic.

OS Homo sapiens.

XX WO9744352-A1.

XX 27-NOV-1997.

XX 22-MAY-1997; 97WO-AU000312.

XX 22-MAY-1996; 96AU-00009990.

XX (NORT-) NORTHSTAR BIOLOGICALS PTY LTD.

XX Gerraty NL, Westbrook SL, Kingston DJ;

XX WPI; 1998-018427/02.

XX New non-naturally occurring peptide(s) - which are based on portions of  
 PT somatostatin, somatostatin receptors and insulin-like growth factor  
 PT binding protein.

PS Disclosure; Page 9; 136pp; English.

XX Peptides AAW45983-W456025 are based on portions of somatostatin,  
 CC somatostatin receptors (SSTR) and insulin-like growth factor binding  
 CC proteins (IGFBP). They are capable of increasing weight gain, birth  
 CC weight, growth rates, milk production, levels of circulating insulin, IGF  
 CC -I and IGF-III, fibre production and muscle weight. They may be used to  
 CC modulate carbohydrate metabolism and in treatment of diabetes. The oil  
 CC carrier may be used for delivery of the peptides

SQ Sequence 7 AA;

Query Match 46.0%; Score 29; DB 2; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 1.7e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7  
 |||||  
 Db 1 TSLDATV 7

RESULT 13

AAR86068

ID AAR86068 standard; peptide; 12 AA.

AC AAR86068;

XX 21-JUN-1996 (first entry)

XX Anti-ELAM-1 binding peptide #45.

XX Peptide mimetic; endothelial leukocyte adhesion molecule; ELAM; selectin;  
 KW receptor; leukocyte; vascular wall; endothelium; extravasation;  
 KW inflammation; sialyl Lewis; cell surface glycoprotein; HL60 cell.

XX Synthetic.

XX WO9531210-A1.

XX 23-NOV-1995.

XX 11-MAY-1995; 95WO-US006315.

XX 11-MAY-1994; 94US-00241054.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Barrett RW, Cwiria SE, Dower WJ, Koller KJ, Lee J, Martens CL;  
 PI Ruhland-Fritsch B;

XX WPI; 1996-010687/01.

XX New peptide(s) that bind to endothelial leukocyte adhesion molecule 1 -  
 PT useful for treating inflammation and other B-selectin mediated diseases.

XX Disclosure; Page 8; 85pp; English.

XX Peptides AAR86024-R86236 are examples of peptides and their mimetics that  
 CC bind to endothelial leukocyte adhesion molecule (ELAM)-1. This molecule  
 CC is a member of the selectin family of receptors and is involved in  
 CC binding of leukocytes to the vascular endothelial wall prior to  
 CC extravasation of the leukocyte, e.g. to a site of inflammation. The  
 CC peptides bind pref. to E-selectin but may also bind L- or P-selectin, and  
 CC can be used to treat conditions mediated by E-selectin, e.g. inflammatory  
 CC conditions. The peptides have strong affinity for the selectin receptors  
 CC and inhibit the binding of the sialyl Lewis (SLe-x) part of cell surface  
 CC glycoproteins to E-selectin. The peptide are small, generally less than 2  
 CC KD, have an IC50 of up to 100 micromole against binding of HL60 cells to  
 CC ELAM-1, have one or more peptide linkages replaced by CH2OC(O)NR,  
 CC phosphonate, CH2SO2NR, CH2NR, CON(R6), or NHCONH linkages where R = H or  
 CC a lower alkyl and R6 = a lower alkyl. The peptides may also have  
 CC substituted N- and C-termini e.g. succinimido, N-benzoyloxycarbonyl or N-  
 CC lower alkyl cpds

XX Sequence 12 AA;

Query Match 44.4%; Score 28; DB 2; Length 12;  
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12  
 :|||  
 Db 7 LWTMM 11



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 12:45:20 ; Search time 187 Seconds  
(without alignments)  
36.922 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDAMIWMM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 4909

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	38.1	10	1 APE_CAPGI	P80474 capnocytoph
2	24	38.1	11	2 Q9UELO	Q9ue10 homo sapien
3	24	38.1	11	2 Q7MIU2	Q7mlu2 oryza sativ
4	20	31.7	10	1 LABA_JATMU	P13270 jatropa mu
5	20	31.7	10	2 Q7MIJ3	Q7mij3 spinacia ol
6	19	30.2	11	2 Q77896	Q77896 oreochromis
7	19	30.2	12	2 Q9UCR3	Q9ucr3 homo sapien
8	18	28.6	8	2 Q81VK3	Q81vk3 homo sapien
9	18	28.6	8	2 Q35835	Q35835 rattus sp.
10	18	28.6	9	2 Q9H3V3	Q9h3v3 homo sapien
11	18	28.6	9	2 Q38366	Q38366 bacterioph
12	18	28.6	9	2 Q801K0	Q801k0 illicura mil
13	18	28.6	9	2 Q801K1	Q801k1 chiroxipha
14	18	28.6	9	2 Q801K2	Q801k2 antilophia
15	18	28.6	10	2 Q7M501	Q7m501 aspergillus
16	18	28.6	10	2 Q8WTT4	Q8wt4 homo sapien
17	18	28.6	10	2 Q8SHB4	Q8shb4 furcifer ve
18	18	28.6	10	2 Q8SHH7	Q8shd7 furcifer ou
19	18	28.6	10	2 Q8SHC0	Q8shc0 furcifer la
20	18	28.6	10	2 Q8SHC3	Q8shc3 furcifer la
21	18	28.6	10	2 Q9ESU5	Q9esu5 mus musculu
22	18	28.6	11	2 Q78118	Q78118 oreochromis
23	18	28.6	11	2 Q78120	Q78120 oreochromis
24	18	28.6	12	2 Q6RA12	Q6ra12 homo sapien
25	18	28.6	12	2 Q9UBJ5	Q9ubj5 homo sapien
26	18	28.6	12	2 Q6RAB8	Q6rab8 pygathrix b
27	18	28.6	12	2 Q6RAB9	Q6rab9 pygathrix n
28	18	28.6	12	2 Q6RAC1	Q6rac1 erythrocebu
29	18	28.6	12	2 Q6RAC2	Q6rac2 macaca mula
30	18	28.6	12	2 Q6RAC3	Q6rac3 trachypithe
31	18	28.6	12	2 Q6RAC4	Q6rac4 trachypithe

32	18	28.6	12	2 Q6RAC5	Q6rac5 hylobates l
33	18	28.6	12	2 Q6RAC6	Q6rac6 hylobates h
34	18	28.6	12	2 Q6RAC9	Q6rac9 pongo pygma
35	18	28.6	12	2 Q6RAD3	Q6rad3 gorilla gor
36	18	28.6	12	2 Q6RAE2	Q6rae2 pan troglod
37	18	28.6	12	2 Q77889	Q77889 oreochromis
38	18	28.6	12	2 Q77890	Q77890 oreochromis
39	18	28.6	12	2 Q77891	Q77891 oreochromis
40	18	28.6	12	2 Q77920	Q77920 pseudotroph
41	18	28.6	12	2 AAS87900	Aas87900 homo sapi
42	18	28.6	12	2 AAS87901	Aas87901 homo sapi
43	18	28.6	12	2 AAS87902	Aas87902 homo sapi
44	18	28.6	12	2 AAS87903	Aas87903 homo sapi
45	18	28.6	12	2 AAS87904	Aas87904 homo sapi

ALIGNMENTS

RESULT 1  
APE\_CAPGI STANDARD; PRT; 10 AA.  
AC P80474;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Aminopeptidase (EC 3.4.11.-) (Fragment).  
OS Capnocytophaga gingivalis.  
OC Bacteria; Bacteroidetes; Flavobacteriales;  
OC Flavobacteriaceae; Capnocytophaga.  
OX NCBI\_TaxID=1017;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=ATCC 33624;  
RX MEDLINE=96118234; PubMed=8574402;  
RA Spratt D.A., Greenman J., Schafer A.G.;  
RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence factor.";  
RL Microbiology 141:3087-3093(1995).  
CC -!- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N-terminal amino acid residues but not N-terminal blocked ones.  
CC Optimum activity is measured at pH 7.5. May be important in the nutrition and pathogenesis of the organism in the human oral cavity.  
CC -!- COFACTOR: Requires magnesium or calcium.  
KW Aminopeptidase; Calcium; Direct protein sequencing; Hydrolase;  
KW Magnesium.  
FT NON\_TER 1 1  
FT NON\_TER 10 10  
SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 38.1%; Score 24; DB 1; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DATMIW 9  
DB 1 DYNMLW 6

RESULT 2  
Q9UELO PRELIMINARY; PRT; 11 AA.  
ID Q9UELO;  
AC Q9UELO;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Fas antigen (CD95 antigen) (Fragment).  
GN Name=CD95;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

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RN RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=9535401; PubMed=7543095;
RA Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
RA Nakanishi Y.;
RT "Transcription Stimulation of the Fas-encoding gene by nuclear factor
RT for interleukin-6 expression upon influenza virus infection.";
RL J. Biol. Chem. 270:18007-18012(1995).
[2]
RN RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Brauninger A., Wolf J., Hanemann M.L., Diehl V.,
RA Kuppers R., Rajewsky K.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[4]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kurth J., Pernio A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kuppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; D11968; BAA20850.1; -
DR EMBL; AJ279011; CAC35539.1; -
DR EMBL; AJ279012; CAC35540.1; -
DR EMBL; AJ279013; CAC35541.1; -
DR EMBL; AJ509179; CAD48929.1; -
DR EMBL; AJ509180; CAD48930.1; -
FT NON_TER 11
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 2;

QY 8 IWTMM 12
DB 4 IWTLL 8

RESULT 3
Q7M1U2 PRELIMINARY; PRT; 11 AA.
AC Q7M1U2;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Unidentified 5.7/35K protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA Komatsu S., Kajiwara H., Hirano H.;
RT "A rice protein library, a data-file of rice proteins separated by
RT two-dimensional electrophoresis.";
RL Theor. Appl. Genet. 86:935-942(1993).
DR PIR; PQ0731; PQ0731.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1319 MW; CBE97F0E53277362 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 5 ATMIW 9
DB 1 ATVMW 5

RESULT 4
LABA_JATMU STANDARD; PRT; 10 AA.
ID LABA_JATMU
AC P13270;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Labaditin.
OS Jatropha multifida (Physic nut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaceae;
OC Jatropha.
OX NCBI_TaxID=3996;
RN [1]
RP SEQUENCE.
RC TISSUE=LateX;
RA Koassi S., van der Sluis W.G., Boslens R., T'Hart L.A., Labadie R.P.;
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha
RT multifida L. (Euphorbiaceae). Isolation and sequence determination by
RT means of two-dimensional NMR.";
RL FEBS Lett. 256:91-96(1989).
CC -!- FUNCTION: Labaditin is an active peptide which inhibits the
CC classical pathway of complement activation in vitro. Activity
CC seems to be based on an interaction with C1.
CC -!- PTM: This is a cyclic peptide.
CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine
CC for treatment of infected wounds, skins infections and scabies.
KW Direct protein sequencing.
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 31.7%; Score 20; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.7e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 2;

QY 8 IWTM 11
DB 3 WVTV 6

RESULT 5
Q7M1J3 PRELIMINARY; PRT; 10 AA.
AC Q7M1J3;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Cystathionine gamma-synthase (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX MEDLINE=95142682; PubMed=7840669;
RA Ravanel S., Proux M., Douce R.;
RT "Methionine biosynthesis in higher plants. I. Purification and
RT characterization of cystathionine gamma-synthase from spinach
RT chloroplasts.";
RL Arch. Biochem. Biophys. 316:572-584(1995).
DR PIR; S69159; S69159.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 873 MW; D88458DDDDAB2CD CRC64;

Query Match 31.7%; Score 20; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.7e+03;
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Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLDATMI 8  
|:|:|  
Db 2 TAVDAAAI 9

RESULT 6  
O77896 PRELIMINARY; PRT; 11 AA.  
AC O77896;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DE MHC class II B locus 12 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCBI\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.,  
RT "Linkage relationships and haplotype polymorphism among cichlid MHC  
class II B loci."  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF050006; AAC41345.1; -.  
FT NON\_TER 1  
FT NON\_TER 11  
SQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;

Query Match 30.2%; Score 19; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.1e+04;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 WTMM 12  
|:|:  
Db 4 WSML 7

RESULT 7  
Q9UCR3 PRELIMINARY; PRT; 12 AA.  
AC Q9UCR3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE AUTOTAXIN (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92129337; PubMed=1733949;  
RA Stracke M.L., Kruttsch H.C., Unsworth E.J., Arestad A., Cioce V.,  
RA Schiffmann E., Liotta L.A.;  
RT "Identification, purification, and partial sequence analysis of  
RT autotaxin, a novel motility-stimulating protein."  
RL J. Biol. Chem. 267:2524-2529(1992).  
FT NON\_TER 1  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1493 MW; 433482B3F335A1A7 CRC64;

Query Match 30.2%; Score 19; DB 2; Length 12;  
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Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLD 4  
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Db 6 TSLD 9

RESULT 8  
Q8IVK3 PRELIMINARY; PRT; 8 AA.  
AC Q8IVK3;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Steerin2 (Fragment).  
GN Name=STERIN2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Feeters P.J., Verhasselt P., Moechars D.W., Luyten W.H.M.L.,  
RA Geysen J.J.G.H.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ488208; CAD32561.1; -.  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 1030 MW; E8A7245417737726 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 8;  
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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIW 9  
|:|:  
Db 1 MLW 3

RESULT 9  
O35835 PRELIMINARY; PRT; 8 AA.  
AC O35835;  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ORF1 protein.  
GN Name=ORF1;  
OS Rattus sp.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10118;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98008057; PubMed=9581555;  
RA Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;  
RT "Human and rat testis express two mRNA species encoding variants of  
RT NR1D convertase, a metalloendopeptidase of the insulinase family."  
RL Biochem. J. 327:773-779(1997).  
DR EMBL; X93208; CAA63695.1; -.  
SQ SEQUENCE 8 AA; 886 MW; EA7EA1B1ADC5A5B6 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 8;  
Best Local Similarity 60.0%; Pred. No. 1.8e+06;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 ATMIW 9  
|:|:  
Db 4 ATTCW 8

RESULT 10  
Q9H3Y3 PRELIMINARY; PRT; 9 AA.  
AC Q9H3Y3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DJ839B11.1 (Novel protein with a Kunitz/Bovine pancreatic trypsin
DE inhibitor domain and WAP-type (Whey Acidic Protein) 'four-disulfide
DE core' domains) (Fragment).
GN Name=dJ461P17.1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AL121778, CAB76844.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1036 MW; 2C417B01B412D1B3 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
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Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTM 11
DB 1 MWTV 4

RESULT 11
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AC Q38366;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E gene product (Fragment).
OS Bacteriophage phi-X174.
OC Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10847;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88118956; PubMed=2963134;
RA Buckley K.J., Hayashi M.;
RT "Role of premature translational termination in the regulation of
RT expression of the phi X174 lysis gene.";
RL J. Mol. Biol. 198.599-607(1987).
DR EMBL, X07809; CAA30668.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1207 MW; C093B37731B36412 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 WTM 11
DB 4 WTL 6

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AC Q801K0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Ilicura militaris (pin-tailed manakin).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Ilicura.
OX NCBI_TaxID=208056;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
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RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL, AY136617; AAN16894.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 WTM 11
DB 7 WTL 9

RESULT 13
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AC Q801K1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Chiroxiphia caudata.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Pipridae; Chiroxiphia.
OX NCBI_TaxID=196027;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL, AY136616; AAN16893.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;

Query Match 28.6%; Score 18; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 WTM 11
DB 7 WTL 9

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AC Q801K2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Beta fibrinogen (Fragment).
GN Name=beta fibrinogen;
OS Antilophia galeata (Helmeted manakin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Tyrannidae; Antilophia.
OX NCBI_TaxID=208054;
RN [1]
RP SEQUENCE FROM N.A.
RA Marini M.A., Hackett S.J.;
RT "A Multifaceted Approach to the Characterization of an Intergeneric
RT Hybrid Manakin (Pipridae) from Brazil.";
RL Auk 119:1114-1120(2002).
DR EMBL, AY136615; AAN16892.1; -.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 992 MW; 8620B378744AB1 CRC64;
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Query Match 28.6%; Score 18; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred.No. 1.8e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 WTM 11  
Db 7 WTL 9

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Q7M501 ID Q7M501 PRELIMINARY; PRT; 10 AA.  
AC Q7M501;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Polygalacturonase (EC 3.2.1.15) IV (Fragment).  
OS Aspergillus sp.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI\_TaxID=5065;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=93151962; PubMed=8427629;  
RA Stratilova E., Markovic O., Skrovinova D., Rexova-Benkova L.,  
RA Jorvall H.;  
RT "Pectinase Aspergillus sp. polygalacturonase: multiplicity,  
RT divergence, and structural patterns linking fungal, bacterial, and  
RT plant polygalacturonases.";  
RL J. Protein Chem. 12:15-22(1993).  
DR PIR; D61440; D61440.  
DR GO; GO:0004650; F:polygalacturonase activity; IEA.  
FT NON\_TER 1  
FT NON\_TER 10  
SQ SEQUENCE 10 AA; 959 MW; 845236CSA1A9D1AE CRC64;

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Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSLDA 5  
Db 6 TSADA 10

Search completed: November 14, 2004, 12:54:38  
Job time : 188 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model.  
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(without alignments)  
31.219 Million cell updates/sec

Title: US-09-831-253F-3  
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Searched: 1568699 seqs, 353819137 residues

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Maximum Match 100%  
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- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	46.0	7	9 US-09-758-128-41	Sequence 41, Appl
2	29	46.0	7	9 US-09-758-128-44	Sequence 44, Appl
3	29	46.0	7	9 US-09-758-426-41	Sequence 41, Appl
4	29	46.0	7	9 US-09-758-426-44	Sequence 44, Appl
5	29	46.0	7	9 US-09-758-198-41	Sequence 41, Appl
6	29	46.0	7	9 US-09-758-198-44	Sequence 44, Appl
7	29	46.0	7	10 US-09-861-661-41	Sequence 41, Appl
8	29	46.0	7	10 US-09-861-661-44	Sequence 44, Appl
9	27	42.9	10	14 US-10-062-109A-642	Sequence 642, App
10	27	42.9	10	14 US-10-062-109A-642	Sequence 642, App
11	26	41.3	9	15 US-10-182-252A-685	Sequence 685, App
12	25	39.7	8	14 US-10-190-082-602	Sequence 602, App
13	25	39.7	9	14 US-10-357-935-20	Sequence 20, Appl

14	25	39.7	9	15	US-10-182-252A-632	Sequence 632, App
15	25	39.7	9	15	US-10-182-252A-657	Sequence 657, App
16	25	39.7	9	15	US-10-182-252A-1216	Sequence 1216, Ap
17	25	39.7	10	14	US-10-200-708-79	Sequence 79, Appl
18	25	39.7	10	14	US-10-200-708-501	Sequence 501, App
19	25	39.7	11	10	US-09-758-109-7	Sequence 7, Appli
20	25	39.7	12	9	US-09-823-829-44	Sequence 44, Appl
21	25	39.7	12	9	US-09-840-277-69	Sequence 69, Appl
22	25	39.7	12	9	US-09-823-823-44	Sequence 44, Appl
23	25	39.7	12	15	US-10-609-217-151	Sequence 151, App
24	25	39.7	12	15	US-10-632-388-151	Sequence 151, App
25	25	39.7	12	15	US-10-651-723-151	Sequence 151, App
26	25	39.7	12	15	US-10-645-761-151	Sequence 151, App
27	25	39.7	12	15	US-10-666-696-151	Sequence 151, App
28	25	39.7	12	15	US-10-653-048-151	Sequence 151, App
29	24	38.1	7	15	US-10-651-165-170	Sequence 170, App
30	24	38.1	9	10	US-09-997-209-82	Sequence 82, Appl
31	24	38.1	9	15	US-10-182-252A-3	Sequence 3, Appli
32	24	38.1	9	15	US-10-182-252A-215	Sequence 215, App
33	24	38.1	9	15	US-10-182-252A-617	Sequence 617, App
34	24	38.1	9	15	US-10-182-252A-631	Sequence 631, App
35	24	38.1	9	15	US-10-182-252A-656	Sequence 656, App
36	24	38.1	9	15	US-10-182-252A-658	Sequence 658, App
37	24	38.1	9	15	US-10-433-206-82	Sequence 82, Appl
38	24	38.1	11	10	US-09-809-391-551	Sequence 551, App
39	24	38.1	11	10	US-09-882-171-551	Sequence 551, App
40	24	38.1	11	14	US-10-092-908-38	Sequence 38, Appl
41	24	38.1	11	14	US-10-164-861-551	Sequence 551, App
42	23	36.5	9	10	US-09-845-042-27	Sequence 27, Appl
43	23	36.5	9	14	US-10-062-109A-13	Sequence 13, Appl
44	23	36.5	9	14	US-10-005-480A-13	Sequence 13, Appl
45	23	36.5	9	15	US-10-182-252A-630	Sequence 630, App

ALIGNMENTS

RESULT 1

US-09-758-128-41  
; Sequence 41, Application US/09758128  
; Patent No. US20020107187A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020107187A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,128  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-128-41

Query Match 46.0%; Score 29; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TSLDATM 7  
Db 1 TSLDATV 7

RESULT 2

US-09-758-128-44

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; Sequence 44, Application US/09758128
; Patent No. US20020107187A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATTY, No. US20020107187A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,128
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-128-44

Query Match 46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 3
US-09-758-426-41
; Sequence 41, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATTY, No. US20020169116A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-426-41

Query Match 46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 4
US-09-758-426-44
; Sequence 44, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATTY, No. US20020169116A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-426-44

Query Match 46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 5
US-09-758-198-41
; Sequence 41, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATTY, No. US20020187925A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-02-05
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-198-41

Query Match 46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 6
US-09-758-198-44
; Sequence 44, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATTY, No. US20020187925A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF
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; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-44

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 7
US-09-861-661-41
; Sequence 41, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-861-661-41

Query Match          46.0%; Score 29; DB 10; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 8
US-09-861-661-44
; Sequence 44, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; APPLICANT: WESTBROOK, SIMON L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-44

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
Db 1 TSLDATV 7

RESULT 9
US-10-062-109A-642
; Sequence 642, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 642
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-642

Query Match          42.9%; Score 27; DB 14; Length 10;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLDATMIW 9
Db 1 TCVESTRIW 9

RESULT 10
US-10-005-480A-642
; Sequence 642, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
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; CURRENT FILING DATE: 2001-11-07  
; NUMBER OF SEQ ID NOS: 765  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 642  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-005-480A-642

Query Match 42.9%; Score 27; DB 14; Length 10;  
Best Local Similarity 44.4%; Pred. No. 2.9e+02;  
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 TSLDATMIW 9  
Db 1 TCVESTRIW 9

## RESULT 11

US-10-182-252A-685  
; Sequence 685, Application US/10182252A  
; Publication No. US20040072162A1  
; GENERAL INFORMATION:  
; APPLICANT: FOMSGAARD, ANDERS  
; APPLICANT: BRUNAK, SOREN  
; APPLICANT: BUUS, SOREN  
; APPLICANT: CORBET, SYLVIE  
; APPLICANT: LAUEMOLLER, SANNE LISE  
; APPLICANT: HANSEN, JAN  
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND  
; FILE REFERENCE: 030307/0205  
; CURRENT APPLICATION NUMBER: US/10/182,252A  
; CURRENT FILING DATE: 2003-04-10  
; PRIOR APPLICATION NUMBER: PCT/DK01/00059  
; PRIOR FILING DATE: 2001-01-29  
; PRIOR APPLICATION NUMBER: EP 00610017.6  
; PRIOR FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: US 60/179,333  
; PRIOR FILING DATE: 2000-01-31  
; NUMBER OF SEQ ID NOS: 1388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 685  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide  
US-10-182-252A-685

Query Match 41.3%; Score 26; DB 15; Length 9;  
Best Local Similarity 33.3%; Pred. No. 1.4e+06;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDATMIWTM 11  
Db 1 IQAIVWTV 9

## RESULT 12

US-10-190-082-602  
; Sequence 602, Application US/10190082  
; Publication No. US20030148264A1  
; GENERAL INFORMATION:  
; APPLICANT: Laeky, Lawrence A.  
; APPLICANT: Sidhu, Sachdev S.  
; APPLICANT: Held, Helke A.  
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
; FILE REFERENCE: E1905R1  
; CURRENT APPLICATION NUMBER: US/10/190,082  
; CURRENT FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/303,634  
; PRIOR FILING DATE: 2001-07-06

; NUMBER OF SEQ ID NOS: 683  
; SEQ ID NO 602  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-190-082-602

Query Match 39.7%; Score 25; DB 14; Length 8;  
Best Local Similarity 37.5%; Pred. No. 1.4e+06;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 DATMIWTM 11  
Db 1 DETSVWVL 8

## RESULT 13

US-10-357-935-20  
; Sequence 20, Application US/10357935  
; Publication No. US20030165958A1  
; GENERAL INFORMATION:  
; APPLICANT: HARDY, John Anthony  
; APPLICANT: GOATE, Alison Mary  
; APPLICANT: MULLAN, Michael John  
; APPLICANT: CHARTIER-HARLIN, Marie-Christine  
; APPLICANT: OWEN, Michael John  
; TITLE OF INVENTION: Test and Model for Alzheimer's Disease  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/357,935  
; FILING DATE: 03-Feb-2003  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,250  
; FILING DATE: 05-Jun-1995  
; APPLICATION NUMBER: 08/104,165  
; FILING DATE: 21-JAN-1992  
; APPLICATION NUMBER: 9101307.8  
; FILING DATE: 21-JAN-1991  
; APPLICATION NUMBER: 9118445.7  
; FILING DATE: 28-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joe  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 16163-000100  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-10-357-935-20

Query Match 39.7%; Score 25; DB 14; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.4e+06;

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 ATMIW 9
|:|:|
Db 2 ATVIW 6

RESULT 14
US-10-182-252A-632
; Sequence 632, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 632
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-632

Query Match 39.7%; Score 25; DB 15; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 5 ATMIWTM 11
|:|:|
Db 3 AIVVWTL 9

RESULT 15
US-10-182-252A-657
; Sequence 657, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 657
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-657

Query Match 39.7%; Score 25; DB 15; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 5 ATMIWTM 11
|:|:|
Db 3 AIVVWTL 9

Search completed: November 14, 2004, 13:06:28
Job time : 137 secs
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OM protein - protein search, using sw model

Run on: November 14, 2004, 12:46:25 ; Search time 36 Seconds  
(without alignments)  
22.106 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDWTMTMM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 130155

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	28	44.4	12	1	US-08-241-054-53
3	28	44.4	12	1	US-08-241-054-61
4	28	44.4	12	1	US-08-390-156A-22
5	28	44.4	12	1	US-08-390-156A-57
6	28	44.4	12	1	US-08-390-156A-61
7	28	44.4	12	1	US-08-439-817-30
8	28	44.4	12	1	US-08-439-817-33
9	28	44.4	12	1	US-08-439-817-41
10	28	44.4	12	1	US-08-485-508-50
11	28	44.4	12	1	US-08-485-508-53
12	28	44.4	12	1	US-08-485-508-61
13	27	42.9	10	3	US-08-396-385-9
14	27	42.9	10	3	US-09-287-221-9
15	25	39.7	9	2	US-08-104-165-20
16	25	39.7	9	3	US-08-464-250-20
17	25	39.7	9	3	US-08-464-250-20
18	25	39.7	11	2	US-08-319-052-7
19	25	39.7	11	3	US-08-442-108B-7
20	25	39.7	12	1	US-08-241-054-55
21	25	39.7	12	1	US-08-241-054-95
22	25	39.7	12	1	US-08-241-054-98
23	25	39.7	12	1	US-08-390-156A-45
24	25	39.7	12	1	US-08-390-156A-58
25	25	39.7	12	1	US-08-390-156A-87
26	25	39.7	12	1	US-08-439-817-35
27	25	39.7	12	1	US-08-439-817-75

28	39.7	12	1	US-08-439-817-78	Sequence 78, Appl
29	39.7	12	1	US-08-439-817-200	Sequence 200, Appl
30	39.7	12	1	US-08-485-508-55	Sequence 55, Appl
31	39.7	12	1	US-08-485-508-95	Sequence 95, Appl
32	39.7	12	1	US-08-485-508-98	Sequence 98, Appl
33	39.7	12	4	US-09-823-823-44	Sequence 44, Appl
34	39.7	12	4	US-09-428-082B-151	Sequence 151, Appl
35	39.7	12	4	US-08-635-886C-170	Sequence 170, Appl
36	38.1	7	4	US-08-974-690C-170	Sequence 170, Appl
37	38.1	7	4	US-08-974-685-170	Sequence 170, Appl
38	38.1	7	4	US-08-974-685-180	Sequence 180, Appl
39	38.1	9	4	US-08-466-601A-160	Sequence 160, Appl
40	38.1	11	4	US-09-149-476-551	Sequence 551, Appl
41	36.5	8	3	US-08-444-818-563	Sequence 563, Appl
42	36.5	8	3	US-08-444-818-564	Sequence 564, Appl
43	36.5	9	3	US-09-171-705-76	Sequence 76, Appl
44	36.5	10	2	US-08-617-929-24	Sequence 24, Appl
45	36.5	11	4	US-09-620-091-443	Sequence 443, Appl

## ALIGNMENTS

RESULT 1  
US-08-241-054-50  
; Sequence 50, Application US/08241054  
; Patent No. 5643873

## GENERAL INFORMATION:

; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Gerald F. Swiss  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-241-054-50

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 7 LWTMM 12  
DB 6 MLWNMM 11

## RESULT 2

US-08-241-054-53  
; Sequence 53, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gerald F. Swiss  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-002  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-241-054-53

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12  
DB :||||

DB 7 LWTMM 11

## RESULT 3

US-08-241-054-61  
; Sequence 61, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gerald F. Swiss  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-002  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-241-054-61

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12  
DB :||||

## RESULT 4

US-08-390-156A-22  
; Sequence 22, Application US/08390156A  
; Patent No. 5648458  
; GENERAL INFORMATION:  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Barrett, Ronald W.

APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
TITLE OF INVENTION: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 22:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-156A-22

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 7 MIWTMM 12  
Db 6 MLWNMM 11

RESULT 5  
US-08-390-156A-57  
Sequence 57, Application US/08390156A  
Patent No. 5648458  
GENERAL INFORMATION:  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
TITLE OF INVENTION: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 57:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-156A-57

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 IWTMM 12  
Db 7 LWTMM 11

RESULT 6  
US-08-390-156A-61  
Sequence 61, Application US/08390156A  
Patent No. 5648458  
GENERAL INFORMATION:  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
TITLE OF INVENTION: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A

```
/
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-496-2300
/ TELEFAX: 415-424-0832
/ INFORMATION FOR SEQ ID NO: 61:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-390-156A-61

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12
Db 7 LWTMM 11

RESULT 7
US-08-439-817-30
; Sequence 30, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
/
US-08-439-817-33

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

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/
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-439-817-30

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 MIWTMM 12
Db 6 MLWNMM 11

RESULT 8
US-08-439-817-33
; Sequence 33, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; TITLE OF INVENTION: Molecule I (ELAM-1)
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Affymax Technologies, NV
; STREET: 4001 Miranda Ave.
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,817
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/241,054
; FILING DATE: 11-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,295
; FILING DATE: 05-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/881,395
; FILING DATE: 06-MAY-1992
; NAME: Stevens, Lauren L.
; REGISTRATION NUMBER: 36,691
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-496-2300
; TELEFAX: 415-424-0832
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
/
US-08-439-817-33

Query Match 44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%; Pred. No. 1e+02;
```

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12  
:||||  
Db 7 LWTMM 11

## RESULT 9

US-08-439-817-41  
; Sequence 41, Application US/08439817  
; Patent No. 5728802  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I (ELAM-1)  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,817  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-439-817-41

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12  
:||||  
Db 7 LWTMM 11

## RESULT 10

US-08-485-508-50  
; Sequence 50, Application US/08485508  
; Patent No. 5786322  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I  
; NUMBER OF SEQUENCES: 162  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,508  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 000324-002/1056  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-485-508-50

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 MIWTMM 12  
:||||  
Db 6 MLNMM 11

## RESULT 11

US-08-485-508-53  
; Sequence 53, Application US/08485508  
; Patent No. 5786322  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.

APPLICANT: Cwirla, Steven E.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice  
TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule 1  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,508  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 000324-002/1056  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-485-508-53

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTTM 12  
DB 7 LWTMM 11

RESULT 12  
US-08-485-508-61  
Sequence 61, Application US/08485508  
Patent No. 5786322  
GENERAL INFORMATION:  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Dower, William J.  
APPLICANT: Koller, Kerry J.  
APPLICANT: Lee, Jung  
APPLICANT: Martens, Christine L.  
APPLICANT: Ruhland-Fritsch, Beatrice

TITLE OF INVENTION: Peptides and Compounds That Bind  
TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
TITLE OF INVENTION: Molecule 1  
NUMBER OF SEQUENCES: 162  
CORRESPONDENCE ADDRESS:  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,508  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Stevens, Lauren L.  
REGISTRATION NUMBER: 36,691  
REFERENCE/DOCKET NUMBER: 000324-002/1056  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 61:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-485-508-61

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTTM 12  
DB 7 LWTMM 11

RESULT 13  
US-08-396-385-9  
Sequence 9, Application US/08396385  
Patent No. 6001349  
GENERAL INFORMATION:  
APPLICANT: Schlom, Jeffrey  
APPLICANT: Panicali, Dennis  
TITLE OF INVENTION: GENERATION OF HUMAN CYTOTOXIC T-CELLS  
TITLE OF INVENTION: SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEWALL P. BRONSTEIN; DIKE, BRONSTEIN, ROBERTS  
ADDRESSEE: & CUSHMAN  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: US

;; ZIP: 02109  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/396,385  
;; FILING DATE:  
;; CLASSIFICATION: 530  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Resnick, David S.  
;; REGISTRATION NUMBER: 34,235  
;; REFERENCE/DOCKET NUMBER: 44933  
;; TELEPHONE: (617) 523-3400  
;; TELEFAX: (617) 523-6440  
;; TELEX: 200291 STRE UR  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown

Query Match 42.9%; Score 27; DB 3; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 DATMIW 9  
DB 3 DATYLM 8  
RESULT 14  
US-09-287-221-9  
Sequence 9, Application US/09287221  
Patent No. 6319496  
GENERAL INFORMATION:  
APPLICANT: Schlom, Jeffrey  
TITLE OF INVENTION: GENERATION OF HUMAN CYTOTOXIC T-CELLS  
SPECIFIC FOR CARCINOMA SELF-ASSOCIATED ANTIGENS AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEWALL P. BRONSTEIN; DIKE, BRONSTEIN, ROBERTS  
STREET: 130 WATER STREET  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: US  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/287,221  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/396,385  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 44933  
TELEPHONE: (617) 523-3400  
TELEFAX: (617) 523-6440

Query Match 42.9%; Score 27; DB 3; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 DATMIW 9  
DB 3 DATYLM 8

RESULT 15  
US-08-104-165-20  
Sequence 20, Application US/08104165  
Patent No. 5877015  
GENERAL INFORMATION:  
APPLICANT: HARDY, John Anthony  
APPLICANT: GOATE, Alison Mary  
APPLICANT: MULLAN, Michael John  
APPLICANT: CHARTIER-HARLIN, Marie-Christine  
APPLICANT: OWEN, Michael John  
TITLE OF INVENTION: Test and Model for Alzheimer's Disease  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourlie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/104,165  
FILING DATE: 21-JAN-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9101307.8  
FILING DATE: 21-JAN-1991  
APPLICATION NUMBER: 9118445.7  
FILING DATE: 28-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joe  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 16163-000100  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-104-165-20  
Query Match 39.7%; Score 25; DB 2; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 ATMIW 9  
DB 2 ATVIW 6

;; TELEX: 200291 STRE UR  
;; INFORMATION FOR SEQ ID NO: 9:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: unknown  
;; TOPOLOGY: unknown  
US-09-287-221-9  
Query Match 42.9%; Score 27; DB 3; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 DATMIW 9  
DB 3 DATYLM 8

RESULT 15  
US-08-104-165-20  
Sequence 20, Application US/08104165  
Patent No. 5877015  
GENERAL INFORMATION:  
APPLICANT: HARDY, John Anthony  
APPLICANT: GOATE, Alison Mary  
APPLICANT: MULLAN, Michael John  
APPLICANT: CHARTIER-HARLIN, Marie-Christine  
APPLICANT: OWEN, Michael John  
TITLE OF INVENTION: Test and Model for Alzheimer's Disease  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourlie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy Disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/104,165  
FILING DATE: 21-JAN-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 9101307.8  
FILING DATE: 21-JAN-1991  
APPLICATION NUMBER: 9118445.7  
FILING DATE: 28-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joe  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 16163-000100  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-104-165-20  
Query Match 39.7%; Score 25; DB 2; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 ATMIW 9  
DB 2 ATVIW 6

Search completed: November 14, 2004, 12:56:03  
Job time : 37 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 7.40425 seconds  
(without alignments)  
155.938 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	47.6	15	2 PH1612	Ig H chain V-D-J r
2	28	44.4	14	2 PH1625	Ig H chain V-D-J r
3	28	44.4	14	2 PH1627	Ig H chain V-D-J r
4	28	44.4	15	2 PH1613	Ig H chain V-D-J r
5	28	44.4	16	2 PH1637	Ig H chain V-D-J r
6	26	41.3	17	2 PH1331	Ig heavy chain DJ
7	25	39.7	17	2 PH1630	Ig H chain V-D-J r
8	25	39.7	22	2 PQ0007	killer toxin - yea
9	25	39.7	23	2 FC4030	rRNA endonuclease
10	24	38.1	11	2 PQ0731	unidentified 5.7/3
11	24	38.1	13	2 PH1636	Ig H chain V-D-J r
12	24	38.1	14	2 PH1594	Ig H chain V-D-J r
13	24	38.1	16	2 PH1638	Ig H chain V-D-J r
14	24	38.1	20	2 A44921	hydroxypyruvate re
15	24	38.1	22	2 S40838	ATF-43 protein - h
16	24	38.1	23	2 T03261	glutamate-ammonia
17	23.5	37.3	19	2 PH1315	Ig heavy chain DJ
18	23	36.5	13	2 PH1620	Ig H chain V-D-J r
19	23	36.5	14	2 A35105	hypothetical prote
20	23	36.5	20	2 PH1358	Ig heavy chain DJ
21	22	34.9	21	2 PH1602	Ig H chain V-D-J r
22	22	34.9	21	2 A44139	RNA-polymerase-ass
23	21.5	34.1	20	2 PH1380	alpha-amylase (EC
24	21	33.3	14	2 PH1327	Ig heavy chain DJ
25	21	33.3	20	2 PL0192	Ig lambda 2 chain
26	21	33.3	20	2 PH1326	Ig heavy chain DJ
27	20	31.7	10	2 S69159	cystathionine gamm
28	20	31.7	14	2 PH1626	Ig H chain V-D-J r
29	20	31.7	18	2 A32220	T-cell receptor de

cytochrome P450-C-  
L-lactate dehydrog  
probable trp opero  
thrABC leader pept  
T-cell receptor be  
Ig heavy chain DJ  
r cell receptor al  
Ig heavy chain DJ  
self-incompatibili  
major outer membra  
Ig heavy chain V r  
Ig heavy chain CDR  
polygalacturonase  
proton-translocati  
collecting duct wa  
aeg-46.5 protein -

ALIGNMENTS

RESULT 1

PH1612  
Ig H chain V-D-J region (wild-type clone 344) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1612

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic.

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1612

A;Molecule type: DNA

A;Residues: 1-15 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 47.6%; Score 30; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 13;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIWT 10

DB 9 EVTMLWT 15

RESULT 2

PH1625  
Ig H chain V-D-J region (clone B-less 109) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1625

R;Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic

A;Reference number: PH1580; MUID:93301609; PMID:8315387

A;Accession: PH1625

A;Molecule type: DNA

A;Residues: 1-14 <LEV>

A;Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 44.4%; Score 28; DB 2; Length 14;  
Best Local Similarity 80.0%; Pred. No. 29;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TMIWT 10

DB 10 TMLWT 14

RESULT 3

PH1627

Ig H chain V-D-J region (clone B-less 120) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1627

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1627

A:Molecule type: DNA

A:Residues: 1-14 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 44.4%; Score 28; DB 2; Length 14;

Best Local Similarity 80.0%; Pred. No. 29;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TWIWT 10

Db 10 TWLWT 14

#### RESULT 4

PH1613

Ig H chain V-D-J region (clone B-less 17) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1613

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1613

A:Molecule type: DNA

A:Residues: 1-15 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 44.4%; Score 28; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 32;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TWIWT 10

Db 11 TWLWT 15

#### RESULT 5

PH1637

Ig H chain V-D-J region (clone B-less 226) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1637

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1637

A:Molecule type: DNA

A:Residues: 1-16 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 44.4%; Score 28; DB 2; Length 16;

Best Local Similarity 80.0%; Pred. No. 34;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TWIWT 10

Db 12 TWLWT 16

#### RESULT 6

PH1331

Ig heavy chain DJ region (clone C148-106) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: PH1331

R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1331

A:Molecule type: DNA

A:Residues: 1-17 <WAS>

C:Keywords: heterotetramer; immunoglobulin

Query Match 41.3%; Score 26; DB 2; Length 17;

Best Local Similarity 44.4%; Pred. No. 89;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 SLDATMIWT 10

Db 3 TLRTTTWT 11

#### RESULT 7

PH1630

Ig H chain V-D-J region (clone B-less 156) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999

C:Accession: PH1630

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A:Reference number: PH1580; MUID:93301609; PMID:8315387

A:Accession: PH1630

A:Molecule type: DNA

A:Residues: 1-17 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 39.7%; Score 25; DB 2; Length 17;

Best Local Similarity 40.0%; Pred. No. 1.4e+02;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TSLDATMIWT 10

Db 8 TTYGRPLWT 17

#### RESULT 8

PQ0007

Killer toxin - yeast (Pichia farinosa) (fragment)

C:Species: Pichia farinosa

C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004

C:Accession: PQ0007

R:Suzuki, C.; Nikkuni, S.

Agric. Biol. Chem. 53, 2599-2604, 1989

A:Title: Purification and properties of the killer toxin produced by a halotolerant yeast

A:Reference number: PQ0007

A:Molecule type: protein

A:Residues: 1-22 <SUZ>

A:Cross-references: UNIPROT:P19372

A:Experimental source: strain KK1

A:Note: the full activity of this toxin depends on NaCl or KCl

Query Match 39.7%; Score 25; DB 2; Length 22;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIW 9

Db 2 EATTIW 7

## RESULT 9

PC4030  
rRNA endonuclease (EC 3.1.27.10) - shiitake mushroom (fragment)  
N:Alternate names: nuclease Le3  
C:Species: Lentinula edodes (shiitake mushroom)  
C:Date: 21-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: PC4030  
R:Kobayashi, H.; Inokuchi, N.; Koyama, T.; Tomita, M.; Irie, M.  
Biosci. Biotechnol. Biochem. 59, 1169-1171, 1995  
A:Title: Purification and characterization of the 2nd 5'-nucleotide-forming nuclease from *Lentinula edodes*  
A:Reference number: PC4030; MUID:95337563; PMID:7613009  
A:Accession: PC4030  
A:Molecule type: DNA  
A:Residues: 1-23 <KOB>  
A:Cross-references: UNIPROT:Q9UR71  
C:Comment: This enzyme has 3'-nucleotidase activity.  
C:Keywords: endonuclease; hydrolase

Query Match 39.7%; Score 25; DB 2; Length 23;  
Best Local Similarity 37.5%; Pred. No. 1.9e+02;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 SLDATMIW 9  
DB 16 ALDPSFVW 23

## RESULT 10

PQ0731  
unidentified 5.7/35K protein [imported] - rice (fragment)  
C:Species: Oryza sativa (rice)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: PQ0731  
R:Komatsu, S.; Kajiwara, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993  
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimensional gel electrophoresis  
A:Reference number: PQ0696  
A:Accession: PQ0731  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-11 <KOM>  
A:Cross-references: UNIPROT:Q7M1U2

Query Match 38.1%; Score 24; DB 2; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 ATMIW 9  
DB 1 ATVW 5

## RESULT 11

PH1636  
Ig H chain V-D-J region (clone B-less 224) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1636  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315387  
A:Accession: PH1636  
A:Molecule type: DNA  
A:Residues: 1-13 <LEV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 38.1%; Score 24; DB 2; Length 13;  
Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWT 10  
DB 10 MVWT 13

## RESULT 12

PH1594  
Ig H chain V-D-J region (wild-type clone 149) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1594  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315387  
A:Accession: PH1594  
A:Molecule type: DNA  
A:Residues: 1-14 <LEV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 38.1%; Score 24; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ATMIWT 10  
DB 9 ATGLWT 14

## RESULT 13

PH1638  
Ig H chain V-D-J region (clone B-less 228) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C:Accession: PH1638  
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A:Reference number: PH1580; MUID:93301609; PMID:8315387  
A:Accession: PH1638  
A:Molecule type: DNA  
A:Residues: 1-16 <LEV>  
A:Experimental source: bone marrow pre-B lymphocyte  
C:Keywords: immunoglobulin

Query Match 38.1%; Score 24; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 2e+02;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 TMWT 10  
DB 12 SMLWT 16

## RESULT 14

A44921  
hydroxypyruvate reductase (EC 1.1.1.81) - Methylobacterium extorquens (fragment)  
C:Species: Methylobacterium extorquens  
C:Date: 01-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: A44921  
R:Chistoserdova, L.V.; Lidstrom, M.E.  
J. Bacteriol. 174, 71-77, 1992  
A:Title: Cloning, mutagenesis, and physiological effect of a hydroxypyruvate reductase gene  
A:Reference number: A44921; MUID:92104992; PMID:1729225  
A:Contents: AM1  
A:Accession: A44921  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-20 <CHI>  
A:Cross-references: GB:M81443; NID:gl50010; PIDN:AAA25378.1; PID:gl50011  
A>Note: sequence extracted from NCBI backbone (NCBIN:75202, NCBIP:75203)

C;Keywords: oxidoreductase

Query Match 38.1%; Score 24; DB 2; Length 20;  
Best Local Similarity 83.3%; Pred. NO. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SLDATM 7  
|||:  
Db 12 SLDATV 17

RESULT 15

S40638  
ATP-43 protein - human (fragments)  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 10-Nov-1995  
C;Accession: S40638  
R;Hurst, H.C.; Totty, N.F.; Jones, N.C.  
Nucleic Acids Res. 19, 4601-4609, 1991  
A;Title: Identification and functional characterisation of the cellular activating trans-  
A;Reference number: S40638; MUID:91367654; PMID:1653949  
A;Accession: S40638  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-22 <HUR>

Query Match 38.1%; Score 24; DB 2; Length 22;  
Best Local Similarity 50.0%; Pred. NO. 2.9e+02;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TSLDATMIWT 10  
||| |:  
Db 12 TSLPQTIVVT 21

Search completed: November 14, 2004, 12:03:10  
Job time : 9.40425 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 32.0426 Seconds  
(without alignments)  
215.479 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 17482

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	39.7	18	2 Q9ZY81	Q9zy81 amitus sp.
2	25	39.7	18	2 Q9S817	Q9s817 oryza sativ
3	25	39.7	18	2 Q9S818	Q9s818 oryza sativ
4	25	39.7	20	2 Q9TWP7	Q9twp7 leishmania
5	25	39.7	23	2 Q9UR71	Q9ur71 leishmania
6	24	38.1	10	1 APE_CAPGI	P80474 capnocytoph
7	24	38.1	11	2 Q9UELO	Q9ue10 homo sapien
8	24	38.1	11	2 Q7MIU2	Q7miu2 oryza sativ
9	24	38.1	17	1 LPW_AZOB	P50871 azospirillum
10	24	38.1	17	2 Q6LDJ9	Q6ld19 rattus norv
11	24	38.1	17	2 Q6LEA8	Q6lea8 xenopus lae
12	24	38.1	17	2 AAA49911	Aaa49911 xenopus l
13	24	38.1	17	2 AAA41680	Aaa41680 rattus no
14	24	38.1	18	2 Q9ZYV8	Q9zyv8 aspirota sp
15	24	38.1	19	2 Q9ZYW5	Q9zyw5 jarra phoro
16	24	38.1	19	2 Q8W128	Q8w128 scaevola pr
17	24	38.1	20	2 Q49132	Q49132 methylobact
18	24	38.1	23	2 Q07939	Q07939 nicotiana t
19	23	36.5	16	2 Q8HUM0	Q8hum0 uncultured
20	23	36.5	16	2 Q8HUM1	Q8hum1 uncultured
21	23	36.5	17	2 Q69074	Q69074 human herpe
22	23	36.5	18	2 Q8ZS29	Q8zsz9 pyrobaculum
23	23	36.5	19	2 Q6PTX6	Q6ptx6 gallus gall
24	23	36.5	19	2 AAS90337	Aas90337 gallus ga
25	22	34.9	15	2 Q9TR62	Q9tr62 oryctolagus
26	22	34.9	19	2 Q9TRP4	Q9trp4 bos taurus
27	22	34.9	21	2 Q95N72	Q95n72 equus cabal
28	22	34.9	22	2 Q48861	Q48861 oryza sativ
29	22	34.9	22	2 Q8CI00	Q8ciq0 rattus norv
30	22	34.9	23	2 Q8HA22	Q8ha22 bacterioph
31	22	34.9	23	2 Q9R570	Q9r570 nitrosomona

Q9r5e8 bacillus sp  
Q9twc0 acanthamoeb  
Q9prf0 oryzias lat  
Q9zyv6 bethyridae  
Q6wa89 myxine glut  
Q865g9 actus azara  
Aaq63924 myxine gl  
Q93r63 yersinia pe  
P13270 jatrophia mu  
Q7mi13 spinacia ol  
Q6vfm5 photobacter  
Aar40451 photobact  
Aar40454 photobact  
Aas16489 photobact

## ALIGNMENTS

RESULT 1  
Q9ZV81 PRELIMINARY; PRT; 18 AA.  
AC Q9ZY81;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytochrome oxidase II (Fragment).  
OS Amitus sp.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Platygastridae;  
OC Platygastridae; Amitus.  
RN [1]\_TaxID=81080;  
RX SEQUENCE FROM N.A.  
RP MEDLINE=99152621; PubMed=10028295;  
RA Downton M., Austin A.D.;  
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in  
RL Mol. Biol. Evol. 16:298-309(1999).  
DR ENBL; AF082920; AAD17780.1; --  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1  
SQ SEQUENCE 18 AA; 2153 MW; 6480609B2C35EC7A CRC64;  
Query Match 39.7%; Score 25; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 1.4e+03;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 TSLDATMIWT 10  
DB 6 TSLNLFKWT 15  
RESULT 2  
Q9S817 PRELIMINARY; PRT; 18 AA.  
AC Q9S817;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE 40 kDa PI 8.5 ABCISSIC acid-induced histidine rich protein  
(Fragment).  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
RN [1]\_TaxID=4530;  
RX SEQUENCE.  
RP MEDLINE=95175599; PubMed=7870812;  
RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;

RT "Molecular and physiological responses to abscisic acid and salts in roots of salt-sensitive and salt-tolerant Indica rice varieties.";  
 RL Plant Physiol. 107:177-186(1995).  
 DR Gramene; Q9S817; -.  
 SQ SEQUENCE 18 AA; 2094 MW; 0CD245DB237E7520 CRC64;

Query Match 39.7%; Score 25; DB 2; Length 18;  
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIWT 10  
 | : : : |  
 Db 10 DESVLWT 16

RESULT 3  
 ID Q9S818 PRELIMINARY; PRT; 18 AA.  
 AC Q9S818;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE 40 kDa PI 8.5 ABSCESSIC acid-induced protein (Fragment).  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC, Ehrhartoideae; Oryzeae; Oryza.  
 OX, NCBI\_TaxID=4530;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95175599; PubMed=7870812;  
 RA Moons A., Bauw G., Prinsen E., Van Montagu M., Van der Straeten D.;  
 RT "Molecular and physiological responses to abscisic acid and salts in roots of salt-sensitive and salt-tolerant Indica rice varieties.";  
 RL Plant Physiol. 107:177-186(1995).  
 DR Gramene; Q9S818; -.  
 SQ SEQUENCE 18 AA; 2097 MW; 146450D9A97BE6D83 CRC64;

Query Match 39.7%; Score 25; DB 2; Length 18;  
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 DATMIWT 10  
 | : : : |  
 Db 10 DESVLWT 16

RESULT 4  
 ID Q9TWP7 PRELIMINARY; PRT; 20 AA.  
 AC Q9TWP7;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE Cathepsin B-like cysteine protease (Fragment).  
 OS Leishmania mexicana.  
 OC Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.  
 OX, NCBI\_TaxID=5665;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=94187801; PubMed=8139620;  
 RA Robertson C.D., Coombs G.H.;  
 RT "Cathepsin B-like cysteine proteases of Leishmania mexicana.";  
 RL Mol. Biochem. Parasitol. 62:271-279(1993).  
 SQ SEQUENCE 20 AA; 2203 MW; FE1A260FA1DBE41F CRC64;

Query Match 39.7%; Score 25; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SLDATMIWTM 11  
 | : : : |  
 Db 5 SPDASEKMPM 14

RESULT 5  
 ID Q9UR71 PRELIMINARY; PRT; 23 AA.

AC Q9UR71;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-MAY-2004 (TREMBlrel. 26, Last annotation update)  
 DE 5'-nucleotide-forming nuclease (Fragment).  
 OS Lentinula edodes (Shiitake mushroom) (Lentinus edodes).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Agaricales; Tricholomataceae; Lentinula.  
 OX, NCBI\_TaxID=5353;  
 RN [1]  
 RP SEQUENCE.

RX MEDLINE=95337563; PubMed=7613009;  
 RA Kobayashi H., Inokuchi N., Koyama T., Tomita M., Irie M.;  
 RT "Purification and characterization of the 2nd 5'-nucleotide-forming RT nuclease from Lentinus edodes.";  
 RL Biosci. Biotechnol. Biochem. 59:1169-1171(1995).  
 DR PIR; PC4030; PC4030.  
 DR InterPro; IPR008947; PLC Nuclease.  
 SQ SEQUENCE 23 AA; 2535 MW; 978082B3B161FCC6 CRC64;

Query Match 39.7%; Score 25; DB 2; Length 23;  
 Best Local Similarity 37.5%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 SLDATMIW 9  
 | : : : |  
 Db 16 ALDPSFVW 23

RESULT 6

APE CAPGI STANDARD; PRT; 10 AA.  
 ID\_APE\_CAPGI  
 AC P80474;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Aminopeptidase (EC 3.4.11.-) (Fragment).  
 OS Capnocytophaga gingivalis.  
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;  
 OC Flavobacteriaceae; Capnocytophaga.  
 OX, NCBI\_TaxID=1017;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=ATCC 33624;  
 RX MEDLINE=96118234; PubMed=8574402;  
 RA Spratt D.A., Greenman J., Schaffer A.G.;  
 RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence factor.";  
 RL Microbiology 141:3087-3093(1995).  
 CC -!- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N-terminal amino acid residues but not N-terminal blocked ones.  
 CC Optimum activity is measured at pH 7.5. May be important in the nutrition and pathogenesis of the organism in the human oral cavity.  
 CC -!- COFACTOR: Requires magnesium or calcium.  
 CC Aminopeptidase; Calcium; Direct protein sequencing; Hydrolase;

KW Magnesium.  
 FT NON\_TER 1 1  
 FT NON\_TER 10 10  
 SQ SEQUENCE 10 AA; 1306 MW; 00C0A6DB43772694 CRC64;

Query Match 38.1%; Score 24; DB 1; Length 10;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+03;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DATMIW 9  
 | : : : |  
 Db 1 DVNMLW 6

```

RESULT 7
Q9UELO PRELIMINARY; PRT; 11 AA.
AC Q9UELO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fas antigen (CD95 antigen) (Fragment).
GN Name=CD95;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX Wada N., Matsumura M., Ohba Y., Kobayashi N., Takizawa T.,
RA Nakanishi Y.;
RT "Transcription Stimulation of the Fas-encoding gene by nuclear factor
RT for interleukin-6 expression upon influenza virus infection.";
RL J. Biol. Chem. 270:18007-18012(1995).
RN [2];
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Brauning A., Wolf J., Hansmann M.L., Diehl V.,
RA Kuppers R., Rajewsky K.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [3];
RP SEQUENCE FROM N.A.
RA Muschen M., Re D., Jungnickel B., Diehl V., Rajewsky K., Kuppers R.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4];
RP SEQUENCE FROM N.A.
RX MEDLINE=22404279; PubMed=12516573;
RA Kurth J., Pernick A., Schmitz R., Iking-Konert C., Chiorazzi N.,
RA Thompson K.M., Winkler T., Rajewsky K., Kuppers R.;
RT "Lack of deleterious somatic mutations in the CD95 gene of
RT plasmablasts from systemic lupus erythematosus patients and
RT autoantibody-producing cell lines.";
RL Eur. J. Immunol. 32:3785-3792(2002).
DR EMBL; D31968; BAA20850.1; -
DR EMBL; AJ279011; CAC35539.1; -
DR EMBL; AJ279012; CAC35540.1; -
DR EMBL; AJ279013; CAC35541.1; -
DR EMBL; AJ509179; CAD48929.1; -
DR EMBL; AJ509180; CAD48930.1; -
FT NON_TER 11
SQ SEQUENCE 11 AA; 1256 MW; 0802145E2731B370 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 ITWM 12
Db 4 ITWL 8

RESULT 8
Q7MIU2 PRELIMINARY; PRT; 11 AA.
AC Q7MIU2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Unidentified 5.7/35K protein (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;

Query Match 38.1%; Score 24; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 ITWM 12
Db 4 ITWL 8

RESULT 9
LPW_AZOBR STANDARD; PRT; 17 AA.
AC P50871;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Trp operon leader peptide.
GN Name=trpL;
OS Azospirillum brasilense.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Azospirillum.
OX NCBI_TaxID=192;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=Sp7;
RX MEDLINE=97094331; PubMed=8939798;
RA de Troch P., Dosselaere F., Keijers V., de Wilde P., Vanderleyden J.;
RT "Isolation and characterization of the Azospirillum brasilense trpE(G)
RT gene, encoding anthranilate synthase.";
RL Curr. Microbiol. 34:27-32(1997).
CC -!- FUNCTION: This protein is involved in control of the biosynthesis
CC of tryptophan.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; U44127; AAC45140.1; -
DR Leader peptide; tryptophan biosynthesis.
SQ SEQUENCE 17 AA; 2114 MW; CD42DDEC3724BC9A CRC64;

Query Match 38.1%; Score 24; DB 1; Length 17;
Best Local Similarity 41.7%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 TSLDATMIWTMM 12
Db 6 TSLSCRWMPVM 17

RESULT 10
Q6LDD9 PRELIMINARY; PRT; 17 AA.
AC Q6LDD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).

```

GN Name=NCAM-C;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN NCBI\_TaxID=101116;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=90287121; PubMed=1694009;  
 RA Chen A., Reyes A., Akesson R.A.;  
 RT "Transcription initiation sites and structural organization of the  
 RT extreme 5' region of the rat neural cell adhesion molecule gene.";  
 RL Mol. Cell. Biol. 10:3314-3324(1990).  
 DR EMBL; M32612; AAA41680.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 17 AA; 2026 MW; AEA1EB5F25284F5 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTM 11  
 Db 7 LIWTL 11

RESULT 11  
 Q6LEA8 PRELIMINARY; PRT; 17 AA.  
 ID Q6LEA8  
 AC Q6LEA8  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Neural cell adhesion molecule (Fragment).  
 GN Name=NCAM;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Johnson A.D., Ovsenek N., Tonissen K.F., Krieg P.A.;  
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; L26396; AAA49911.1; -;  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTM 11  
 Db 7 LIWTL 11

RESULT 12  
 AAA49911 PRELIMINARY; PRT; 17 AA.  
 ID AAA49911  
 AC AAA49911  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Neural cell adhesion molecule (Fragment).  
 GN NCAM.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RA Johnson A.D., Ovsenek N., Tonissen K.F., Krieg P.A.;  
 RT "The Xenopus NCAM promoter: Appropriate expression in response to  
 RT neural inducing signals and identification of a conserved sequence  
 RT element.";  
 RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; L26396; AAA49911.1; -;  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTM 11  
 Db 7 LIWTL 11

RESULT 13  
 AAA41680 PRELIMINARY; PRT; 17 AA.  
 ID AAA41680  
 AC AAA41680  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Neural cell adhesion molecule (Fragment).  
 GN NCAM-C.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=101116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=90287121; PubMed=1694009;  
 RA Chen A., Reyes A., Akesson R.A.;  
 RT "Transcription initiation sites and structural organization of the  
 RT extreme 5' region of the rat neural cell adhesion molecule gene.";  
 RL Mol. Cell. Biol. 10:3314-3324(1990).  
 DR EMBL; M32612; AAA41680.1; -;  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 2026 MW; AEA1EB5F25284F5 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 17;  
 Best Local Similarity 60.0%; Pred. No. 2e+03;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTM 11  
 Db 7 LIWTL 11

RESULT 14  
 Q9ZYV8 PRELIMINARY; PRT; 18 AA.  
 ID Q9ZYV8  
 AC Q9ZYV8  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome oxidase II (Fragment).  
 OS Aspilota sp.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;  
 OC Braconidae; Alysiinae; Aspilota.  
 OX NCBI\_TaxID=61200;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99152621; PubMed=10028295;  
 RA Dowton M., Austin A.D.;  
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in  
 RT the hymenoptera.";  
 RL Mol. Biol. Evol. 16:298-309(1999).



DR EMBL; AF034603; AAC79751.1; -  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1 1  
 SQ SEQUENCE 18 AA; 2181 MW; F83846FDAEB8DCD6 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 18;  
 Best Local Similarity 62.5%; Pred. No. 2.1e+03;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 SLDATMIW 9  
 |||||  
 Db 7 SLKIFMIW 14

## RESULT 15

O9ZYW5 PRELIMINARY; PRT; 19 AA.  
 AC O9ZYW5;  
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome oxidase II (Fragment).  
 OS Jarra phorocantha.  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonoides;  
 OC Braconidae; Doryctinae; Jarra.  
 OX NCBI\_TaxID=64830;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99152621; PubMed=10028295;  
 RA Downton M., Austin A.D.;  
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in  
 the hymenoptera.";  
 RL Mol. Biol. Evol. 16:298-309(1999).  
 DR EMBL; AF034596; AAC79744.1; -  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1 1  
 SQ SEQUENCE 19 AA; 2291 MW; B964CCC7FDAC36C3 CRC64;

Query Match 38.1%; Score 24; DB 2; Length 19;  
 Best Local Similarity 41.7%; Pred. No. 2.2e+03;  
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 TSLDATMIWTMM 12  
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 Db 6 TSLNSFFNWLKM 17

Search completed: November 14, 2004, 12:07:29  
 Job time : 35.0426 secs

**This Page Blank (uspio)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:26 ; Search time 9.44681 Seconds  
(without alignments)  
84.242 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 202416

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCFUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	44.4	12	1	US-08-241-054-50
2	28	44.4	12	1	US-08-241-054-53
3	28	44.4	12	1	US-08-241-054-61
4	28	44.4	12	1	US-08-390-156A-22
5	28	44.4	12	1	US-08-390-156A-57
6	28	44.4	12	1	US-08-390-156A-61
7	28	44.4	12	1	US-08-439-817-30
8	28	44.4	12	1	US-08-439-817-33
9	28	44.4	12	1	US-08-439-817-41
10	28	44.4	12	1	US-08-485-508-50
11	28	44.4	12	1	US-08-485-508-53
12	28	44.4	12	1	US-08-485-508-61
13	28	44.4	13	1	US-07-920-519-12
14	28	44.4	13	1	US-08-086-410-9
15	28	44.4	13	1	US-08-314-586-12
16	27	42.9	10	3	US-08-396-385-9
17	27	42.9	10	3	US-09-287-221-9
18	26	41.3	15	4	US-09-255-501-106
19	26	41.3	15	4	US-09-255-501-107
20	25	39.7	9	2	US-08-104-165-20
21	25	39.7	9	3	US-08-464-250-20
22	25	39.7	9	3	US-08-464-250-20
23	25	39.7	11	2	US-08-319-052-7
24	25	39.7	12	1	US-08-442-108B-7
25	25	39.7	12	1	US-08-241-054-55
26	25	39.7	12	1	US-08-241-054-95
27	25	39.7	12	1	US-08-241-054-98

28	25	39.7	12	1	US-08-390-156A-45	Sequence 45, Appl
29	25	39.7	12	1	US-08-390-156A-58	Sequence 58, Appl
30	25	39.7	12	1	US-08-390-156A-87	Sequence 87, Appl
31	25	39.7	12	1	US-08-439-817-35	Sequence 35, Appl
32	25	39.7	12	1	US-08-439-817-75	Sequence 75, Appl
33	25	39.7	12	1	US-08-439-817-78	Sequence 78, Appl
34	25	39.7	12	1	US-08-439-817-200	Sequence 200, Appl
35	25	39.7	12	1	US-08-485-508-55	Sequence 55, Appl
36	25	39.7	12	1	US-08-485-508-95	Sequence 95, Appl
37	25	39.7	12	1	US-08-485-508-98	Sequence 98, Appl
38	25	39.7	12	4	US-09-823-823-44	Sequence 44, Appl
39	25	39.7	12	4	US-09-428-082B-151	Sequence 151, Appl
40	25	39.7	15	4	US-09-255-501-108	Sequence 108, Appl
41	25	39.7	20	1	US-08-382-013A-18	Sequence 18, Appl
42	25	39.7	20	1	US-08-241-054-81	Sequence 81, Appl
43	25	39.7	20	1	US-08-390-156A-38	Sequence 38, Appl
44	25	39.7	20	1	US-08-439-817-61	Sequence 61, Appl
45	25	39.7	20	1	US-08-485-508-81	Sequence 81, Appl

ALIGNMENTS

RESULT 1  
US-08-241-054-50  
; Sequence 50, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/241,054  
FILING DATE: 11-MAY-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Gerald F. Swiss  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 000324-002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-7400  
TELEFAX: 415-854-8275  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-241-054-50

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 1; Gaps 0;

QY 7 MLWTMM 12  
Db 6 MLWNMM 11

## RESULT 2

US-08-241-054-53  
; Sequence 53, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gerald F. Swiss  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-241-054-53

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12  
:||||

Db 7 LWTMM 11

## RESULT 3

US-08-241-054-61  
; Sequence 61, Application US/08241054  
; Patent No. 5643873  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelium Leukocyte Adhesion  
; NUMBER OF SEQUENCES: 169  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22313  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/241,054  
; FILING DATE: 11-MAY-1994  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gerald F. Swiss  
; REGISTRATION NUMBER: 30,113  
; REFERENCE/DOCKET NUMBER: 000324-002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-854-7400  
; TELEFAX: 415-854-8275  
; INFORMATION FOR SEQ ID NO: 61:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-241-054-61

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12  
:||||

Db 7 LWTMM 11

## RESULT 4

US-08-390-156A-22  
; Sequence 22, Application US/08390156A  
; Patent No. 5648458  
; GENERAL INFORMATION:  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Barrett, Ronald W.

APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
NUMBER OF SEQUENCES: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-424-0832  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-156A-22

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 7 MIWTMM 12  
Db 6 MLWNMM 11

RESULT 5  
US-08-390-156A-57  
Sequence 57, Application US/08390156A  
Patent No. 5648458  
GENERAL INFORMATION:  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
NUMBER OF SEQUENCES: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-496-2300  
TELEFAX: 415-424-0832  
INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-390-156A-57  
Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 8 IWTMM 12  
Db 7 LWTMM 11  
RESULT 6  
US-08-390-156A-61  
Sequence 61, Application US/08390156A  
Patent No. 5648458  
GENERAL INFORMATION:  
APPLICANT: Cwirla, Steven E.  
APPLICANT: Barrett, Ronald W.  
APPLICANT: Dower, William J.  
APPLICANT: Martens, Christine L.  
TITLE OF INVENTION: Peptides and Compounds That Bind to  
NUMBER OF SEQUENCES: ELAM-1  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Affymax Technologies, N.V.  
STREET: 4001 Miranda Ave.  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/390,156A  
FILING DATE: 16-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/057,295  
FILING DATE: 05-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/881,395  
FILING DATE: 06-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Swiss, Gerald F.  
REGISTRATION NUMBER: 30,113  
REFERENCE/DOCKET NUMBER: 1023.1A

```

, , TELECOMMUNICATION INFORMATION:
, ,
, , TELEPHONE: 415-496-2300
, , TELEFAX: 415-424-0832
, , INFORMATION FOR SEQ ID NO: 61:
, ,
, , SEQUENCE CHARACTERISTICS:
, , LENGTH: 12 amino acids
, , TYPE: amino acid
, , STRANDEDNESS: single
, , TOPOLOGY: linear
, , MOLECULE TYPE: peptide
, , US-08-390-156A-61

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Query Match      44.4%; Score 28; DB 1; Length 12;
Best Local Similarity 80.0%;
Matches 4; Conservative 1; Mismatches 0; Indels
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Qy 8 IWMM 12  
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Db 7 LWMM 11

```

RESULT 7
US-08-439-817-30
; Sequence 30, Application US/08439817
; Patent No. 5728802
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Cwirla, Steven E.
; APPLICANT: Dower, William J.
; APPLICANT: Koller, Kerry J.
; APPLICANT: Lee, Jung
; APPLICANT: Martens, Christine L.
; APPLICANT: Ruhland-Fritsch, Beatrice
; TITLE OF INVENTION: Peptides and Compounds That Bind
; TO AND/OR Inhibit Endothelial Leukocyte Adhesion
; MOLECULE I (ELAM-I)
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion
; MOLECULE I (ELAM-I)

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-439-817-30

Query Match          44.4%;      Score 28;   DB 1;   Length 12;
Best Local Similarity 66.7%;      Pred. No. 1e+02;
Matches 4;   Conservative 1;   Mismatches 1;   Indels

Qy      7  MIWTMM 12
      | | | |
Db      6  MLNNMM 11

```

RESULT 8  
 US-08-439-817-33  
 ; Sequence 33, Application US/08439817  
 ; Patent No. 5728802  
 ;  
 ; GENERAL INVENTION:  
 ;  
 ; APPLICANT: Barrett, Ronald W.  
 ; APPLICANT: Cwirla, Steven E.  
 ; APPLICANT: Dower, William J.  
 ; APPLICANT: Koller, Kerry J.  
 ; APPLICANT: Lee, Jung  
 ; APPLICANT: Martens, Christine L.  
 ; APPLICANT: Ruhland-Eritsch, Beatrice  
 ;  
 ; TITLE OF INVENTION: Peptides and Compounds That Bind  
 ; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
 ; TITLE OF INVENTION: Molecule I (ELAM-1)  
 ; NUMBER OF SEQUENCES: 209  
 ; CORRESPONDENCE ADDRESS:

Query Match	44.4%	Score 28; DB 1; Length 12;
. Best Local Similarity	80.0%	Pred. No. 1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12  
:||||  
Db 7 LWTMM 11

## RESULT 9

US-08-439-817-41  
; Sequence 41, Application US/08439817  
; Patent No. 5728802  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I (ELAM-1)  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/439,817  
; FILING DATE: 12-MAY-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 000324-046/1056.1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-439-817-41

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 IWTMM 12  
:||||  
Db 7 LWTMM 11

## RESULT 10

US-08-485-508-50  
; Sequence 50, Application US/08485508  
; Patent No. 5786322  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritsch, Beatrice  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Peptides and Compounds That Bind  
; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
; TITLE OF INVENTION: Molecule I  
; NUMBER OF SEQUENCES: 162  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Affymax Technologies, NV  
; STREET: 4001 Miranda Ave.  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,508  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/241,054  
; FILING DATE: 11-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/057,295  
; FILING DATE: 05-MAY-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/881,395  
; FILING DATE: 06-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stevens, Lauren L.  
; REGISTRATION NUMBER: 36,691  
; REFERENCE/DOCKET NUMBER: 000324-002/1056  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-496-2300  
; TELEFAX: 415-424-0832  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-485-508-50

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 66.7%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 MIWTMM 12  
:|:|:|  
Db 6 MLWNMM 11

## RESULT 11

US-08-485-508-53  
; Sequence 53, Application US/08485508  
; Patent No. 5786322  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.

;; APPLICANT: Cwirla, Steven B.  
;; APPLICANT: Dower, William J.  
;; APPLICANT: Koller, Kerry J.  
;; APPLICANT: Lee, Jung  
;; APPLICANT: Martens, Christine L.  
;; APPLICANT: Ruhland-Fritch, Beatrice  
;; TITLE OF INVENTION: Peptides and Compounds That Bind  
;; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
;; TITLE OF INVENTION: Molecule I  
;; NUMBER OF SEQUENCES: 162  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Affymax Technologies, NV  
;; STREET: 4001 Miranda Ave.  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION NUMBER: US/08/485,508  
;; FILING DATE: Herewith  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/241,054  
;; FILING DATE: 11-MAY-1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION NUMBER: US 08/057,295  
;; FILING DATE: 05-MAY-1993  
;; APPLICATION NUMBER: US 07/881,395  
;; FILING DATE: 06-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Stevens, Lauren L.  
;; REGISTRATION NUMBER: 36,691  
;; REFERENCE/DOCKET NUMBER: 000324-002/1056  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-496-2300  
;; TELEFAX: 415-424-0832  
;; INFORMATION FOR SEQ ID NO: 53:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-485-508-53

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12  
:||||  
DB 7 LWTMM 11

RESULT 12  
US-08-485-508-61  
; Sequence 61, Application US/08485508  
; Patent No. 5786322  
; GENERAL INFORMATION:  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven B.  
; APPLICANT: Dower, William J.  
; APPLICANT: Koller, Kerry J.  
; APPLICANT: Lee, Jung  
; APPLICANT: Martens, Christine L.  
; APPLICANT: Ruhland-Fritch, Beatrice

;; TITLE OF INVENTION: Peptides and Compounds That Bind  
;; TITLE OF INVENTION: Selectins Including Endothelial Leukocyte Adhesion  
;; TITLE OF INVENTION: Molecule I  
;; NUMBER OF SEQUENCES: 162  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Affymax Technologies, NV  
;; STREET: 4001 Miranda Ave.  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION NUMBER: US/08/485,508  
;; FILING DATE: Herewith  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/241,054  
;; FILING DATE: 11-MAY-1994  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION NUMBER: US 08/057,295  
;; FILING DATE: 05-MAY-1993  
;; APPLICATION NUMBER: US 07/881,395  
;; FILING DATE: 06-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Stevens, Lauren L.  
;; REGISTRATION NUMBER: 36,691  
;; REFERENCE/DOCKET NUMBER: 000324-002/1056  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-496-2300  
;; TELEFAX: 415-424-0832  
;; INFORMATION FOR SEQ ID NO: 61:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 12 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-485-508-61

Query Match 44.4%; Score 28; DB 1; Length 12;  
Best Local Similarity 80.0%; Pred. No. 1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IWTMM 12  
:||||  
DB 7 LWTMM 11

RESULT 13  
US-07-920-519-12  
; Sequence 12, Application US/07920519  
; Patent No. 5382518  
; GENERAL INFORMATION:  
; APPLICANT: CAPUT, DANIEL  
; APPLICANT: FERRARA, PASCUAL  
; APPLICANT: GUILLEMOT, JEAN-CLAUDE  
; APPLICANT: KAGHAD, MOURAD  
; APPLICANT: LEGOUX, RICHARD  
; APPLICANT: LOISON, GERARD  
; APPLICANT: LARBE, ELIZABETH  
; APPLICANT: LUPKER, JOHANNES  
; APPLICANT: LEPLATOIS, PASCUAL  
; APPLICANT: SALOME, MARK  
; TITLE OF INVENTION: URATE OXIDASE ACTIVITY PROTEIN,  
; TITLE OF INVENTION: RECOMBINANT GENE CODING THEREFOR, EXPRESSION VECTOR,  
; TITLE OF INVENTION: MICRO-ORGANISMS AND TRANSFORMED CELLS





;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/659,408  
;; FILING DATE: 25-APR-1991  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BENT, Stephen A.  
;; REGISTRATION NUMBER: 29,768  
;; REFERENCE/DOCKET NUMBER: 16781/509/BEDL  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (703)836-9300  
;; TELEFAX: (703)883-4109  
;; TELEX: 899149  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 13 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; HYPOTHETICAL: NO  
;; IMMEDIATE SOURCE:  
;; CLONE: Hydrolysis product T 28  
US-08-314-586-12

Query Match 44.4%; Score 28; DB 1; Length 13;  
Best Local Similarity 55.6%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TSLDATMIW 9  
| : || |  
Db 4 TDVDTWQW 12

Search completed: November 14, 2004, 12:08:47  
Job time : 10.4468 secs

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Original Use Only

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 14, 2004, 11:57:25 ; Search time 34.7234 Seconds  
(without alignments)  
123.973 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 718658

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23sep04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	63	100.0	12	3 AAY92947	Aay92947 Transform
2	63	100.0	12	3 AAY93008	Aay93008 Transform
3	58	92.1	12	3 AAY93009	Aay93009 Transform
4	50	79.4	11	3 AAY93094	Aay93094 Transform
5	50	79.4	14	3 AAY93098	Aay93098 Transform
6	50	79.4	14	3 AAY92950	Aay92950 Transform
7	48	76.2	12	3 AAY93093	Aay93093 Transform
8	37	58.7	12	3 AAY93007	Aay93007 Transform
9	36.5	57.9	9	3 AAY93096	Aay93096 Transform
10	36.5	57.9	9	3 AAY92949	Aay92949 Transform
11	35	55.6	7	3 AAY93095	Aay93095 Transform
12	35	55.6	12	3 AAY93010	Aay93010 Transform
13	31.5	50.0	9	3 AAY93097	Aay93097 Transform
14	31	49.2	14	4 AAB88161	Aab88161 CD66 pept
15	31	49.2	20	7 ADC99257	Adc99257 Cancer-re
16	30	47.6	13	4 AAU05001	Aau05001 N-termina
17	30	47.6	13	5 AAU06061	Aau06061 Human glu
18	30	47.6	16	7 ADF69672	Adf69672 Trpzip pe
19	29	46.0	7	2 AAW46010	Aaw46010 Peptide #
20	29	46.0	16	7 ADF69670	Adf69670 Trpzip pe
21	29	46.0	18	2 AAW69116	Aaw69116 Neuronal
22	28	44.4	12	2 AAR86068	Aar86068 Anti-ELAM
23	28	44.4	12	2 AAR86065	Aar86065 Anti-ELAM
24	28	44.4	12	2 AAW26904	Aaw26904 ELAM-1 b1
25	28	44.4	12	2 AAW26900	Aaw26900 ELAM-1 b1

## ALIGNMENTS

RESULT 1

AA92947

ID AAY92947 standard; peptide; 12 AA.

XX AC AAY92947;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide #3.

XX KW Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Homo sapiens.

XX PN WO2000311135-Al.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

(CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
Borras Cuesta F;

WPI; 2000-411935/35.

Peptides that antagonize binding of transforming growth factor betal,  
useful for treatment of liver disease, especially cirrhosis, are partial  
sequences of the factor or its receptors.

Claim 4; Page 80; 86pp; Spanish.

The invention relates to synthetic peptides that antagonise the binding  
of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
vivo which have partial amino acid sequences identical, or similar, with  
those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
examples of the peptides of the invention. The peptides act by  
competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
they are inhibitors of stimulation of collagen synthesis in liver cells  
and inhibitors of synthesis of proteolytic enzymes able to degrade the  
extracellular matrix. The peptides, their mimetopes and/or DNA (or  
expression systems) encoding the peptides are used for treatment of liver  
disease, specifically cirrhosis

Aaw26865 ELAM-1 b1  
Aaw3875 ELAM-1 pe  
Aaw3886 ELAM-1 pe  
Aaw3878 ELAM-1 pe  
Aar13972 [Asp14]Me  
Aau06698 Peptide r  
Abj38668 VH-CDR3 p  
Ada89077 Human c1o  
Adg74329 Human VH-  
Ade7540 Human 161  
Ade66432 Human 161  
Ade7609 Human 161  
Ade70007 Human 161  
Ade67387 Human 161  
Ade69708 Human 161  
Aab88091 CD66 pept  
Ade70131 Human 161  
Ade70548 Human 161  
Ade70592 Human 161

26 28 44.4 12 2 AAW26865  
27 28 44.4 12 2 AAW3875  
28 28 44.4 12 2 AAW3886  
29 28 44.4 12 2 AAW3878  
30 28 44.4 15 2 AAR13972  
31 28 44.4 15 2 AAR61463  
32 28 44.4 17 4 AAU06698  
33 28 44.4 17 6 ABJ38668  
34 28 44.4 17 6 ADA89077  
35 28 44.4 17 7 ADG74329  
36 27 42.9 9 7 ADE7540  
37 27 42.9 10 7 ADE66432  
38 27 42.9 10 7 ADE7609  
39 27 42.9 10 7 ADE70007  
40 27 42.9 10 7 ADE67387  
41 27 42.9 10 7 ADE69708  
42 27 42.9 14 4 AAB88091  
43 27 42.9 15 7 ADE70131  
44 27 42.9 15 7 ADE70548  
45 27 42.9 15 7 ADE70592

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XX SQ Sequence 12 AA;
Query Match 100.0%; Score 63; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TSLDATMIWTMM 12
Db 1 TSLDATMIWTMM 12
|||||

RESULT 2
AAV93008
ID AAY93008 standard; peptide; 12 AA.
XX
AC AAY93008;
XX
DT 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide P54.
XX
DE Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
OS Rattus sp.
XX
PN WO200031135-A1.
XX
PD 02-JUN-2000.
XX
PF 23-NOV-1999; 99WO-ES000375.
XX
PR 24-NOV-1998; 98ES-00002465.
XX
XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.
XX
PI Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;
PI Borrás Cuesta F;
XX
XX WPI; 2000-411935/35.
XX
XX Peptides that antagonize binding of transforming growth factor beta1,
PT useful for treatment of liver disease, especially cirrhosis, are partial
PT sequences of the factor or its receptors.
XX
XX Disclosure; Page 27; 86pp; Spanish.
XX
XX The invention relates to synthetic peptides that antagonise the binding
CC of transforming growth (TGF) factor beta1 (TGF-beta1) to its receptor in
CC vivo which have partial amino acid sequences identical, or similar, with
CC those of TGF-beta1 and/or its receptors. Peptides AAY92945-Y93133 represent
CC examples of the peptides of the invention. The peptides act by
CC competitive inhibition of the binding of TGF-beta1 to its receptors, e.g.
CC they are inhibitors of stimulation of collagen synthesis in liver cells
CC and inhibitors of synthesis of proteolytic enzymes able to degrade the
CC extracellular matrix. The peptides, their mimetopes and/or DNA (or
CC expression systems) encoding the peptides are used for treatment of liver
CC disease, specifically cirrhosis
XX
XX Sequence 12 AA;
Query Match 92.1%; Score 58; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 SLDATMIWTMM 12
Db 1 SLDATMIWTMM 11
|||||

RESULT 4
AAV93094
ID AAY93094 standard; peptide; 11 AA.
XX
AC AAY93094;
XX
DT 08-NOV-2000 (first entry)
XX
XX Transforming growth factor inhibitory peptide P140.
XX
DE Hepatotropic; antagonist; transforming growth factor beta1; TGF-beta1;
KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;
KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.
XX
XX

```



CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX  
 SQ Sequence 14 AA;

Query Match 79.4%; Score 50; DB 3; Length 14;  
 Best Local Similarity 75.0%; Pred. No. 0.03;  
 Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TSLDATMIWTMM 12  
 |||||:||||  
 DB 1 TSLDASIIWAMM 12

## RESULT 7

AA93093  
 ID AAY93093 standard; peptide; 12 AA.

AC AAY93093;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide P139.

XX Hepatotrophic; antagonist; transforming growth factor betal; TGF- $\beta$ 1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Homo sapiens.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

XX Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF- $\beta$ 1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX

XX Sequence 12 AA;

Query Match 76.2%; Score 48; DB 3; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 0.058;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TSLDATMIW 9  
 |||||:  
 DB 1 TSLDATMIW 9

## RESULT 8

AA93007  
 ID AAY93007 standard; peptide; 12 AA.

XX AAY93007;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide P53.

XX Hepatotrophic; antagonist; transforming growth factor betal; TGF- $\beta$ 1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Rattus sp.

XX WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

XX Borras Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX Disclosure; Page 27; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF- $\beta$ 1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF- $\beta$ 1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF- $\beta$ 1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX

XX Sequence 12 AA;

Query Match 58.7%; Score 37; DB 3; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 5.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATMI 8  
 |||||:  
 DB 5 TSLDATMI 12

## RESULT 9

AA93096  
 ID AAY93096 standard; peptide; 9 AA.

XX AAY93096;

XX

DT 08-NOV-2000 (first entry)  
 XX Transforming growth factor inhibitory peptide P142.  
 DE Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 KW Homo sapiens.  
 XX OS  
 XX PN WO200031135-A1.  
 XX PD  
 XX 02-JUN-2000.  
 XX PF  
 XX 23-NOV-1999; 99WO-ES000375.  
 XX PR  
 XX 24-NOV-1998; 98ES-00002465.  
 XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;  
 XX WPI; 2000-411935/35.  
 XX Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 XX sequences of the factor or its receptors.  
 XX Disclosure; Page 31; 86pp; Spanish.  
 XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX SQ Sequence 9 AA;  
 XX Query Match 57.9%; Score 36.5; DB 3; Length 9;  
 XX Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 1 TSLDATMIWTMM 12  
 DB ||| |||||  
 1 TSL---MIWTMM 9  
 RESULT 10  
 AAY92949  
 ID AAY92949 standard; peptide; 9 AA.  
 XX AC AAY92949;  
 XX DT 08-NOV-2000 (first entry)  
 XX Transforming growth factor inhibitory peptide #5.  
 DE Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 XX competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX Homo sapiens.  
 XX OS  
 XX PN WO200031135-A1.  
 XX PD 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.  
 XX 24-NOV-1998; 98ES-00002465.  
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;  
 XX WPI; 2000-411935/35.  
 XX Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 XX sequences of the factor or its receptors.  
 XX Claim 6; Page 81; 86pp; Spanish.  
 XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betal (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY92945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis  
 XX SQ Sequence 9 AA;  
 XX Query Match 57.9%; Score 36.5; DB 3; Length 9;  
 XX Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
 XX Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 1 TSLDATMIWTMM 12  
 DB ||| |||||  
 1 TSL---MIWTMM 9  
 RESULT 11  
 AAY93095  
 ID AAY93095 standard; peptide; 7 AA.  
 XX AC AAY93095;  
 XX DT 08-NOV-2000 (first entry)  
 XX Transforming growth factor inhibitory peptide P141.  
 DE Hepatotropic; antagonist; transforming growth factor betal; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.  
 XX Homo sapiens.  
 XX OS  
 XX PN WO200031135-A1.  
 XX PD 02-JUN-2000.  
 XX 23-NOV-1999; 99WO-ES000375.  
 XX 24-NOV-1998; 98ES-00002465.  
 XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.  
 XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;  
 PI Borrás Cuesta F;  
 XX WPI; 2000-411935/35.  
 XX Peptides that antagonize binding of transforming growth factor betal,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 XX sequences of the factor or its receptors.

PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betel (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY2945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis

XX Sequence 7 AA;

Query Match 55.6%; Score 35; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DATMIW 9  
 |||||  
 Db 1 DATMIW 6

RESULT 12

AAY93010  
 ID AAY93010 standard; peptide; 12 AA.

AC AAY93010;

DT 08-NOV-2000 (first entry)

DE Transforming growth factor inhibitory peptide P56.

XX Hepatotrophic; antagonist; transforming growth factor betel; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX Rattus sp.

PN WO200031135-A1.

XX 02-JUN-2000.

XX 23-NOV-1999; 99WO-ES000375.

XX 24-NOV-1998; 98ES-00002465.

XX (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

PI Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betel,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX Disclosure; Page 27; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betel (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY2945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the

CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis

XX Sequence 12 AA;

Query Match 55.6%; Score 35; DB 3; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MIWTMM 12  
 |||||

Db 1 MIWTMM 6

RESULT 13

AAY93097

ID AAY93097 standard; peptide; 9 AA.

XX AC AAY93097;

XX DT 08-NOV-2000 (first entry)

XX DE Transforming growth factor inhibitory peptide P143.

XX Hepatotrophic; antagonist; transforming growth factor betel; TGF-b1;  
 KW competitive inhibition; collagen synthesis stimulation inhibitor; liver;  
 KW extracellular matrix degradation inhibitor; mimetope; cirrhosis.

XX OS Homo sapiens.

XX PN WO200031135-A1.

XX PD 02-JUN-2000.

XX PF 23-NOV-1999; 99WO-ES000375.

XX PR 24-NOV-1998; 98ES-00002465.

XX PA (CIEN-) INST CIENTIFICO & TECNOLÓGICO NAVARRA.

XX Ezquerro Saenz IJ, Lasarte Sagastibelza JJ, Prieto Valtuena J;

PI Borrás Cuesta F;

XX WPI; 2000-411935/35.

XX Peptides that antagonize binding of transforming growth factor betel,  
 PT useful for treatment of liver disease, especially cirrhosis, are partial  
 PT sequences of the factor or its receptors.

XX Disclosure; Page 31; 86pp; Spanish.

XX The invention relates to synthetic peptides that antagonise the binding  
 CC of transforming growth (TGF) factor betel (TGF-b1) to its receptor in  
 CC vivo which have partial amino acid sequences identical, or similar, with  
 CC those of TGF-b1 and/or its receptors. Peptides AAY2945-Y93133 represent  
 CC examples of the peptides of the invention. The peptides act by  
 CC competitive inhibition of the binding of TGF-b1 to its receptors, e.g.  
 CC they are inhibitors of stimulation of collagen synthesis in liver cells  
 CC and inhibitors of synthesis of proteolytic enzymes able to degrade the  
 CC extracellular matrix. The peptides, their mimetopes and/or DNA (or  
 CC expression systems) encoding the peptides are used for treatment of liver  
 CC disease, specifically cirrhosis

XX Sequence 9 AA;

Query Match 50.0%; Score 31.5; DB 3; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 TSLDATMIWTMM 12  
 |||||

Db 1 TSLDAT---TMM 9



## RESULT 14

AAB88161  
ID AAB88161 standard; peptide; 14 AA.

XX AC AAB88161;

XX DT 17-MAY-2001 (first entry)

XX DE CD66 peptide CD66f(11)-10.

XX KW CD66; CBACAM; adhesion molecule; antiviral; antibacterial;

XX KW antiinflammatory; cytostatic; neutrophil activation; proliferation;

XX KW differentiation; cancer; angiogenesis.

XX OS Unidentified.

XX PN WO200113937-A1.

XX PD 01-MAR-2001.

XX PF 25-AUG-2000; 2000WO-US023482.

XX PR 26-AUG-1999; 99US-0150791P.

XX PR 02-SEP-1999; 99US-0152501P.

XX PA (SKUB/) SKUBITZ K M.

XX PA (SKUB/) SKUBITZ A P N.

XX PI Skubitz KM, Skubitz APN;

XX DR WPI; 2001-234981/24.

XX PT Novel peptides useful for activating neutrophils or blocking activation  
PT of neutrophils, modulating homotypic or heterotypic adhesion of CD66  
PT polypeptides, and modulating immune cell activation.

XX PS Claim 1; Page 54; 102pp; English.

XX CC The present sequence is an isolated peptide that was tested for its  
CC ability to modulate the function of CD66 family polypeptides and CD66  
CC ligands. 106 sequences of 13 or 14 amino acids in length, and their  
CC analogues, were identified that modulate the function of at least one  
CC CD66 family polypeptide and/or at least one ligand of the polypeptide.  
CC The peptides are capable of modulating activation of neutrophils,  
CC activation or inhibition, proliferation and/or differentiation of T-  
CC cells, B-cells, NK cells, LAK cells, dendritic cells, or other immune  
CC system cells, proliferation and/or differentiation of epithelial cells,  
CC homotypic and/or heterotypic adhesion among CD66 family polypeptides and  
CC adhesion of CD66 family polypeptides to other ligands. The peptides are  
CC useful for delivering a therapeutically active agent to a patient, for  
CC modifying the metastasis of malignant cells, for altering bacterial or  
CC viral binding to cells or a biomaterial, for altering cell adhesion to a  
CC biomaterial, for detecting tumours, for detecting inflammation, for  
CC detecting a CD66 protein or its ligand, for altering angiogenesis by  
CC contacting endothelial cells, tumour cells or immune cells, for altering  
CC an immune response, and for altering keratinocyte proliferation

XX SQ Sequence 14 AA;

Query Match 49.2%; Score 31; DB 4; Length 14;

Best Local Similarity 50.0%; Pred. No. 80;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 SLDATMIWTM 11

Db :|||:|

3 TLDASYLWMM 12

## RESULT 15

ADC99257

ID ADC99257 standard; peptide; 20 AA.

XX AC ADC99257;

XX DT 01-JAN-2004 (first entry)

XX DE Cancer-related DGI-2-binder peptide - SEQ ID 90.

XX KW cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;  
KW leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;  
KW VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR;  
KW kinase insert domain protein receptor; EGFR; epidermal growth factor;  
KW FGFR1; fibroblast growth factor; tie-1.

XX OS Unidentified.

XX PN WO2003035839-A2.

XX PD 01-MAY-2003.

XX PF 24-OCT-2002; 2002WO-US034021.

XX PR 24-OCT-2001; 2001US-0345471P.

XX PA (DGI-2) DGI BIOTECHNOLOGIES INC.

XX PI Pillutla RC, Brissette R, Spruyt M, Dedova O, Blume A;

XX PI Prendergast J, Goldstein N;

XX DR WPI; 2003-457332/43.

XX PT Selecting target and target binder pairs for preparing a composition for  
PT treating cancer by mixing in a reaction vessel phage expressing  
PT biological targets and phage expressing target binders.

XX PS Claim 26; SEQ ID NO 90; 172pp; English.

XX CC The invention relates to a novel method of selecting target and target  
CC binder pairs comprising mixing in a reaction vessel phage expressing  
CC biological targets and phage expressing target binders, each having  
CC distinguishable selection markers and selecting target and target binder  
CC pairs based on the selection markers. The molecules of the invention  
CC demonstrate cytostatic activity whilst the method may be useful for  
CC selecting target and target binder pairs for preparing a composition for  
CC treating cancer. Furthermore, the method may be utilised during gene  
CC therapy procedures. The current sequence is that of the cancer-related  
CC DGI-2-binder peptide of the invention.

XX SQ Sequence 20 AA;

Query Match 49.2%; Score 31; DB 7; Length 20;

Best Local Similarity 75.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 DATMIWTM 11

Db :|||:|

5 DAGMIWFM 12

Search completed: November 14, 2004, 12:02:06

Job time : 35.7234 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2004, 12:03:21 ; Search time 28.3404 Seconds  
(without alignments)  
149.815 Million cell updates/sec

Title: US-09-831-253F-3  
Perfect score: 63  
Sequence: 1 TSLDATMIWTMM 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 294451

Minimum DB seq length: 0  
Maximum DB seq length: 23

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	49.2	20	14	US-10-280-066-90
2	31	49.2	22	16	US-10-742-379-441
3	30	47.6	13	9	US-09-753-126-97
4	30	47.6	13	10	US-09-896-896A-61
5	30	47.6	13	15	US-10-330-697-97
6	30	47.6	16	10	US-09-836-770-7
7	29	46.0	7	9	US-09-758-128-41
8	29	46.0	7	9	US-09-758-128-44
9	29	46.0	7	9	US-09-758-426-41
10	29	46.0	7	9	US-09-758-426-44
11	29	46.0	7	9	US-09-758-198-41
12	29	46.0	7	9	US-09-758-198-44
13	29	46.0	7	10	US-09-861-661-41

14	29	46.0	7	10	US-09-861-661-44	Sequence 44, Appl
15	29	46.0	16	10	US-09-836-770-5	Sequence 5, Appl
16	29	46.0	22	14	US-10-195-730-319	Sequence 319, App
17	29	46.0	22	16	US-10-799-747-319	Sequence 319, App
18	28	44.4	27	14	US-10-176-791A-76	Sequence 76, Appl
19	27	42.9	10	14	US-10-062-109A-642	Sequence 642, App
20	27	42.9	10	14	US-10-005-480A-642	Sequence 4789, A
21	27	42.9	22	9	US-09-864-761-47789	Sequence 439, App
22	27	42.9	22	16	US-10-742-379-439	Sequence 685, App
23	26	41.3	9	15	US-10-182-252A-685	Sequence 101, App
24	26	41.3	14	14	US-10-435-766-101	Sequence 39131, A
25	26	41.3	17	9	US-09-864-761-39131	Sequence 1841, Ap
26	26	41.3	17	14	US-10-225-567A-1841	Sequence 2023, Ap
27	26	41.3	20	14	US-10-283-017-2023	Sequence 2024, Ap
28	26	41.3	20	14	US-10-283-017-2024	Sequence 86, Appl
29	26	41.3	22	15	US-10-410-764-86	Sequence 602, App
30	25	39.7	8	14	US-10-190-082-602	Sequence 20, Appl
31	25	39.7	9	14	US-10-357-935-20	Sequence 632, App
32	25	39.7	9	15	US-10-182-252A-632	Sequence 657, App
33	25	39.7	9	15	US-10-182-252A-657	Sequence 1216, Ap
34	25	39.7	9	15	US-10-182-252A-1216	Sequence 79, Appl
35	25	39.7	10	14	US-10-200-708-79	Sequence 501, App
36	25	39.7	10	14	US-10-200-708-501	Sequence 7, Appl
37	25	39.7	11	10	US-09-755-109-7	Sequence 44, Appl
38	25	39.7	12	9	US-09-823-829-44	Sequence 69, Appl
39	25	39.7	12	9	US-09-840-277-69	Sequence 44, Appl
40	25	39.7	12	9	US-09-823-823-44	Sequence 151, App
41	25	39.7	12	15	US-10-609-217-151	Sequence 151, App
42	25	39.7	12	15	US-10-632-388-151	Sequence 151, App
43	25	39.7	12	15	US-10-651-723-151	Sequence 151, App
44	25	39.7	12	15	US-10-645-761-151	Sequence 151, App
45	25	39.7	12	15	US-10-666-696-151	Sequence 151, App

ALIGNMENTS

RESULT 1  
US-10-280-066-90  
; Sequence 90, Application US/102800066  
; Publication No. US20030180718A1  
; GENERAL INFORMATION:  
; APPLICANT: Pillutla, Renuka C.  
; APPLICANT: Brissette, Renee  
; APPLICANT: Spruyt, Michael  
; APPLICANT: Dedova, Olga  
; APPLICANT: Blume, Arthur J.  
; APPLICANT: Prendergast, John  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIN  
; FILE REFERENCE: 2598-4009US1  
; CURRENT APPLICATION NUMBER: US/10/280,066  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: 60/345,471  
; PRIOR FILING DATE: 2001-10-24  
; NUMBER OF SEQ ID NOS: 537  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 90  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; OTHER INFORMATION: DGI-2-20R-4-B6  
US-10-280-066-90

Query Match 49.2%; Score 31; DB 14; Length 20;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DATMIWTM 11

Db 5 DAGMIWFM 12

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RESULT 2
US-10-742-379-441
; Sequence 441, Application US/10742379
; Publication No. US20040181033A1
; GENERAL INFORMATION:
; APPLICANT: Han, HQ
; APPLICANT: Min, Hosung
; APPLICANT: Boone, Thomas Charles
; TITLE OF INVENTION: BINDING AGENTS WHICH INHIBIT MYOSTATIN
; FILE REFERENCE: A-828 (US)
; CURRENT APPLICATION NUMBER: US/10/742,379
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/435,923
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 634
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 441
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Myostatin Binding Peptide
US-10-742-379-441

Query Match          49.2%; Score 31; DB 16; Length 22;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY      1 TSLDMSLWMTMM 12
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Db      1 TSDMSLLWELL 12

RESULT 3
US-09-753-126-97
; Sequence 97, Application US/09753126
; Patent No. US20020127219A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-0006000S
; CURRENT APPLICATION NUMBER: US/09/753,126
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/210,984
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: 60/211,124
; PRIOR FILING DATE: 2000-06-12
; PRIOR APPLICATION NUMBER: PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/217,497
; PRIOR FILING DATE: 2000-07-11
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 97
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-753-126-97
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Query Match          47.6%; Score 30; DB 9; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 SLDATMTWT 10
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Db      1 AVNATMWT 9

RESULT 4
US-09-896-896A-61
; Sequence 61, Application US/09896896A
; Publication No. US20030036181A1
; GENERAL INFORMATION:
; APPLICANT: MAXYGEN APS
; TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
; FILE REFERENCE: 0217u8210
; CURRENT APPLICATION NUMBER: US/09/896,896A
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/217,497
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: US 60/225,558
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: DK PA 2000 01027
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DK PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: PCT/DK00/00743
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: PCT/DK01/00090
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 61
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-896-896A-61

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Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 SLDATMTWT 10
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Db      1 AVNATMWT 9

RESULT 5
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; Sequence 97, Application US/10330697
; Publication No. US20040009165A1
; GENERAL INFORMATION:
; APPLICANT: OKKELS, JENS SIGURD
; APPLICANT: JENSEN, ANNE DAM
; APPLICANT: HALKIER, TORBEN
; APPLICANT: JENSEN, RIKKE BOLDING
; TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMES AND LYSOSOMAL ENZYME
; TITLE OF INVENTION: ACTIVATORS
; FILE REFERENCE: 31-0006000S
; CURRENT APPLICATION NUMBER: US/10/330,697
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: US/09/753,126
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: PA 1999 01891
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: 60/174,652
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PA 200 00865
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; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 60/210,984  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: 60/211,124  
; PRIOR FILING DATE: 2000-06-12  
; PRIOR APPLICATION NUMBER: PA 2000 01027  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/217,497  
; PRIOR FILING DATE: 2000-07-11  
; NUMBER OF SEQ ID NOS: 147  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 97  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-330-697-97.

Query Match 47.6%; Score 30; DB 15; Length 13;  
Best Local Similarity 55.6%; Pred. No. 1.1e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLDATMIWT 10  
Db :::|||||  
1 AVNATMNWT 9

## RESULT 6

US-09-836-770-7  
; Sequence 7, Application US/09836770  
; Publication No. US20030175799A1  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Andrea G.  
; APPLICANT: Starovaenik, Melissa A.  
; APPLICANT: Skelton, Nicholas  
; TITLE OF INVENTION: HAIRPIN PEPTIDES WITH A NOVEL STRUCTURAL MOTIF AND  
; TITLE OF INVENTION: METHODS RELATING THERETO  
; FILE REFERENCE: P1875  
; CURRENT APPLICATION NUMBER: US/09/836,770  
; CURRENT FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 7  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide  
US-09-836-770-7

Query Match 47.6%; Score 30; DB 10; Length 16;  
Best Local Similarity 52.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 DATMIWTM 11  
Db :|||::|  
7 DATKTWTV 14

## RESULT 7

US-09-758-128-41  
; Sequence 41, Application US/09758128  
; Patent No. US20020107187A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,128  
; CURRENT FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 41  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-758-128-41

Query Match 46.0%; Score 29; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7  
Db :|||::|  
1 TSLDATV 7

## RESULT 8

US-09-758-128-44  
; Sequence 44, Application US/09758128  
; Patent No. US20020107187A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: GERRATY, No. US20020107187A1man L.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,128  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Rat  
US-09-758-128-44

Query Match 46.0%; Score 29; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7  
Db :|||::|  
1 TSLDATV 7

## RESULT 9

US-09-758-426-41  
; Sequence 41, Application US/09758426  
; Patent No. US20020169116A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, David J.  
; APPLICANT: WESTBROOK, Simon L.  
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS  
; TITLE OF INVENTION: - PEPTIDES, ANTIBODIES, VACCINES AND USES THEREOF  
; FILE REFERENCE: 016786/0214  
; CURRENT APPLICATION NUMBER: US/09/758,426  
; CURRENT FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 58

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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-426-41

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
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Db 1 TSLDATV 7

RESULT 10
US-09-758-426-44
; Sequence 44, Application US/09758426
; Patent No. US20020169116A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020169116A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,426
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9390
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-426-44

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
   |||||:
Db 1 TSLDATV 7

RESULT 11
US-09-758-198-41
; Sequence 41, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020187925A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US/09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-861-661-41

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
   |||||:
Db 1 TSLDATV 7

RESULT 12
US-09-758-198-44
; Sequence 44, Application US/09758198
; Publication No. US20020187925A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, David J.
; APPLICANT: GERRATY, No. US20020187925A1man L.
; TITLE OF INVENTION: MODULATING THE ACTIVITY OF HORMONES OR THEIR RECEPTORS
; FILE REFERENCE: 016786/0214
; CURRENT APPLICATION NUMBER: US/09/758,198
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: US/09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: PCT/AU97/00312
; PRIOR FILING DATE: 1997-05-22
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Rat
US-09-758-198-44

Query Match          46.0%; Score 29; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7
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Db 1 TSLDATV 7

RESULT 13
US-09-861-661-41
; Sequence 41, Application US/09861661
; Publication No. US20030045676A1
; GENERAL INFORMATION:
; APPLICANT: KINGSTON, DAVID J.
; APPLICANT: GERRATY, NORMAN L.
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF
; FILE REFERENCE: 054270/0135
; CURRENT APPLICATION NUMBER: US/09/861,661
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: 09/194,218
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: AU PN9990
; PRIOR FILING DATE: 1996-05-22
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-861-661-41
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Search completed: November 14, 2004, 12:26:59  
Job time : 29.3404 secs

Query Match 46.0%; Score 29; DB 10; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7  
Db 1 TSLDATV 7

RESULT 14  
US-09-861-661-44  
; Sequence 44, Application US/09861661  
; Publication No. US20030045676A1  
; GENERAL INFORMATION:  
; APPLICANT: KINGSTON, DAVID J.  
; APPLICANT: GERRATY, NORMAN L.  
; APPLICANT: WESTBROOK, SIMON L.  
; TITLE OF INVENTION: PEPTIDES, ANTIBODIES, VACCINES & USES THEREOF  
; FILE REFERENCE: 054270/0135  
; CURRENT APPLICATION NUMBER: US/09/861,661  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: 09/194,218  
; PRIOR FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: AU PN9990  
; PRIOR FILING DATE: 1996-05-22  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 44  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Rattus sp.  
US-09-861-661-44

Query Match 46.0%; Score 29; DB 10; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TSLDATM 7  
Db 1 TSLDATV 7

RESULT 15  
US-09-836-770-5  
; Sequence 5, Application US/09836770  
; Publication No. US20030175799A1  
; GENERAL INFORMATION:  
; APPLICANT: Cochran, Andrea G.  
; APPLICANT: Starovashnik, Melissa A.  
; APPLICANT: Skelton, Nicholas  
; TITLE OF INVENTION: HAIRPIN PEPTIDES WITH A NOVEL STRUCTURAL MOTIF AND  
; TITLE OF INVENTION: METHODS RELATING THERETO  
; FILE REFERENCE: P1875  
; CURRENT APPLICATION NUMBER: US/09/836,770  
; CURRENT FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 5  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide  
US-09-836-770-5

Query Match 46.0%; Score 29; DB 10; Length 16;  
Best Local Similarity 71.4%; Pred. No. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 DATMTWT 10  
Db 7 DATKTWT 13

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